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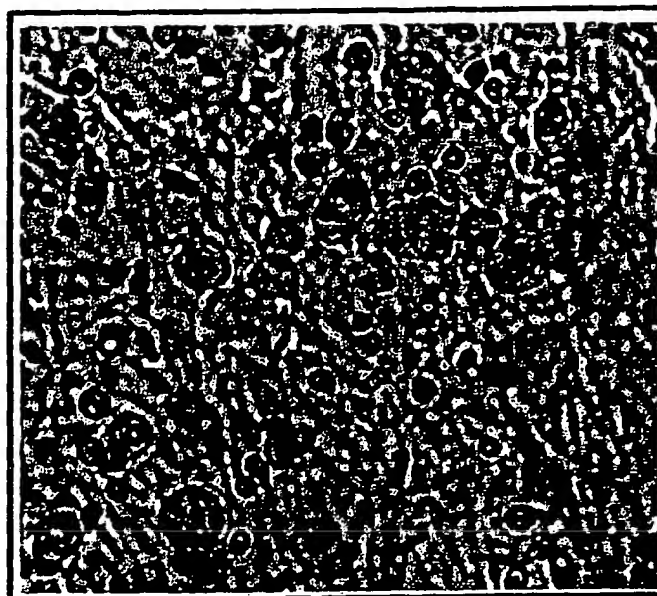
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(54) Title: HUMAN MESENCHYMAL PROGENITOR CELL



(57) Abstract: Pluri-differentiated human mesenchymal progenitor cells (MPCs) are isolated. A method isolates and purifies human mesenchymal progenitor cells from Dexter-type cultures for characterization of and uses, particularly therapeutic uses for such cells. Specifically, isolated MPCs can be used for diagnostic purposes, to enhance the engraftment of hematopoietic progenitor cells, enhance bone marrow transplantation, or aid in the treatment or prevention of graft versus host disease.



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HUMAN MESENCHYMAL PROGENITOR CELL

FIELD OF THE INVENTION

The present invention generally relates to pluri-differentiated mesenchymal progenitor cells and therapeutic uses for the same. More specifically, 5 the isolated mesenchymal progenitor cells are isolated from hematopoietic cells and macrophages in Dexter-type cultures cells.

BACKGROUND OF THE INVENTION

Bone marrow, the site of blood cell production and home to various leukemia and lymphoma cells, comprises a complex cellular population including 10 hematopoietic progenitor or stem cells and the stromal cells that support them. Hematopoietic stem cells have the capacity for self-regeneration and for generating all blood cell lineages while stromal stem cells have the capacity for self-renewal and for producing the hematopoietic microenvironment.

Two bone-marrow culture systems introduced in the mid-1970's have 15 evolved as favored media for the *in vitro* analysis of mesengensis and hematopoiesis. The Friedenstein culture system was introduced in 1976 as a media for the analysis and study of mesengensis. (Friedenstein, et al, in *Exp Hematol* 4,267-74 (1976). In order to obtain mesenchymal stem cells (MSCs) for expansion in the culture medium, it is necessary to first isolate rare pluripotent mesenchymal 20 stem cells from other cells in the bone marrow. In the Friedenstein culture system, isolating the nonhematopoietic cells is achieved by utilizing their tendency to adhere to plastic. Once isolated, a monolayer of homogeneous, undifferentiated stromal cells is then grown in the culture medium, in the absence of hematopoietic cells. The stromal cells from this system have the potential to differentiate into discrete 25 mesenchymal tissues, namely bone, cartilage, adipose tissue and muscle depending on specific growth supplements. These MSCs have been the target of extensive investigation including exploration of their potential clinical utility in repair or replacement of genetically damaged mesenchymal tissues.

In 1977, Dexter, *et al.* developed another bone marrow culture system 30 for the study of hematopoiesis. (Dexter et al. *J Cell Physiol* 91, 335-44 (1977). The Dexter culture does not require isolation of the mesenchymal cells before culturing. Thus, the monolayer of stromal cells is grown in the presence of hematopoietic cells. Greenberger later modified the Dexter system by the addition of hydrocortisone to

for matched sibling donors to 50% in the cases of matched, unrelated donors and un-matched donors from the patient's family.

The potential benefits of bone marrow transplantation have stimulated research on the cause and prevention of GvHD. The removal of T cells from the bone marrow obtained from matched unrelated or unmatched sibling donors results in a decreased incidence of graft versus host reactions, but an increased incidence of rejection of the allogeneic bone marrow graft by the patient.

Current therapy for GvHD is imperfect, and the disease can be disfiguring and/or lethal. Thus, risk of GvHD restricts the use of bone marrow transplantation to patients with otherwise fatal diseases, such as severe immunodeficiency disorders, severe aplastic anemia, and malignancies.

The potential to enhance engraftment of bone marrow or stem cells from antigenically mis-matched donors to patients without graft rejection or GvHD would greatly extend the availability of bone marrow transplantation to those patients without an antigenically matched sibling donor.

Thus, it would be useful to develop methods of improving and/or enhance bone marrow transplantation by enhancing the engraftment of bone marrow or hematopoietic progenitor cells and/or decreasing the occurrence of graft rejection or GvHD in allogenic transplants.

Studies of hematopoiesis and mesengogenesis and the urgent need for improved methods of treatment in the field of bone marrow transplants have led to the isolation of MSCs from bone marrow stroma. These MSCs are the same pluri-potential cells that result from expansion in Friedenstein type cultures. Several patents describe the isolation and therapeutic uses of these MSCs.

U.S. Patent No. 5,486,359, to Caplan, *et al.*, discloses isolated human MSCs, and a method for their isolation, purification, and culturing. Caplan, *et al.* also describes methods for characterizing and using the purified mesenchymal stem cells for research, diagnostic, and therapeutic purposes. The invention in '359, to Caplan, *et al.*, describes pluri-potential cells that remain pluri-potential, even after cultural expansion. Caplan, *et al.* also teaches that it is necessary to first isolate the pluri-potent MSCs from other cells in the bone marrow and then, in some applications, uses culture medium to expand the population of the isolated MSCs. The Caplan *et al.* patent fails to disclose the use of Dexter-type cultures, pluri-

cell culture preparation by the Dexter method, treating the cells to obtain a cell suspension, removing macrophages, fractionating the cells, and collecting the fraction of pluri-differentiated mesenchymal progenitor cells.

5 The present invention also provides a method for enhancing bone marrow engraftment in a mammal in need thereof which includes administering to the mammal (i) isolated pluri-differentiated mesenchymal progenitor cells and (ii) a bone marrow graft, wherein the pluri-differentiated mesenchymal progenitor cells are administered in an amount effective to promote engraftment of the bone marrow in the mammal.

10 The present invention provides a method for enhancing engraftment of hematopoietic progenitor cells in a mammal in need thereof which includes the step of administering to the mammal (i) isolated pluri-differentiated mesenchymal progenitor cells and (ii) hematopoietic progenitor cells, wherein the pluri-differentiated mesenchymal progenitor cells are administered in an amount effective
15 to promote engraftment of the hematopoietic progenitor cells in the mammal.

Another embodiment of the present invention provides a method for treating graft-versus-host disease (GvHD) in a mammal about to undergo bone marrow or organ transplantation or suffering from GvHD caused by bone marrow or organ transplantation, by administering to the mammal an effective amount of
20 isolated pluri-differentiated mesenchymal progenitor cells.

Yet another embodiment of the present invention provides a method for diagnosing a disease state by: a) establishing gene expression patterns of normal state bone marrow derived isolated pluri-differentiated mesenchymal progenitor cells; b) establishing gene expression patterns of various leukemic state
25 bone marrow derived isolated pluri-differentiated mesenchymal progenitor cells; c) identifying gene sets that are unique to a given state; and d) comparing a profile of bone marrow derived isolated mesenchymal progenitor cell of unknown state to the gene sets.

Additionally, the present invention provides a method for identifying
30 therapeutic targets for treatment of hematopoietic function by: a) determining the median gene expression profile of bone marrow isolated pluri-differentiated mesenchymal progenitor cells associated with each disease state of interest; b)

Vectastain Elite ABC Kit). (Figure 4C) Immunostain using anti-CD45 antibody (Dako, Clone PD7/26 & 2B11; ABC Kit). (Figure 4D) Periodic acid-Schiff (Sigma). (Figure 4E) Nile Red (Sigma), counterstained with DAPI (Vector). (Figure 4F) Alkaline phosphatase (Sigma Kit No. 85), counterstained with Nuclear Fast Red (Baker).
 5 (Figure 4G) Immunostain using antibody to fibronectin (Immunotech, Clone 120.5; ABC Kit). (Figure 4H) Immunostain using anti-muscle actin antibody (Ventana, clone HUC 1-1; Ventana system using a section of formalin-fixed, paraffin-embedded cell block, instead of a cytospin). Appropriate positive controls and isotype-matched negative controls were employed to ascertain antibody staining-specificity. All parts
 10 of figure as shown, except 4E and 4H, have clearly identifiable built-in cell controls. The morphological features of the cells are listed in row 1 of Table 1.

Figure 5 is a photograph which shows a transmission electron micrograph of an MPC of the present invention bearing microvilli, irregular nucleus, and pools of glycogen (6) in the ectoplasm (x 4,600).

15 Figure 6A-M are photographs which show Northern blot analysis of bone marrow stromal cell RNAs for expression of genes specific for multiple mesenchymal cell lineages. Figures 6A-M represent different gene probes used for hybridization. The following outlines the sources of the gene probes employed and the approximate sizes of the major transcripts observed (shown in parentheses):
 20 Figure 6A) CD68 (Clone ID 3176179, Genome Systems, Inc (GSI); 2-3 kb); Figure 6B) Cathepsin B (Clone ID 2806166, GSI; 2-3 kb); Figure 6C) GAPDH probe (generated using PCR primers from R&D Systems, Inc; ~2 kb) hybridized to same blot as A and B; Figure 6D) Adipsin (probe generated using PCR primers as described, Ref 20; 0.5-1 kb); Figure 6E) Osteoblast-specific cadherin-11 (Clone ID
 25 434771, GSI; ~3 kb); Figure 6F) Chondroitin sulfate proteoglycan 2 (Clone ID 1623237, GSI; >10 kb); Figure 6G) Collagen type I alpha 1 (Clone ID 782235, GSI; >10 kb); Figure 6H) Decorin (Clone ID 3820761, GSI; 2-3 kb); Figure 6I) GAPDH probe hybridized to same blot as D-H; Figure 6J) Fibronectin (Clone ID 3553729, GSI; >10 kb); Figure 6K) Caldesmon (Clone ID 1319608, GSI; ~4 kb); Figure 6L)
 30 Transgelin (Clone ID 4049957, GSI; ~1.5 kb); and Figure 6M) GAPDH probe hybridized to same blot as J-L.

Figure 7 is a photograph which shows RT-PCR analysis for expression of representative hematopoietic growth factors (G-CSF and SCF) and extracellular

(arrow; autoradiogram exposed for only 45 minutes). Figure 12B shows EcoR1 digest of thymic genomic DNA from SCID mice. Figure 12C shows EcoR1 digest of lymph node genomic DNA from SCID mice. Figure 13A and Figure 13 B show graphs comparing the survival rate and engraftment of human hematopoietic cells in SCID mice cotransplanted with the purified bone marrow MPCs of the present invention vs. unpurified bone marrow stromal cells. In the line graphs provided the line with diamonds represents MPCs and bone marrow mononuclear cells, squares represents bone marrow mononuclear cells only, triangles represents unfractionated bone marrow stromal cells, the Xs represent MPCs only, and the circles represent the control. In the bar graphs, the gray bars represent mice that survived and the black bars represent mice with engraftment. Figures 14A-C are photographs which demonstrate apoptosis by TUNEL assay in organs of SCID mice that died after transplantation. Figure 14A shows a serial section of the liver of the mouse that survived. Figure 14B shows a serial section of the liver of the mouse that died. Figure 14C shows a serial section of the spleen of the mouse that survived. Figure 14D shows a serial section of the spleen of the mouse that died.

Figure 15 shows photomicrographs of single-cell MPCs that were isolated by laser capture microdissection (LCM) and subsequently targeted for microarray analysis.

Figure 16 shows a Venn diagram displaying the stromal-cell gene-list. Stromal cell genes are operationally defined as being active in at least 9 out of 10 single cell MPCs AND 4 out of 5 collective MPC samples AND 7 out of 8 collective USC samples, i.e., 20 of 23 samples tested. This criterion was very stringent and automatically excluded the outliers, independently of filtering for genes with weak expressions on the basis of control strength (referred to as C or CS). The stromal cell gene list of 2755 includes 13 AFFX microarray-assay positive controls.

Figure 17 shows a two-dimensional hierarchical clustering of 2755 stromal cell genes based on the expression profiles of 23 samples. The gene tree is displayed on top and the experiment or sample tree is shown on left. Accordingly, each column represents a particular gene on the chip and each row represents a separate stromal cell sample.

Figure 18 shows composite gene-expression plots of 2755 stromal cell genes comparing collective purified stromal cell samples (cMPC), collective

Generally, the present invention provides isolated and purified mesenchymal progenitor cells that are pluri-differentiated. Also provided by the present invention is a therapeutic composition including an effective amount of isolated and purified pluri-differentiated mesenchymal progenitor cells and a
5 pharmaceutically acceptable carrier.

The terms "enhance" or "improve" as used herein are intended to indicate that there is a more beneficial end result. In other words, the product provides a more effective result.

The term "pluri-differentiated" as used herein refers to cells that are a
10 single cell type co-expressing genes specific for multiple lineages. The term "pluri-potential" as used herein refers to cells that are undifferentiated and have the potential to be differentiated into discrete mesenchymal tissues.

Dexter-type cultures contain stromal cells that co-express multiple message lineage markers. These pluri-differentiated cells are referred to by the
15 inventor as mesenchymal progenitor cells (MPCs). Disclosed herein is a process for isolating and purifying MPCs from Dexter-type cultures. Purified MPCs provide a sufficiently defined system to permit detailed elucidation of the role of bone marrow in normal and leukemic hematopoiesis.

The present invention also provides various methods for using MPCs
20 to enhance bone marrow transplantation, enhance hematopoietic progenitor cell engraftment, for diagnostic purposes, or for the treatment of GvHD.

The exact cell types in Dexter cultures have been identified. No evidence was found for the existence of discrete cellular populations, such as adipocytes, osteoblasts, fibroblasts, smooth muscle cells and endothelial cells,
25 notwithstanding the abundance of literature and wide spread belief (*See*, J.L. Liesveld *et al.*, *Blood* 73, 1794 (1989); A.K. Sullivan, D. Claxton, G. Shematek *et al.*, *Lab Invest* 60, 667 (1989); K. Dorshkind, *Ann Rev Immunol* 8, 126 (1990); S. Perkins, R.A. Fleischman, *Blood* 75, 620 (1990); I.A. Denkers, R.H. Beelen, G.J. Ossenkoppele *et al.*, *Ann Hematol* 64, 210 (1992); P.E. Penn, D.Z. Jiang, R.G. Fei
30 *et al.*, *Blood* 81, 1205 (1993); E. de Wynter *et al.*, *J Cell Sci* 106, 761 (1993); A. Ferrajoli *et al.*, *Stem Cells (Dayt)* 12, 638 (1994); B.R. Clark, A. Keating, *Ann NY Acad Sci* 770, 70 (1995); B.S. Wilkins, D.B. Jones, *Br J Haematol* 90, 757 (1995); S. Gronthos, P.J. Simmons, *J Hematother* 5, 15 (1996); D. Soligo *et al.*, Abstract

The MPCs in Dexter type cultures were characterized using a variety of techniques. Cytospins were prepared using aliquots of unfractionated cells for performance of various cytological, cytochemical and immunocytochemical stains. Reactivity patterns of the bone marrow culture cells are outlined in Table 1. Figures 4A-E illustrate morphologic and phenotypic characteristics, as uncovered by staining for representative cell lineage markers.

Only rarely have investigators in this field taken the approach of preparing a cell suspension and staining cells on cytospins as was done to characterize the cells of the present invention (Simmons, *et al.*, *Nature* 328, p429-32 (1987)) and no other group has used this method to address the issue of pluridifferentiation by bone marrow stromal cells. Almost all of the published studies in the field, with a rare exception (Simmons, *et al.*, *Nature*, 328, p429-32 (1987)), conducted cytochemical and immunocytochemical staining on layers of stromal cells grown to confluence on coverslips. In this situation, the stromal cultures appear very complex especially in the areas of hematopoietic activity, so-called "cobblestones" with macrophages and hematopoietic cells enmeshed in them. Macrophages and nonhematopoietic cells spread themselves and assume varied shapes when they adhere to and grow on plastic or glass. This spreading further contributes to the perceived heterogeneity and complexity. The complexity precludes a clear morphological visualization of the nonhematopoietic cells and consequently interferes with the determination of what percent of what cell type is positive for any given marker.

In terms of lineage markers, up to 100% of the nonhematopoietic cells or MPCs of the present invention expressed two fat cell markers (Nile Red (Figure 4E) and Oil Red O); an osteoblast marker (alkaline phosphatase (Figure 4F)); and two fibroblast markers (fibronectin (Figure 4G) and prolyl-4-hydroxylase). Greater than 85% of the MPCs were also positive for a muscle marker, actin (Figure 4H). There was no evidence of expression of endothelial cell differentiation, as judged by immunohistochemical staining for CD34 and CD31.

In addition, the Dexter type stromal cells had not previously been subjected to Periodic Acid-Schiff (PAS) staining, which revealed a strong and uniform positivity by almost 100% of the MPCs studied. This indicates the presence of large stores of glycogen (Figure 4D). The presence of glycogen (6) was confirmed

Percoll gradient centrifugation (Figure 2). The isolated MPCs were then collected and washed.

The purity of the nonhematopoietic cells was demonstrated by a near complete absence of two macrophage markers, CD68 and cathepsin B (as shown by Northern blotting data, Figure 6A and 6B). As a positive control, bone marrow mononuclear cells rich in myelomonocytic cells abundantly expressed CD68 (lanes 5 & 6, Figure 6A). The Northern blot results are consistent with a purity estimate of ~95% (vs. 60% in unfractionated samples) based on morphology and immunocytochemical staining for CD68.

A purified source of MPCs is desirable for a number of reasons. The relative ease with which large numbers of the MPCs can be purified and their distinctive phenotypic characteristics make them valuable targets for future investigations. Purified MPCs provide a sufficiently defined system to permit detailed elucidation of the role of bone marrow in normal and leukemic hematopoiesis in addition to aiding in bone marrow transplantation.

Another major reason that purified cells are desirable is that Dexter cultures also contain a significant percentage of highly immunogenic macrophages that can cause onset of GvHD after transplantation. The MPCs of the present invention are purified to ~95% free of macrophages and hematopoietic cells. Note the increased survival rate in Severe Combined Immunodeficiency Disease (SCID) mice that received purified MPCs versus those that received unfractionated bone marrow stromal cells in Figure 13B. This data establishes that stromal cells in combination with engraftment or other similar procedures enhances the effectiveness of the treatment.

The present invention also provides methods of enhancing the engraftment of hematopoietic cells and of enhancing the engraftment of bone marrow. The hematopoietic support capacity of the Dexter-type cultures has been repeatedly demonstrated by a number of investigators. RT-PCR analysis showed that Dexter cultures and Friedenstein cultures expressed a similar pattern of cytokine and growth factor mRNAs; yet, Dexter cultures were found to be more efficient than Friedenstein cultures in achieving preservation of hematopoietic progenitors (Majumdar, *et al.*, *J.Cell.Physiol.*, 176, 57-66.). The pluri-differentiated MPC is capable of supporting hematopoiesis, as shown by its ability to express

invention represent a single pluridifferentiated MPC which allows for genomic study of the stromal cells and the development of new, more objective diagnostic tools for patients suffering from leukemia conditions.

The present invention provides a comprehensive phenotype of cultured
5 bone marrow stromal cells at single cell level for the first time. These findings pave the road for ultimate identification and investigation of these cells in fresh samples of marrow, normal as well as diseased, in which they occur at a low frequency and are extremely difficult to study at the present time. The development of this phenotype forms the basis for various diagnostic tests including a comprehensive test that can
10 be used to screen for different abnormalities of bone marrow stromal cells in various hematologic diseases and other diseases effecting stromal cells.

Results show that isolated single stromal cells simultaneously express transcripts for osteoblasts, fibroblasts, muscle cells and adipocytes. Furthermore, there is shown that isolated single stromal cells simultaneously express transcripts
15 for epithelial cells and neural/glia cells as well as transcripts for CD45, CD19, CD10, CD79a, and representative proto-oncogenes and transcription factors, typically known to be affiliated with normal and neoplastic hematopoietic cells. These findings are evidence of existence of a progenitor cell that is common to nonhematopoietic mesenchymal cells and hematopoietic cells, particularly B-lymphocytes. "Lineage
20 burst" characterized by simultaneous activation of diverse differentiation pathways within the same cell appears to be the signature profile of a stromal cell, indicating that a "pluripotent" cell is "pluridifferentiated" at the molecular level. That is, prior to a selective and full-fledged lineage differentiation, progenitors express genes associated with multiple lineages to which they might possibly commit, thus
25 providing insight into the molecular basis of cellular plasticity.

Transcriptomic analysis has been undeniably contributing to the molecular definition of new disease categories with demonstrable therapeutic benefit. The present invention contributes to the further definition of the stromal cell by refining its molecular signature. The *in vivo* identification of the stromal cell and its
30 possible ontogenic variants as they might occur in different hematological diseases and subsequent targeting of these cells holds the key to ultimately treating some, if not all, of these diseases.

The present invention also provides for a method of preventing or treating GvHD. The highest mortality rate, Figure 13B, was observed in mice receiving the unpurified whole marrow stroma and the bone marrow mononuclear cells. The increased mortality observed is related to the presence of highly immunogenic macrophages and consequent GvHD. The mice with the highest survival rate, shown in Figure 13A, were the mice receiving purified MPCs and bone marrow mononuclear cells.

Notably, there is discrete TUNEL-positive nuclei in the liver of the expired mouse in Figure 14B and complete absence of staining in the liver of the surviving mouse (see Figure 14A). While some ill-defined globules of staining are observed in the spleen of the mouse that survived, the nuclear integrity of most of the cells is well preserved suggesting minimal or no apoptosis (Figure 14C). In contrast, the dead mouse spleen (Figure 14D) showed extensive TUNEL positivity precluding accurate interpretation. Control mouse liver and spleen showed results similar to those of the mouse that survived.

The above results indicate that purified MPCs can support human hematopoiesis in SCID mice as effectively as whole marrow stroma. Equally important is that the purified MPCs increased the survival rate. The evidence shows that the increased survival is due to a reduction in GvHD.

Allogeneic bone marrow transplantation is the preferred method of treatment for a variety of malignant and genetic diseases of the blood and blood forming cells. However, failure of hematopoietic cell engraftment can occur for a number of reasons. These include, microenvironmental defects as part of the underlying disease itself (e.g., aplastic anemia), and/ or stromal cell damage caused by chemoradiotherapy and/ or microenvironmental damage as part of GvHD which is a dreaded complication following bone marrow transplantation. In GvHD, donor T cells present in the hematopoietic cell graft destroy host tissues. GvHD can involve multiple organs such as skin, liver, GI system etc. The current treatment modalities for preventing or treating graft failure or GvHD are cumbersome, costly and involve some form of immunosuppression. Stromal cell lesions, either primary to the disease process or secondarily induced by allogeneic bone marrow transplantation, play a prominent role in the success or failure of the hematopoietic cell graft. Cotransplantation of MPC not only enhances hematopoietic cell engraftment but

administration are solutions in sterile isotonic aqueous buffer. Where necessary, the composition can also include a local anesthetic to ameliorate any pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a cryopreserved concentrate in a hermetically sealed container such as an ampoule indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients can be mixed prior to administration.

The present invention paves the way for applications of mesenchymal progenitor cells in the field of transplantation with respect to hematopoietic support, immunoregulation, and graft facilitation. MPCs can be used as a supporting cell type in bone marrow transplantation, particularly in diseases where defects in the hematopoietic stromal microenvironment are believed to prevail, such as aplastic anemia, myelofibrosis, and bone marrow failure following high dose chemotherapy and radiation therapy.

Another aspect of the invention provides a method for diagnosing various disease states in mammals by identifying new diagnostic markers, specifically the classification and diagnosis of leukemia. Prior to the present invention, stromal cells were not carefully investigated in terms of genomics because of the widespread belief that they represent a heterogeneous mixture of cell types and cellular heterogeneity presents significant challenges for the application of genetic analysis such as microarray technology. The isolated MPCs of the present invention represent a single cell type and allow for genomic study of the stromal cells.

Using the methods of the present invention, it has been determined that bone marrow stromal cells in leukemia patients are functionally and structurally defective regardless of the damage caused by chemotherapy and radiation therapy. Given the almost 25 year history and intense interest in bone marrow stromal cell cultures, previous documentation of stromal cell abnormalities has been disappointingly low (Martinez & Martinez, *Exp. Hematol* 11:522-26 (1983); Budak-Alpdogan, *et al.*, *Am.J.Hematol*, 62:212-20 (1999); Nagao, *et al.*, *Blood*, 61:589-92

(1983); Peled, et al., Exp.Hematol 24:728-37 (1996); Bhatia, et al., Blood 85:3636-45 (1995); Agarwal, et al., Blood 85:1306-12 (1995); Diana, et al., Blood 96:357a(2000)). By identifying gene sets that are unique to a given state, these differences in the stromal cells can be utilized for diagnostic purposes.

5 In one embodiment of the invention, isolated MPCs from a patient are assayed for expression of a large number of genes. The gene expression profile is projected into a profile of gene set expression values according to the definition of gene sets. A reference database containing a number of reference projected profiles is also created from the isolated MPCs of patients with known states, such
10 as normal and various leukemic disease states. The projected profile is then compared with the reference database containing the reference projected profiles. If the projected profile of the patient matches best with the profile of a particular disease state in the database, the patient is diagnosed as having such disease state. Various computer systems and software (see Example 5) can be utilized for
15 implementing the analytical methods of this invention and are apparent to one of skill in the art. Some of these software programs include Cluster & TreeView (Stanford, URLs: rana.lbl.gov or www.microarray.org), GeneCluster (MIT/Whitehead Institute, URL: MPR/GeneCluster/GeneCluster.html), Array Explorer (SpotFire Inc, URL: <http://www.spotfire.com/products/scicomp.asp#SAE>) and GeneSpring (Silicon
20 Genetics Inc, URL: <http://www.sigenetics.com/Products/GeneSpring/index.html>) (for computer systems and software, see also U.S. Patent No. 6,203,987).

The methods of the present invention can also be useful for monitoring the progression of diseases and the effectiveness of treatments. For example, by comparing the projected profile prior to treatment with the profile after treatment.

25 One aspect of the present invention provides methods for therapeutic and drug discovery utilizing bone marrow derived isolated mesenchymal progenitor cells. The present invention can be utilized to identify stromal cell genes that can be therapeutic targets for improvement of normal hematopoietic function, which is constantly compromised, in leukemic patients. In one embodiment, gene sets are
30 defined using cluster analysis. The genes within a gene set are indicated as potentially co-regulated under the conditions of interest. Co-regulated genes are further explored as potentially being involved in a regulatory pathway. Identification

of genes involved in a regulatory pathway provides useful information for designing and screening new drugs.

Some embodiments of the present invention employ gene set definition and projection to identify drug action pathways. In one embodiment, the expression changes of a large number of genes in response to the application of a drug are measured. The expression change profile is projected into a gene set expression change profile. In some cases, each of the gene sets represents one particular pathway with a defined biological purpose. By examining the change of gene sets, the action pathway can be deciphered. In some other cases, the expression change profile is compared with a database of projected profiles obtained by perturbing many different pathways. If the projected profile is similar to a projected profile derived from a known perturbation, the action pathway of the drug is indicated as similar to the known perturbation. Identification of drug action pathways is useful for drug discovery. See, Stoughton and Friend, Methods for Identifying pathways of Drug Action, U.S. patent application Ser. No. 09/074,983.

The present invention provides a genomics strategy method for identifying genes differentially expressed in MPCs. The method begins with the preparation of total RNA from MPC samples, which leads to the generation of cDNA. From the cDNA, ds DNA can be prepared for *in vitro* transcription into cRNA. The cRNA is then fragmented for the hybridization of target RNA to a microarray of known genes (Affymetrix genechip containing DNA from ~12,000 known human genes, e.g., U95A oligonucleotide microarray). Finally, analysis of differentially expressed genes is accomplished using appropriate software (GeneSpring) to discern the patterns of gene expression or genomic signatures by a given MPC type (e.g., up-regulation or down-regulation).

Up-regulated and down-regulated gene sets for a given disease-associated or cytokine-stimulated MPC are combined. The combination enables those of skill in the art to identify gene sets with minimal number of elements that are unique to a given MPC type with a capability to discriminate one MPC type from another (this can be accomplished by means of a series of Venn diagrams and lists of required genes obtained via GeneSpring). Such gene sets are of immense diagnostic value as they can be routinely used in assays that are simpler than microarray analysis (for example "real-time" quantitative PCR). Such gene sets also

provide insights into pathogenesis and targets for design of new drugs. For example, the method allows one to establish transcriptional profiles of MPC genes that are pathologically altered.

Those of skill in the art can use the data and methods contained herein for the following: a) study select gene or sets of genes that are relevant to hematopoietic disease conditions by using relatively inexpensive but low-throughput technologies such as Northern blotting, RNase protection assays and/or PCR intended for gene expression analysis; b) identify newer drug targets and diagnostic markers relevant to specific diseases, such as MM or CML etc depending on the research interests of the individual investigators.

The present invention also provides a large-format 2-D gel electrophoretic system for the reproducible separation of MPC proteins and for preparing 2-D PAGE protein maps for normal bone marrow-derived MPCs (untreated and treated with representative cytokines, e.g., TNF- α and/or IL-4) and for MPCs derived from patients with representative pre-leukemic/ premalignant and leukemic/ malignant conditions. The pre-leukemic conditions include myelodysplastic syndromes (MDS) and the leukemic conditions include chronic myeloid leukemia (CML), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), acute lymphocytic leukemia (ALL), and multiple myeloma (MM). The protein samples consist of culture supernatants/secreted proteins, extracellular matrix (ECM) proteins, plasma membrane proteins solubilized using a three-step differential extraction protocol, employing conditions of progressively increasing solubility; and whole cell lysate proteins similarly solubilized using the three-step differential extraction protocol. This subproteome approach not only simplifies the 2-D PAGE electrophoretic protein patterns but also reveals additional proteins, which would otherwise have gone undetected.

The 2-D system described herein utilizes an immobilized pH gradient gel (pH 4-7) in the first dimension and a mini non-denaturing but high-resolution lithium dodecyl sulfate-polyacrylamide gel electrophoresis (LDS-PAGE) in the second dimension. As identified by silver staining, this system has resolved greater than 800 protein spots in a pH interval of 2.5 units (4.25-6.75, the isoelectric pH range for most of plasma membrane proteins to migrate) and a molecular mass range of 10-150 kDa. Equally important, the system is compatible with high sample

loads (up to 1.5 to 2.0 mg of total protein in up to 350 μ l sample volume). All the protein species identifiable by a silver stain that is compatible with subsequent mass spectrometric analysis have been analyzed by a 2-D gel software with respect to isoelectric point, molecular weight and mass abundance. The lectin-binding status of these proteins has also been determined by lectin blotting. Lectin blots and Western blots have subsequently been stained by a gold stain for detection of total proteins on the same PVDF membrane. Although gold-staining of the Western blot is not as sensitive as silver-staining of the gel, gold-staining of the Western blot generates the necessary landmarks for alignment with the silver stained gel, facilitating excision of spots of interest from the gel for identification by MALDI-MS. Representative protein spots were excised from gel and subjected to mass spectrometric profiling (MALDI-MS) and/or sequencing (Nano ESI MS/MS) with subsequent database searching, resulting in a productive identification of ten proteins.

The invention is further described in detail by reference to the following experimental examples. These examples are provided for the purpose of illustration only, and are not intended to be limiting unless otherwise specified. Thus, the invention should in no way be construed as being limited to the following examples, but rather, should be construed to encompass any and all variations which become evident as a result of the teaching provided herein.

20 EXAMPLES

The examples presented herein can be summarized as follows. The data disclosed herein demonstrate that Dexter cultures consist of only three cell types macrophages (~35%), hematopoietic cells (~5%), and nonhematopoietic cells (~60%). Using a percoll gradient centrifugation technique, the nonhematopoietic mesenchymal progenitor cells were isolated, free of macrophages and hematopoietic cells. A variety of techniques were used to identify the isolated cells as a multi-differentiated mesenchymal cell lineage co-expressing genes specific for multiple mesenchymal cell lineages including adipocytes, osteoblasts, fibroblasts and muscle cells.

30 Evidence that this multi- or pluri-differentiated mesenchymal progenitor cell is capable of supporting hematopoiesis is shown by the expression of a number of hematopoietic growth factors and extracellular matrix receptors. The SCID mouse experimental data provides evidence that since the MPCs can be purified to near

homogeneity (95%) with relative ease, MPCs can be of value for enhancing engraftment of hematopoietic stem cells and bone marrow transplants. Additionally, increased survival rate in the SCID mouse model indicates that isolated MPCs can also be useful for the treatment of GvHD. An example of the administration of bone marrow cells and MPCs to breast cancer patients treated with chemotherapy is also provided.

A stepwise genomics strategy and an example of the genomic changes observed in leukemia associated MPCs is also provided. Cluster analysis was performed to show gene expression patterns in isolated MPCs of a normal individual and individuals with different leukemic conditions. The approach presented provides the basis for a new more objective means to diagnose patients suffering from leukemic conditions.

EXAMPLE 1

Isolation and Characterization of MPCs from Dexter-Type Bone Marrow Stromal Cell Culture Systems

Bone marrow culture:

Bone marrow samples were obtained from posterior superior iliac crest under general anesthesia for standard marrow transplantation. Marrow stromal cell cultures were set up using the residual cells recovered from the filters of Fenwal Bone Marrow Collection System after complete filtration of the marrow samples. The filters were rinsed with phosphate-buffered saline without Ca^{2+} and Mg^{2+} (PBS-CMF). The cell suspension was subjected to Ficoll gradient isolation of the mononuclear cells (bone marrow MNCs). The bone marrow MNCs were washed (x2) in PBS-CMF and suspended in McCoy's 5A with HEPES medium containing 12.5% fetal bovine serum (FBS), 12.5% horse serum, 1 $\mu\text{M/L}$ hydrocortisone and 1% penicillin/streptomycin (for this study McCoy's complete medium) and cultured under standard stromal-cell culture conditions (Figure 1) (Seshi, *et al. Blood* 83, 2399 (1994) and Gartner, *et al. Proc Natl Acad Sci USA* 77, 4756 (1980). After two weeks, confluent stromal cell cultures were trypsinized (first passage), followed by splitting each T75 flask into two T150 flasks.

Morphologic and phenotypic characteristics of MPCs as uncovered by staining for representative mesenchymal cell lineage markers:

Two weeks after the first passage (above), confluent stromal cells were again trypsinized. Cytospins were prepared using aliquots of unfractionated cells for performance of various cytological, cytochemical and immunocytochemical stains.

Reactivity patterns of the bone marrow culture cells are outlined in Table 1. Figures 4A-E illustrate morphologic and phenotypic characteristics, as uncovered by staining for representative cell lineage markers. As illustrated in Table 1 and Figures 3 and 4A, Wright-Giemsa staining revealed three morphologically identifiable cell populations in Dexter type stromal cell cultures, macrophages, hematopoietic cells, and nonhematopoietic cells (labeled 4, 3, and 5, respectively).

The identity of macrophages was confirmed by immunostain using anti-CD68 antibody (Figure 4B) and cytochemical stains for acid phosphatase and Sudan black. The identity of hematopoietic cells (including macrophages) was confirmed by immunostain using anti-CD45 antibody (Figure 4C).

The remaining nonhematopoietic cells stained intensely positive for Periodic acid-Schiff, which was diastase sensitive, signifying the presence of large stores of glycogen (Figure 4D). The presence of glycogen (6) was confirmed by electron microscopy (see Figure 5). In this respect, MPCs are reminiscent of the glycogen-laden reticular cells in the developing bone marrow of human fetuses (observed by L-T. Chen, L. Weiss, *Blood* 46, 389 (1975)). Glycogen deposition is viewed to be a developmentally regulated process during morphogenesis (H. Ohshima, J. Wartiovaara, I. Thesleff, *Cell Tissue Res.* 297, 271 (1999)).

In terms of lineage markers, up to 100% of the nonhematopoietic cells expressed two fat cell markers (Nile Red (Figure 4E) and Oil Red O); an osteoblast marker (alkaline phosphatase (Figure 4F)); and two fibroblast markers (fibronectin (Figure 4G) and prolyl-4-hydroxylase). Greater than 85% of the nonhematopoietic cells were also positive for a muscle marker, actin (Figure 4H). There was no evidence of expression of endothelial cell differentiation, as judged by immunohistochemical staining for CD34 and CD31 (data not shown).

The results indicate that the nonhematopoietic cells of the Dexter cultures are in fact a single, pluri-differentiated cell type co-expressing multiple mesenchymal cell lineage markers. The pluri-differentiated mesenchymal progenitor cells reported here are to be distinguished from the pluri-potential, but

undifferentiated, MSCs that are generated in the absence of hematopoietic cells, such as in Friedenstein-type cultures.

Table 1. Reactivity patterns of bone marrow stromal cells based on cytological, cytochemical and immunocytochemical stains*,***

5

| | Figure | Test Utilized | Macrophages | Hematopoietic cells | Mesenchymal progenitor cells |
|----|----------|---|--|---|--|
| 1 | 3 and 4A | Wright-Giemsa (Harleco) | Large cells with a small round nucleus & foamy cytoplasm: 35% of total cells | Small cells with minimal amount of cytoplasm: 5% of total cells | Large cells with a relatively irregular nucleus & cytoplasm compartmentalized into ectoplasm and endoplasm: 60% of total cells |
| 2 | 4D | Periodic acid-Schiff (PAS) (Sigma) | 0 | 0 | ~100% MPCs: staining restricted to ectoplasm in a ring-like fashion; and completely abolished by diastase digestion |
| 3 | 4C | CD45 (Dako, PD7/26 & 2B11) | 100% macrophages (MΦ) | 100% HCs | 0 |
| 4 | 4B | CD68 (Immunotect h, clone PG-M1) | 100% MΦ | 0 | 0 |
| 5 | | Sudan Black (Sigma) | ~100% MΦ | 0 | 0 |
| 6 | | Acid phosphatase (Sigma Kit No. 387) | 100% MΦ; positive granules packed throughout cytoplasm | 0 | 100% MPCs; positive granules in moderate amounts; staining restricted to endoplasm |
| 7 | 4E | Nile Red (Sigma) | 0 | 0 | ~100% MPCs: staining restricted to endoplasm |
| 8 | | Oil Red O (Sigma) | 0 | 0 | ~ 95% MPCs: variable number of positive granules; staining preferentially in the endoplasm |
| 9 | 4F | Alkaline phosphatase (Sigma Kit No. 85) | 0 | 0 | ~100% MPCs: variable number of positive granules; staining restricted to endoplasm & plasma membrane** |
| 10 | 4G | Fibronectin (Immunotect h, clone 120.5) | 0 | 0 | ~100% MPCs: staining restricted to endoplasm |
| 11 | | Prolyl-4-hydroxylase (Dako, | 0 | 0 | ~100% MPCs: staining preferentially in the endoplasm |

| | | | | | |
|--------|----|---|---|---|---|
| | | clone 5B5) | | | |
| 1 2 | 4H | Muscle actin (Ventana, clone HUC 1-1) | 0 | 0 | > 85% MPCs; variable staining restricted to ectoplasm |

*The lineages of the markers tested above are: 3, hematopoietic cell marker; 4, 5 and 6, monocyte/macrophage markers; 7 and 8, adipocyte markers; 9, osteoblast marker; 10 and 11, fibroblast markers; 12 muscle marker.

5 **One earlier study (Simmons, *et al.*, Nature 328, 429-432) interpreted the localization of alkaline phosphatase staining as confined to the plasma membrane when in fact it is predominately present within the endoplasm (compare Figure 1C of this reference with Figure 4F).

10 *** While well-accepted mesenchymal lineage markers were used, these markers do not necessarily lend themselves to simultaneous assessment of the same cell. For example, muscle-specific actin antibody worked only on formalin-fixed, paraffin embedded material, whereas stains like alkaline phosphatase, Oil Red and Nile Red are not anti-body based and involve varying fixing and staining conditions. Thus, the evidence shows that close to 100% of members of a morphologically distinct
15 population express multiple lineage markers of interest.

Bone marrow mesenchymal progenitor cell (MPC) purification:

To further investigate the characteristics of the MPCs, the nonhematopoietic stromal cells were then purified from the macrophages (~95% pure), the dominant "contaminating" cell type using the following method. Confluent
20 monolayers of stromal cells resulting from first passage, above, were washed for three minutes in $\text{Ca}^{2+}/\text{Mg}^{2+}$ free Hanks' balanced salt solution. Cells were incubated at room temperature for 45 minutes with intermittent mixing in serum-free McCoy's medium containing 10 mM L-leucine methyl ester (LME, Sigma). LME is a
25 lysosomotropic agent that selectively kills and detaches macrophages. The detached macrophages were removed by washing the monolayers twice in McCoy's complete medium, followed by trypsinization of the monolayers. The resulting single cell suspensions were fractionated by discontinuous Percoll gradient (70%, 50%, 30%, 20%, 10%) centrifugation at 800xG for 15 minutes at 4°C in a fixed angle rotor (Avanti-J25 Beckman centrifuge) (Figure 2). Low-density cells representing the

macrophages resistant to detachment by LME separate as a band at the interface of serum and 10% Percoll and were discarded (1). High-density nonhematopoietic cells representing MPCs form a layer in the region of 30-50% Percoll (2). These were collected and washed twice by centrifugation through PBS-CMF. This protocol is conservatively expected to yield, $>2.5 \times 10^6$ MPCs per T-150 flask (i.e., $>50 \times 10^6$ MPCs per batch of 20 flasks). The purity of these preparations, typically about 95%, was routinely monitored by Wright-Giemsa staining.

Northern Blotting:

Additional sets of multiple mesenchymal lineage markers were assessed by Northern blotting to eliminate any observer bias that might be inherent in morphological assessment. Figures 6A-M represent different gene probes used for hybridization. The sources of the gene probes employed and the major transcripts observed are outlined in the brief description of the figures.

Total RNA was prepared by dissolving the high-density cell pellets in Trizol (Life-Technologies). Total RNA samples from unfractionated stromal cells and BM-MNCs were similarly prepared. The RNA samples were electrophoresed in a standard 1% agarose gel containing 2% formaldehyde in MOPS/EDTA buffer and blotted onto Immobilon-Ny+ membrane. Probes were labeled using Prime-A-Gene Kit (Promega) and $\alpha^{32}\text{P}$ dCTP (NEN). Hybridization was performed at 65°C in modified Church's hybridization solution using 3×10^6 counts/ml in 10 ml (Millipore, 1998).

In Figures 6A-M, Northern blot analysis was performed side-by-side on fractionated stromal cells, non-hematopoietic cells freed of macrophages, and initial bone marrow mononuclear cell samples. Lanes 1 and 2 represent total RNA samples (10µg each) from unfractionated stromal cells (subjects S1 and S2, respectively). Lanes 3 and 4 represent total RNA samples (10µg each) from purified stromal MPCs (subjects S1 and S2, respectively). Lanes 5 and 6 represent total RNA samples (10µg each) from bone marrow mononuclear cells, the starting cells for bone marrow cell cultures (subjects S3 and S4, respectively).

The large transcripts, especially of collagen (lane 1, Figure 6G) and fibronectin (lane 1, Figure 6J), in RNA extracted from unfractionated stromal cells of subject 1 showed difficulty migrating into the gel. This observation correlates with the presence of an artifact of unresolved positive material in lane 1, Figure 6A. Since

the RNA extracted from unfractionated stromal cells of the subject 2 did not present this problem (lane 2, Figure 6G, Figure 6J and Figure 6A), the observation does not impact on the overall interpretation of the results (see text). The lineages of markers tested were: monocyte/macrophage markers, CD68 and cathepsin B; adipocyte marker, adipsin; osteoblast markers, osteoblast-specific cadherin-11, chondroitin sulfate proteoglycan 2, collagen type I alpha 1 and decorin; fibroblast marker, fibronectin; muscle markers, caldesmon and transgelin. Marker signals were normalized to the amount of RNA loaded, which was based on densitometry of the GAPDH signals on the corresponding blot (Bio-Rad Model GS-700 Imaging Densitometer). Attenuation or enhancement of the marker signals in the purified stromal MPCs (i.e., lanes 3 and 4) relative to unfractionated stromal cells (i.e., lanes 1 and 2, respectively) is shown as fold Δ (decrease/increase) underneath the lanes 3 and 4; ND, means not determined.

The purity of the nonhematopoietic cells was demonstrated by a near complete absence of two macrophage markers, CD68 and cathepsin B (as shown by Northern blotting data, Figure 6A and 6B). As a positive control, bone marrow mononuclear cells rich in myelomonocytic cells abundantly expressed CD68 (lanes 5 & 6, Figure 6A). The Northern blot results are consistent with a purity estimate of ~95% (vs. 60% in unfractionated samples) based on morphology and immunocytochemical staining for CD68.

Compared to unfractionated cells, the purified nonhematopoietic cells expressed significantly higher levels of markers representing fat cells (adipsin, Figure 6D); osteoblasts (osteoblast-specific cadherin-11, chondroitin sulfate, collagen type 1 and decorin, Figures 6E-H); fibroblasts (fibronectin, Figure 6J); and smooth muscle cells (caldesmon and transgelin, Figures 6K-L).

No trace of osteoblast, fibroblast, or smooth muscle cell markers were detected in the bone marrow mononuclear cells, suggesting a less than detectable level of stromal cells or their precursors in bone marrow mononuclear cells. However, the fat cell marker, adipsin, was detected in all samples including the bone marrow mononuclear cells.

Taken together, the morphologic, cytochemical and immunocytochemical results (Figure 4A-H and Table 1), and the Northern blotting data (Figure 6A-M) indicate that the nonhematopoietic stromal cells of the Dexter

cultures co-express markers specific for at least four different mesenchymal cell lineages.

This finding is especially intriguing because pluri-differentiation is often a feature of neoplastic cells (Brambilla and Brambilla, *Rev. Mal. Respir.* 3,235 (1986); Pfeifer et al., *Cancer Res.* 51, 3793-3801 (1991); Tolmay et al., *Virchow's Arch* 430, 209-12 (1997). However, a cytogenetic analysis of the Percoll-gradient purified MPCs showed a normal GTW banding pattern.

RT-PCR Analysis for expression of representative hematopoietic growth factors and extracellular matrix receptors by MPCs

RT-PCR was conducted in a total reaction volume of 100 µl using 2 µg each of total RNA; corresponding primers; and a master mix of the PCR reagents. The RT conditions included sequential incubations at 42°C for 15 minutes, 99°C for five minutes, and 5°C for five minutes. The PCR conditions included: initial melting at 94°C for four minutes; and cyclical melting at 94°C for 45 seconds, annealing at 55°C for 45 seconds and extension at 72°C for 45 seconds with 34 cycles. PCR was terminated after final extension at 72°C for ten minutes. Reaction products (G-CSF, SCF, each 25 µl; VCAM-1, ALCAM, each 50 µl; ICAM-1, 75 µl) were concentrated as necessary; electrophoresed along with a 100-bp DNA ladder (GIBCO-BRL) in a standard agarose (1%) gel in TAE buffer; and stained with ethidium bromide.

PCR products, shown in Figure 7 lanes labeled 1-2, were generated using aliquots of the same RNA samples from purified stromal MPCs, as used for Northern blotting shown under Figure 6 lanes 3 and 4 respectively. The gene transcripts amplified were as follows: G-CSF (granulocyte-colony stimulating factor); (Tachibana et al., *Br. J. Cancer*, 76, 163-74 (1997); SCF (stem cell factor, i.e., c-Kit ligand); (Saito et al., *Biochem. Biophys. Res. Commun.*, 13, 1762-69 (1994); ICAM-1 (intercellular adhesion molecule-1, CD54) and VCAM-1 (vascular cell adhesion molecule-1, CD106) (primers from R&D); and ALCAM (activated leukocyte cell adhesion molecule, CD166) (Bruder et al., *J. Bone Miner. Res.*, 13, 655-63 (1998)).

The observed PCR products for G-CSF (600 bp, i.e., the top bright band) and ALCAM (175 bp) were significantly different from the expected sizes (278 bp; 372 bp, respectively). However, sequencing of the gel-purified PCR bands and subsequent BLAST search showed a 99-100% identity with respective members. Attempts to detect c-Kit (i.e., SCF receptor) using primers as described (Saito et al.,

Biochem, Biophys. Res. Commun., 13, 1762-69 (1994)) amplified a PCR product of ~300 bp with no homology to c-Kit (data not shown). The observed product sizes for SCF (~730 bp); ICAM-1 (~750 bp); and VCAM-1 (~500 bp) were as expected.

As illustrated in Figure 7, RT-PCR analysis showed that purified, multi-
5 differentiated MPCs express both critical hematopoietic growth factor/cytokines, such as G-CSF and SCF as well as matrix receptors/hematopoietic cell adhesion molecules, i.e. ICAM-1, VCAM-1, and ALCAM.

EXAMPLE 2

Comparison of the Ability to Support in vitro Hematopoiesis by Purified MPCs vs.

10 *Unfractionated Bone Marrow Stromal Cells*

CD34+ positive cells (hematopoietic progenitor cells) were purified (DynaL kit) and cocultured with irradiated stromal monolayers for five weeks, followed by performance of standard colony assays for hematopoietic progenitors using methylcellulose medium supplemented with colony stimulating factors (using
15 MethoCult medium from Stem Cell Technologies, Inc, Canada). Unfractionated bone marrow stromal cells and purified MPCs were prepared in the same manner as in Example 1. Data in Figure 8 represents results from three experiments. Purified MPC provides increased preservation of hematopoietic progenitor cells compared to unfractionated stromal cells.

EXAMPLE 3

20

Animal Model for Enhanced Engraftment Capacity of MPCs

The Severe Combined Immunodeficiency Disease (SCID) mouse model is an ideal system in which to investigate MPC function. Engraftment of human hematopoietic progenitors in SCID mice requires either coadministration of
25 exogenous human cytokines, or cotransplantation of human bone marrow plugs or bone fragments.

There has been discovered a convenient, new source for human bone marrow stromal cells for enhancing transplantation that does not require cytokines, bone fragment, or marrow. Unlike prior methods, the isolated cells of the present
30 invention support human hematopoiesis in the SCID mouse model as effectively as whole marrow stroma. The transplantation of human marrow mononuclear cells combined with purified MPCs results in dramatically vigorous engraftment of human cells in spleen, bone marrow, liver, pancreas, lungs, stomach, and paravertebral

neuronal ganglia of SCID mice. By contrast, mice receiving human bone marrow mononuclear cells alone or MPCs alone expectedly showed no detectable evidence of human hematopoietic cell engraftment. Also notably, the mortality rate was highest in mice that received unfractionated whole marrow stroma whereas purified MPC increased the survival rate which can be due to reduction in GvHD.

Transplantation of human cells in SCID mice:

Homozygous CB-17 scid/scid mice, six to eight weeks of age, were used. Lyophilized anti-asialo GM1 rabbit antibody (Wako Chemicals) was suspended in 1 ml sterile ddH₂O, followed by pretreatment of mice with an IP injection of 20 ml (600 mg) ASGM1 antibody (to specifically deplete mouse macrophages and NK cells). Alternatively, one could use NOD/SCID mice lacking NK cell function, however, in light of highly promising preliminary results it was elected to continue use of scid/scid mice. The antibody treatment schedule included four-hour pre-engraftment and every seven days thereafter for the duration of the experiment. On the day of transplantation, the mice were irradiated with 200 or 300 cGy gamma-irradiation from a ¹³⁷Cs source. Approximately 2.5×10^6 MPCs suspended in 0.5 ml McCoy's medium and/ or 25×10^6 MNCs suspended in 0.2 ml were injected per mouse, intraperitoneally. Hematopoietic cell engraftment was assessed after five weeks by harvesting and analyzing representative hematopoietic and nonhematopoietic organs including blood, spleen, bone marrow (from two femurs and tibia) from euthanized mice.

Flow Cytometric Evidence

Figure 9A and 9B are flow cytometric evidence of human hemopoietic cells in a SCID mouse cotransplanted with marrow MPC. Figure 9A shows the presence of CD45+/CD34+ progenitors in the marrow. Figure 9B shows CD45/CD34- mature hematopoietic cells circulating in the mouse's blood.

Photomicrographs of Cells

Figures 10A-H shows engraftment of human hematopoietic cells in a SCID mouse cotransplanted with the purified marrow MPCs of the present invention. Figure 10A shows a serial section of a mouse spleen stained with H & E. Figure 10B shows a serial section of a mouse spleen stained with immunoperoxidase stain for CD45. Figure 10C shows bone marrow stained for CD45. Figure 10D shows a serial section of the mouse liver stained with H&E depicting involvement of periportal

areas. Figure 10E shows a serial section of the mouse stomach stained with H&E showing transmural infiltration. Figure 10F shows a serial section of the mouse lung stained with H&E showing involvement of peribronchial area. Figure 10G shows a serial section of the mouse pancreas stained with H&E. Figure 10H shows a serial
5 section of the mouse paravertebral ganglia stained with H&E.

Figure 11A is a photomicrograph of a serial section of the spleen of a normal BALB/C mouse showing white pulp populated by darkly staining lymphocytes (H&E). Figure 11B is a photomicrograph of the spleen of a SCID mouse showing white pulp largely consisting of lightly staining stromal framework (H&E). Figure 11C
10 is a photomicrograph of the spleen of a SCID mouse cotransplanted with human bone marrow MNC and the purified bone marrow MPCs of the present invention showing homing (engraftment) of human B cells to white pulp.

Southern Blotting Data

15 Hybridization of sample DNA using a DNA probe specific for human chromosome 17 alpha satellite DNA (p17H8) shows linear signal intensity with a 2.7 Kb band (arrow; autoradiogram exposed for only 45 minutes) (Figure 12A). Lanes 1-10 contain human DNA starting 1000 ng to 100 ng admixed with 0 ng 900 ng of mouse DNA, total amount DNA loaded in each lane being 1 ug, allowing
20 construction of a standard curve. The reported limit of detection with this technique is 0.05% human cells, which is more reliable than flow cytometry in detecting very low levels of human cell engraftment.

Figure 12B is a Southern blot of EcoR1 digest of thymic genomic DNA from SCID mice. Lanes 1-5 were loaded with 500 through 100 ng human DNA.
25 Lanes 6, 9-11 were loaded with DNA from mice which received unfractionated bone marrow stroma plus bone marrow mononuclear cells. Lanes 7, 8, 14, 15 were loaded with DNA from mice that received MPCs plus bone marrow mononuclear cells. Lanes 12, 13 were loaded with DNA from mice that received bone marrow mononuclear cells only. There is evidence of human cell engraftment in the mouse
30 thymus in lanes 9 and 11 and lanes 14 and 15 evidenced by the 2.7 Kb band. There was no evidence of engraftment in mice that only received only bone marrow mononuclear cells, lanes 12 and 13.

Figure 12C is EcoRI digest of Lymph Node genomic DNA from SCID mice. Lanes 1-5 were loaded with 500 through 100 ng human DNA. Lanes 6, 9-11 were loaded with DNA from mice which received unfractionated bone marrow stroma plus bone marrow mononuclear cells. Lanes 7, 8, 14, 15 were loaded with DNA from mice that received MPCs plus bone marrow mononuclear cells. Lanes 12, 13 were loaded with DNA from mice that received bone marrow mononuclear cells only. While there was evidence of engraftment of human cells in the mouse lymph nodes for mice that received unfractionated bone marrow stromal cells and MPCs, there was no evidence of engraftment in mice that only received only bone marrow mononuclear cells, lanes 12 and 13.

Increased Survival and Evidence of MPC Effect on GvHD

Figure 13A and Figure 13 B show graphs comparing the survival rate and engraftment of human hematopoietic cells in SCID mice cotransplanted with the purified bone marrow MPCs of the present invention versus unpurified bone marrow stromal cells. Mice in Figure 13A received 300 cGy irradiation dose and mice in Figure 13B received 200 cGy of irradiation. Figure 13A and Figure 13B show comparable engraftment of human hematopoietic cells in SCID mice cotransplanted with purified MPCs versus unpurified bone marrow stromal cells and the markedly enhanced survival of mice receiving purified MPCs. Notably, no engraftment was observed in mice receiving bone marrow mononuclear cells alone.

The highest mortality rate, Figure 13B, was observed in mice receiving the unpurified stromal cells and the bone marrow mononuclear cells. The increased mortality observed can be related to the presence of highly immunogenic macrophages and consequent GvHD. The mice with the highest survival rate, as shown in Figure 13A, were the mice receiving purified MPCs and bone marrow mononuclear cells.

Figures 14A-C demonstrate apoptosis by TUNEL assay in organs of SCID mice that died after transplantation with human bone marrow mononuclear cells and unpurified bone marrow stromal cells. Figure 14A shows a serial section of the liver of the mouse that survived. Figure 14B shows a serial section of the liver of the mouse that died. Figure 14C shows a serial section of the spleen of the mouse that survived. Figure 14D shows a serial section of the spleen of the mouse that died. Hematoxylin counterstain was applied to sections in Figure 14A and Figure

14C. Methylgreen counterstain was applied to sections in Figure 14B and Figure 14D.

Notably, there is discrete TUNEL-positive nuclei in the liver of the expired mouse in Figure 14B and complete absence of staining in the liver of the surviving mouse Figure 14A. While some ill-defined globules of staining are observed in the spleen of the mouse that survived, the nuclear integrity of most of the cells is well preserved suggesting minimal or no apoptosis (Figure 14C). By contrast, the dead mouse spleen (Figure 14D) showed extensive TUNEL positivity precluding accurate interpretation. Control mouse liver and spleen showed results similar to those of the mouse that survived.

The size of the spleens from the mice that survived and the mice that died were compared. The dead mice were observed to have small and atrophic spleens correlating with lymphoid cell depletion and apoptosis.

The above results indicate that purified MPC can support human hematopoiesis in SCID mice as effectively as whole marrow stroma. Equally important is that the purified MPCs increased the survival rate. Evidence suggests that the increased survival can be due to a reduction in GVHD.

EXAMPLE 4

Administration of Bone Marrow Cells and Mesenchymal Progenitor Cells to Breast Cancer Patients Treated with Chemotherapy

A breast cancer patient undergoes a diagnostic posterior iliac crest bone marrow aspiration and biopsy using a local anesthetic. A small portion (2 to 3 ml) of the aliquot (10 to 20 ml) of marrow is submitted for routine histologic testing and determination of the presence of tumor cells using immunoperoxidase testing. The remainder of the cells are Dexter cultured for MPCs as described above in Example 1.

The patient also undergoes placement of a pheresis central venous catheter, and receives subcutaneous injections of G-CSF (filgrastin) 10µg/kg/day as described in Peters, et al, Blood, Vol. 81, pgs. 1709-1719 (1993); Chao, et al, Blood, Vol. 81, pgs. 2031-2035 (1993); Sheridan, et al, The Lancet, Vol. 2, pgs. 891-895 (1989); and Winter, et al, Blood, Vol. 82, pg. 293a (1993). G-CSF injections begin at least three days before the first pheresis is initiated. G-CSF therapy is withheld if the

white blood cell count rises above 40,000/ μ L and is resumed once the white blood cell count drops to less than 20,000/ μ L.

If the patient is receiving only G-CSF as the vehicle for "mobilization" of peripheral blood progenitor cells, the patient must not have received chemotherapy within four weeks of the planned pheresis. If the patient has received both
5 conventional chemotherapy and G-CSF treatment for mobilization, the patient must not have received chemotherapy within ten days of the planned pheresis, and the white blood cell count must be at least 800/ μ L and the platelet count at least 30,000/ μ L.

10 Daily pheresis procedures are performed using a Cobe Spectra instrument (Cobe, Lakewood, Col.), and each cellular collection is cryopreserved using a controlled-rate liquid nitrogen freezer, until at least 15×10^8 mononuclear cells/kg are collected (Lazarus, et al., Bone Marrow Transplant, Vol. 7, pgs. 241-246 (1991)). Each peripheral blood progenitor cell is processed and cryopreserved
15 according to previously published techniques. (Lazarus, et al., J. Clin. Oncol., Vol. 10, pgs. 1682-1689) (1992); Lazarus et al., (1991)).

Eight days before the patient is infused with the autologous peripheral blood progenitor cells, the patient receives chemotherapy over a period of 96 hours (four days), with the following chemotherapy agents: 1) Cyclophosphamide in a total
20 dosage of 6 g/m^2 (1.5 g/m^2 /day for four days) is given via continuous intravenous infusion at 500 mg/m^2 in 1,000 ml normal saline every eight hours; 2) Thiotepa in a total dosage of 500 mg/m^2 /day for four days) is given via continuous intravenous infusion at 125 mg/m^2 in 1,000 ml normal saline every 24 hours; and 3) Carboplatin in
25 intravenous infusion at 200 mg/m^2 in 1,000 ml of 5% dextrose in water every 24 hours.

The patient also receives 500 mg of Mesna in 50 ml normal saline IV over 15 minutes every four hours for six days (144 hours), beginning with the first dose of cyclophosphamide.

30 At least 72 hours after the completion of the chemotherapy, the MPCs are harvested from the Dexter culture(s). MPCs are collected and purified as described in Example 1. Cells are resuspended at approximately 10^6 cells/ml, and

injected slowly intravenously over 15 minutes to provide a total dosage of from 10 to about 5×10^6 cells.

MPCs can also be frozen and thawed to use when needed. For example, unfractionated cells from a Dexter culture are frozen. Upon thawing the cells are plated for about two days. The MPCs are then purified as in Example 1 above. The MPCs are then replated with serum or in a serum free media and can remain stable for up to six days.

The day after the patient receives the MPCs, the frozen autologous peripheral blood progenitor cells are removed from the liquid nitrogen refrigerator, transported to the patient in liquid nitrogen, submersed in a 37°C to 40°C sterile water bath, and infused rapidly intravenously without additional filtering or washing steps. GM-CSF in an amount of 250 $\mu\text{g}/\text{m}^2$ then is given as a daily subcutaneous injection, beginning three hours after completion of the autologous blood progenitor cell infusion. The GM-CSF is given daily until the peripheral blood neutrophil count exceeds 1,000/ μL for three consecutive days.

EXAMPLE 5

Genomic Changes Observed in Leukemia Associated MPCs

The following is one example of how normal hematopoiesis might be compromised in leukemic conditions. The cellular interactions that underlie leukemic bone marrow involve stromal cells, leukemia/ lymphoma cells, and normal hematopoietic progenitors (including those of myelopoiesis, erythropoiesis and megakaryocytopoiesis). In addition to displacing normal hematopoietic cells, the leukemia/ lymphoma cells can potentially cause direct damage to the hematopoietic supportive stromal cells by inducing unwanted gene expression profiles and adversely affecting the normal hematopoiesis. The cellular interactions can be schematized as:

Leukemia/lymphoma cells stromal cells normal hematopoietic progenitors.

The point of this scheme is that regardless of whether stromal cell lesions are primary or secondary to leukemogenesis, the normal hematopoietic function is invariably compromised in leukemic conditions, though different leukemias affect myelopoiesis, erythropoiesis and megakaryocytopoiesis differentially. Contrary to the prevailing notion (see Marini, F *et al.*, Mesenchymal Stem Cells from Patients with Chronic Myelogenous Leukemia Patients can be

Transduced with Common Gene Transfer Vectors at High Efficiency, and are Genotypically Normal, 42nd Annual Meeting of the American Society of Hematology, Dec. 1-5, 2000 Poster # 665), there has been observed extensive and striking gene expression changes in leukemia-associated bone marrow MPCs by using high-resolution genomics. Therefore, one embodiment of the present invention is to use transplantation of tissue-culture expanded, purified normal MPCs to improve granulopoiesis, erythropoiesis and thrombopoiesis, in for example MDS (most of MDS patients do not die from blast transformation but from complications related to cytopenias, i.e., hematopoietic failure).

The studies targeted acute myeloid leukemia (AML), chronic myeloid leukemia (CML) and multiple myeloma (MM), one case of each. The AML patient was a 57 year-old woman with 52% myeloblasts in the bone marrow with immunophenotype confirmed by flow cytometry and a karyotypic abnormality of 45, XX, -7(6)/46, XX [6]. Together with morphology, the diagnosis was AML arising in a background of myelodysplasia. The CML patient was a 35 year-old man with 2% blasts in the bone marrow and karyotypic abnormalities of Philadelphia chromosome and BCR/ABL gene rearrangement. Together with morphology, the diagnosis was CML in chronic phase. The MM patient was a 61 year-old woman with a IgA myeloma. The serum IgA level was 2.4 g/dl and the marrow plasma cell count was 37%. None of the patients was treated prior to obtaining marrow samples used in this study, to avoid any therapy-induced changes complicating the disease-associated changes.

The leukemic samples consisted of marrow aspirates that remained unused after clinical diagnostic studies were preformed. A bone marrow sample obtained from an adult healthy male who had consented to donate bone marrow for standard marrow transplantation was simultaneously studied. The normal bone marrow sample consisted of residual cells recovered from the filters after complete filtration of the marrow sample. Setting up of Dexter-type stromal cell cultures and isolation of MPC were as described in Example 1. The normal stromal cells were studied without and after stimulation with $\text{TNF}\alpha$ because $\text{TNF}\alpha$ (and IL-4) are regarded as negative regulators of hematopoiesis. Notably these cytokines, especially $\text{TNF}\alpha$, are elevated in marrow plasma of patients with myelodysplastic syndromes (MDS), the clinical hallmarks of which are anemia, leukopenia and

thrombocytopenia (i.e., pancytopenia). $\text{TNF}\alpha$ and IL-4 are considered possible mediators of hematopoietic dysregulation typical of MDS.

A stepwise genomics strategy encompassed:

Preparation of total RNA from MPC samples \rightarrow generation of cDNA \rightarrow
5 preparation of ds DNA \rightarrow *in vitro* transcription into cRNA \rightarrow fragmentation of cRNA
 \rightarrow hybridization of target RNA to a microarray of known genes (Affymetrix genechip
containing DNA from ~12,000 known human genes, e.g., U95A oligonucleotide
microarray) \rightarrow analysis of differentially expressed genes using an appropriate
software (GeneSpring) to discern the patterns of gene expression or genomic
10 signatures by a given MPC type.

*Cluster analysis showing gene expression patterns in bone marrow MPC isolated
from a normal individual and patients with different leukemic conditions.*

Genes with correlated expression across bone marrow MPC types:

GeneSpring was used for cluster analysis. Prior to application of an agglomerative
15 hierarchical clustering algorithm, microarray signals were normalized across
experiments (i.e., from one MPC type to another) making the median value of all of
measurements unity, so different experiments are comparable to one another. The
signals were also normalized across genes in order to remove the differing intensity
signals from multiple experimental readings. Genes that are inactive across all
20 samples were eliminated from analysis. Notably, 7398 genes out of 12,626 genes
(present on the Affymetrix genechip used) passed the filter of a normalized signal
intensity of at least 0.1 across at least one of the five experiments performed.
Cluster analysis was performed with standard correlation (same as Pearson
correlation around zero) as the distance metric, a separation ratio of 0.5 and a
25 minimum distance of 0.001 as provided by the software application. A closer
relationship between CML- and MM-associated MPCs was observed, which in turn
are related to AML-associated MPC, thus transforming global patterns of gene
expression into potentially meaningful relationships.

Two-dimensional cluster analysis of tissue vs. gene expression
30 *vectors:* A gene tree was constructed. Genes cluster near each other on the "gene
tree" if they exhibit a strong correlation across MPC experiments and MPC tree
branches move near each other if they exhibit a similar gene expression profile. The
data indicated that the two-way clustering readjusted the location of a number of

genes resulting in accentuation of genomic signatures of each cell type. Investigators can usefully catalog genes composing any unique or signature cluster of interest by creating a gene list and disclosing their identities.

Self-organizing map (SOM) clusters (6x5) show differential gene expression in bone marrow MPC isolated from different hematopoietic conditions.

Generation of SOM clusters involved prior normalization and filtering of the data. SOM algorithm was applied as provided by GeneSpring. Visualization of SOM clusters in combination with hierarchical clustering (i.e., MPC tree) revealed correlated meaningful patterns of gene expression. Predicated on the basis of SOM operating principle, the related SOM clusters tend to be located physically close to each other. For example, the juxtaposition of the SOM clusters with the common denominator containing genes that are up-regulated in AML/MDS-associated MPC. Whole or part of any SOM cluster can be selected to make a gene list providing the identities of the genes involved.

Genes highly expressed in normal MPC but absent or minimally expressed in leukemia-associated MPC

Lists of genes that are down-regulated in leukemia-associated MPC (AML/MDS, CML and MM) were created in comparison to normal MPC. A Venn diagram was made using these three gene lists. GeneSpring allows creation of sublists of genes corresponding to union, intersection and exclusion. Transcriptional profiles of any of these sublists of genes can be visualized across MPC samples of interest. The following is one such sublist of genes containing genes that are highly expressed in normal MPC and down-regulated in leukemia-associated MPCs revealing the identity of the subset of genes of interest: putative, wg66h09.x1 Soares Homo sapiens cDNA clone, Homo sapiens mRNA for CMP-N-acetylneuraminic acid hydroxylase, Homo sapiens cDNA clone DKFZp586G0421 (symptom: hute1), Human mRNA for histone H1x, Putative monocarboxylate transporterHomo sapiens gene for LD78 alpha precursor, Interacts with SH3 proteins; similar to c-cbl proto-oncogene product, wg82b12.x1 Soares Homo sapiens cDNA clone, Human atrial natriuretic peptide clearance receptor (ANP C-receptor) mRNA, Human 71 kDa 2'5' oligoadenylate synthetase (p69 2-5A synthetase) mRNA, Homo sapiens hMmTRA1b mRNA, Human G0S2 protein gene, Preproenkephalin, Human guanylate binding protein isoform I (GBP-2) mRNA, Human gene for

hepatitis C associated microtubular aggregate protein p44, 17-kDa protein, Human insulin-like growth factor binding protein 5 (IGFBP5) mRNA, GS3686, Human monoamine oxidase B (MAOB) mRNA, Insulin-like growth factor II precursor, Human insulin-like growth factor binding protein 5 (IGFBP5) mRNA, Similar to ribosomal protein L21, X-linked mental retardation candidate gene, and Homo sapiens mRNA; cDNA DKFZp434A202. *Genes not expressed in normal MPC but highly expressed in leukemia-associated MPC*

Lists of genes that are upregulated (instead of down-regulated) in leukemia-associated MPCs (AML/MDS, CML and MM) were created in comparison to normal MPC and a Venn diagram was made. The following is one such sublist of genes containing genes that are inactive in normal MPC but up-regulated in leukemia-associated MPCs revealing the identity of the subset of genes of interest: Beta- tropomyosin, Homo sapiens clone 24659 mRNA sequence, Human mRNA for DNA helicase Q1, OSF; contains SH3 domain and ankyrin repeat, ym22b12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone, Human mRNA for pre-mRNA splicing factor SRp20, Human mRNA for golgi alpha-mannosidaseII, OSF-2os, Homo sapiens gene for Proline synthetase, hk02952 cDNA clone for KIAA0683, wi24g10.x1 Homo sapiens cDNA clone, Lysosomal enzyme; deficient in Sanfilippo B syndrome, CTP synthetase (AA 1-591), WD repeat protein; similar to petunia AN11, Human mRNA for 5'-terminal region of UMK, complete cds, Homo sapiens chemokine exodus-1 mRNA, complete cds, Human GPI-H mRNA, complete cds, Homo sapiens mRNA encoding RAMP1, Transforming growth factor-beta-2 precursor, and Homo sapiens mRNA for KIAA0763 protein.

Visualizing expression of phenotypically & functionally relevant genes across samples of normal & disease-associated BM MPC.

Although GeneSpring is a highly flexible and user-friendly software application, it lacks the facility to create functionally relevant gene lists containing user-defined key words. This limitation was overcome by devising the following method via Microsoft Excel. A stepwise protocol to create such a gene list using Excel includes: Open the annotated microarray genome file (e.g., Affymetrix U95A) in Excel → select the column with gene names → select Data from pull-down menu → Filter → AutoFilter → Custom → enter key words (e.g., cell adhesion or cell cycle) → OK → generates a new Excel worksheet with the list of genes containing the key

words. Copy and paste the list of genes containing the key words into GeneSpring and save the gene list with a meaningful name. Twenty-two (22) such functionally relevant gene lists (Table 2) were created.

The resulting approach is a simple and powerful way to peer into the expression profiles of focused sets of functionally relevant genes across samples of interest. For example, the human vascular cell adhesion molecule-1 (VCAM-1) gene is completely down-regulated in AML/MDS and the human insulin-like growth factor binding protein (hIGFBP1) gene is up-regulated in AML compared to all other samples. Similarly, *Homo sapiens* gene for LD78 alpha precursor is down-regulated in all of leukemia-associated MPCs. Finally, the lineage markers CD45 and CD68 are essentially absent from the leukemia-associated MPCs attesting to the high degree of purity achieved by the sample preparation technique of the present invention.

Results

The genomic changes observed in leukemia-associated MPCs are striking. As shown in Table 2, the changes (up-regulation and/ or down-regulation) involved hundreds of genes. These changes were most dramatic in MPC associated with AML arising in a background of MDS and involved multiple classes of genes (Tables 1-2). Expectedly, the TNFa-induced changes were extensive. Given the high level of purity of MPC preparations, the enormous genomic changes observed are reflective of the underlying pathologic lesions in the MPCs themselves (and not due to the contaminating leukemic cells and/ or macrophages). These studies strongly support the hypothesis that stromal cells in a leukemic patient are functionally defective and therefore purified MPCs are of value in restoring the loss of hematopoietic function in leukemic patients.

Table 2. Magnitude of global gene expression changes in leukemia-associated and TNFa-stimulated MPCs in comparison to normal MPC

| | AML/MDS MPC | CML MPC | MM MPC | TNFa MPC |
|---------------------------|----------------|---------|--------|----------|
| # of genes up-regulated | 234 | 112 | 108 | 279 |
| # of genes down-regulated | 379 | 208 | 251 | 164 |

Table 3. Functional classes of genes analyzed across normal and leukemia-associated MPCs

| | | |
|---|--|---|
| Annexins (14) Caspases & apoptosis-related transcripts (33) Cadherins (50) Calmodulins/ calmodulin-dependent kinases (25) Cell adhesion molecules (20) Cathepsins (19) Collagens (71) | Cell division cycle-related transcripts (36) Cytokines (19) Epidermal growth factors and related transcripts (22) Fibroblast growth factors (21) Fibronectins (6) Galectins (6) Growth factors (136) | IGF system (24) Interleukins/ receptors (76) Integrins/ disintegrins (70) Lineage-related markers (19) Laminins (13) Platelet-derived growth factors & receptors (12) TNF alpha-related transcripts (29) TGF beta-related transcripts (25) |
|---|--|---|

5 The gene lists in Table 3 were created as described above and analyzed using GeneSpring. The numerical value in parenthesis refers to the number of transcripts in the corresponding class of genes analyzed.

Example 6

10 The present invention provides the following benefits: a) identification and documentation of BM stromal cell gene expression patterns under varied, normal, and leukemic hematopoietic conditions; b) identification of stromal cell genes that can be therapeutic targets for improvement of normal hematopoietic function that is constantly compromised in leukemic patients, and identification of similar targets for arresting the growth and progression of neoplastic clones since
15 stromal cells provide the necessary support for preferential growth of leukemic cells (CLL, MM) within BM and protect the leukemic cells from chemotherapy-induced death (MM); and c) identification of new biological bases and new diagnostic markers for refinement of the classification and diagnosis of leukemia. This present invention can also lead to important insights into the pathogenesis of leukemia. In
20 broad terms, analysis of global gene expression or transcriptome (transcriptional profile composed of all transcribed regions of the genome) is considered a nonbiased discovery-driven (as opposed to hypothesis-driven) approach to the analysis of gene expression. A stepwise genomic strategy encompasses preparation of total RNA from cells of interest, to generation of cDNA, to preparation of ds DNA,
25 to *in vitro* transcription into cRNA, to fragmentation of cRNA, to hybridization of target RNA, to a microarray of known genes (and/or ESTs), to analysis of

differentially expressed genes using an appropriate software to discern the patterns of gene expression or genomic signatures by a given disease-associated cell type.

Further test utility of sample preparation technology applied to normal EM-derived MPCs (untreated and treated with representative cytokines) and MPCs
5 derived from patients with representative pre-leukemic and leukemic conditions for performance of high-resolution DNA microarray technology (Affymetrix genechip containing DNA from 12,000 known human genes, e.g., U95A oligonucleotide microarray).

Representative cytokines which are pathologically altered in
10 hematopoietic conditions and that can be used in this study include TNF- α , TGF- β and interferon- γ . The pre-leukemic conditions include myelodysplastic syndromes (MDS) and the leukemic conditions include chronic myeloid leukemia (CML), acute myeloid leukemia (AML), acute lymphocytic leukemia (ALL), and multiple myeloma (MM).

15 The front-end strategy of microarray analysis involves the use of Percoll-gradient purified MPCs. As a follow-up strategy, to validate the stromal cell origin of the differentially expressed genes, MPCs obtained from cytopins of BM stromal cells by laser-capture microdissection (LCM) selected on the basis of morphology (Figure 3) are used followed by "real-time" quantitative polymerase
20 chain reaction (PCR). This can be performed with an LGM system as well as a "real-time" QPCR system. Validation can be performed on at least one sample from each of 6 normal BM M7NC/ MPC types and on one sample from each of 5 leukemia-associated MPC types. Validation is considered successful if the microarray results and PCR results on a given MPC sample match using a suite of 20 genes selected
25 based on median pattern of microarray results for the given cell type. This approach not only validates the microarray results but also ascertains the stromal cell origin of the expressed genes. The standard published protocols involving LGM and "real-time" quantitative PCR and the instructions accompanying the equipment are used for performing the experiments.

30 Stepwise LCMJ real-time QPCR protocol entails the following. Cytopins are made from BM stromal cells. The cytopins are stained with hematoxylin and MPC is selected for based on morphology. Microdissect up to 1,000 MPC from each sample. RNA is extracted and reverse transcribed into cDNA.

The cDNA is amplified using gene-specific primers and "real-time" quantitative PCR.

By applying the combined power of different analytical techniques (such as hierarchical clustering and self-organizing maps) together with the recently developed sample preparation technology for stromal cells the present invention provides a molecular biological basis that can allow refinement of the classification and diagnosis of leukemias and lymphomas, uncovering the suspected disease heterogeneity. This enables the deciphering of the genomic expression profiles or signatures of bone marrow stromal cells in about 10 different physiologic states and about 20 different leukemic states. In addition to aiding in refinement of the classification and diagnosis of the hematopoietic malignancies, the data provides clues to potential novel drug targets and insights into pathogenesis.

The present invention functions by identifying the MPC genes that are differentially expressed after stimulation with different hematopoietic cytokines implicated in the pathogenesis of pre-leukemic conditions (MDS); in actual pre-leukemic disorders (MDS); and in overt leukemias (CML, AML, CLL, ALL, MM) as well as in lymphomas that have a leukemic phase with involvement of BM.

The present invention is accomplished by first determining the median gene expression profiles for MPCs associated with each disease and stimulated by each cytokine of interest (this objective can be achieved by treating the gene expression vectors of individual cases in each MPC category as replicates; this capability is available in GeneSpring software application). Then the gene groups that are up regulated and down regulated and that are common to all the members in a given MPC category are identified (this is accomplished using a series of Venn diagrams and creating required gene lists via GeneSpring). Finally, the up-regulated and down-regulated gene sets for a given disease-associated or cytokine-stimulated MPC are combined. This allows the identification of gene sets with minimal number of elements that are unique to a given MPC type with a capability to discriminate one MPC type from another (this can also be accomplished by means of a series of Venn diagrams and lists of required genes obtained via GeneSpring). Such gene sets can be of immense diagnostic value as they can be routinely used in an assay simpler than microarray analysis (for example "real-time" quantitative PCR). Such gene sets can additionally provide insights into pathogenesis and possible targets for design of new drugs.

Determine expression profiles of MPC genes which are regulated as a result of exposure of normal MPCs to cytokines that are known to have a hematopoietic support role and/or are abnormally elevated in pre-leukemic/leukemic conditions, i.e., TNF α ; IL-4; TNF α + IL-4; interferon γ ; TGF β ; PDGF; FGF; EGF; and calmodulin.

TNF α , IL-4 and IFN γ are potent negative regulators of hematopoiesis. Notably these cytokines, especially TNF α , are elevated in marrow plasma of patients with myelodysplastic syndromes (MDS), the clinical hallmarks of which are anemia, leukopenia and thrombocytopenia (i.e., pancytopenia). TNF α and IL-4 are thus possible mediators of hematopoietic dysregulation typical of MDS. Studies regarding these regulators can uncover the molecular pathways leading to cytopenias in MDS patients. As indicated earlier, myeloproliferative disorders are another, in some ways similar, group of hematopoietic disorders that are clonal in origin but not overtly malignant clinically. These MPDs include polycythemia vera, essential thrombocythemia, idiopathic myelofibrosis (agnogenic myeloid metaplasia) and chronic myelogenous leukemia. These disorders have the potential to change from one to the other at any time, however the signals that trigger such conversion remain enigmatic. Idiopathic myelofibrosis (IMF), in which stromal cells seem to play a profound pathogenetic role, is characterized by fibrosis of the marrow cavity, extramedullary hematopoiesis, splenomegaly, and anemia and leukoerythroblastic features in the peripheral blood. While myeloproliferation is known to be a clonal process, the accompanying stromal cell proliferation and fibrosis are believed to be a polyclonal reactive process that is likely to be due to increased intramedullary activity of a number of cytokines including TGF β , PDGF, FGF, EGF and calmodulin, as shown by other investigators.

Cancer genomics is a rapidly expanding area of investigation. The focus is unique however in emphasizing not the leukemic cells themselves but rather BM stromal cells that provide a haven to various types of pre-leukemia and leukemia cells, non-Hodgkin's lymphomas (NHLs) and metastatic cancers (METs). Pre-leukemic clonal neoplastic conditions include myelodysplastic syndromes (MDSs) and myeloproliferative disorders (MPDs). Stromal cells are known to produce and/or respond to growth factors such as EGF, PDGF, FGF, VEGF, and cytokines such as IL-1 or TNF α , partially explaining the interactive relationship between stromal cells

and cancer cells, especially in MDS and CML.

In spite of similarities between BM stroma and non-BM stroma, certain sharp distinctions do stand out. Non-BM stromal cells are terminally differentiated fibroblasts, while BM stromal cells represent a unique pluripotent or pluridifferentiated mesenchymal cell type, thus exhibiting preserved developmental "plasticity". Using 5-10 cc BM aspirate samples from adult leukemic patients and 3-5 cc BM samples from pediatric patients with ALL, the study can analyze the BM stroma. One cc of marrow sample can produce at least 1 T-150 flask of stromal cells. One concern is that it can be hard to obtain marrow samples from cases like CML and myelofibrosis. In such cases stromal cells are grown using peripheral blood samples as described in the prior art. At least one flask of stromal cells (i.e., 1 cc marrow) to yield the RNA required for analysis. About 10 cases of each type of leukemia/lymphoma were studied. The study provided important insights into the functioning of the BM microenvironment in normal and leukemic hematopoiesis.

A database including all of the above information and that can include age, gender and associated major illness in terms of clinical/pathologic diagnosis for each subject/patient can be created. This can also include information on cytogenetic, molecular and flow cytometric studies. Finally, also included can be the information on clinical course in terms of disease progression and response to treatment exercising adequate care to protect the identity of individual patients. The study analyzed genomic expression profiles or signatures of bone marrow stromal cells derived from about 12 different normal bone marrow states and about 19 different leukemia/lymphoma states, approximately 10 cases of each as shown in Table 4, accounting for a total of 310 samples.

Using the information of the present invention, those of skill in the art can: a) study select gene or sets of genes as relevant to hematopoietic disease conditions using relatively inexpensive but low-throughput technologies such as Northern blotting, RNase protection assays and/or PCR intended for gene expression analysis; b) reanalyze the primary data by using newer and more powerful bioinformatic tools as they become available; and/or c) identify newer drug targets and diagnostic markers relevant to specific diseases, such as MM or CML etc.

Table 4 Scope of human BM samples targeted for DNA microarray analysis
(approximately 10 cases of each)

Normal BM mononuclear cells (NMNC)

Normal BM stromal cells, unfractionated and unstimulated (NBMS)

Normal purified mesenchymal progenitor cells, unstimulated (NMPC)

NMPC stimulated with 9 different cytokines:

- 5 NMPC stimulated with TNF α (TNF α MPC)
- NMPC stimulated with TGF β (TGF β MPC)
- NMPC stimulated with interferon γ (IFN γ MPC)
- NMPC stimulated with IL-4 (IL-4 MPC)
- NMPC stimulated with TNF α + IL-4 (TNF α + IL-4 MPC)
- 10 NMPC stimulated with PDGF (PDGF MPC)
- NMPC stimulated with EGF (EGF MPC)
- NMPC stimulated with FGF (FGF MPC)
- NMPC stimulated with calmodulin (calmodulin MPC)
- MDS - Refractory anemia (MDS-RA MPC)
- 15 MDS - Refractory anemia with ringed sideroblasts (MDS-RARS MPC)
- MDS - Refractory anemia with excess blasts (MDS-RAEB MPC)
- MDS - Chronic myelomonocytic leukemia (M1)S-CMML MPC)
- MPD - Polycythemia vera (MPD-PV MPC)
- MPD - Essential thrombocythemia (MPD-ET MPC)
- 20 MPD - Myelofibrosis (MPD-LMF MPC)
- CML (CML MPC)
- AML-M0/M1/M2 (AML-M0/M1/M2 MPC)
- AML-M3 (APL) (AML-M3 MPC)
- AML-M4/M5 (myelomonocytic) (AML-M4/M5 MPC)
- 25 ALL-L1/L2 (lymphoblastic) (ALL-L1/L2 MPC)
- ALL-L3 (Burkitt's) (ALL-L3 MPC)
- Multiple myeloma (MM MPC)
- CLL/SLL (CLL/SLL MPC)
- Follicle center cell lymphoma (FCL MPC)
- 30 Mantle cell lymphoma (MCL MPC)
- Lymphoplasmacytic lymphoma (LPL MPC)
- Marginal zone lymphoma (MZL MPC).

Human Subjects

- This study involves the use of bone marrow (BM) samples from human
- 35 subjects. BM samples can be obtained from normal subjects (male and female 20-45 years) as well as leukemic patients after informed consent is obtained. Leukemic cells can be obtained from diagnostic samples of BM of adult and pediatric patients (in those cases in which cells remain unused after clinical diagnostic studies are

performed; i.e., about 90% of cases).

Example 7

In broad terms, global gene expression analysis is considered a nonbiased discovery-driven (as opposed to hypothesis-driven) approach to the analysis of protein expression. A stepwise proteomics strategy encompasses: solubilization of proteins from cells of interest; 2-D gel electrophoresis (IPG DALT); staining and image analysis of gels; excision of protein spots of interest; trypsin digestion of proteins; mass spectrometry (MALDI-TOF MS and/or ESI MS/MS) performed on tryptic fragments; identification of proteins by database searching. The present invention provides a method to analyze the population of expressed proteins (i.e., proteome) of BM MPCs in relation to hematopoiesis in collaboration with a state-of-the-art mass spectrometry facility.

The large-format 2-D gel electrophoretic system is used for reproducible separation of MPC proteins and to prepare 2-D PAGE protein maps for normal bone marrow-derived MPCs (untreated and treated with representative cytokines, e.g., TNF α and/or IL-4) and for MPCs derived from patients with representative pre-leukemic/premalignant and leukemic/malignant conditions. The pre-leukemic conditions include myelodysplastic syndromes (MDS) and the leukemic conditions include chronic myeloid leukemia (CML), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), acute lymphocytic leukemia (ALL), and multiple myeloma (MM). The protein samples can consist of culture supernatants/secreted proteins; extracellular matrix (ECM) proteins; plasma membrane proteins solubilized using a three-step differential extraction protocol, employing conditions of progressively increasing solubility; and whole cell lysate proteins similarly solubilized using the three-step differential extraction protocol. This subproteome approach not only simplifies the 2-D PAGE electrophoretic protein patterns but also reveals additional proteins, which would otherwise have gone undetected.

The system of the present invention can be used to differentially express MPC proteins (i.e., those that increased or decreased in intensity as compared to 2-D PAGE protein maps of normal, unstimulated MPCs) using mass spectrometry (MALDI-MS and/or nanoelectrospray ionization MS/MS) and/or Western blotting and/or Western-ligand blotting.

Using high-resolution proteomics with the added power of high-

throughput robotics, enables the system to identify on a larger (semi-comprehensive) scale the MPC proteins that are differentially expressed in conditions that simulate pre-leukemic bone marrow (following stimulation with different cytokines); and in actual pre-leukemic disorders (MDS) as well as in overt
5 leukemias (CML, AML, CLL, ALL, MM).

The system of the present invention enables the identification of MPC proteins whose expression is regulated as a result of exposure of normal MPCs to cytokines that are known to have a hematopoietic support role and/or are abnormally elevated in pre-leukemic/leukemic conditions, i.e., TNF α ; IL-4; TNF α + IL-4;
10 interferon γ ; TGF β ; PDGF; FGF; EGF; and calmodulin.

The system of the present invention also enables the identification of MPC proteins for which expression is altered as a result of exposure of normal MPCs to agents that are clinically used for mobilization of hematopoietic stem cells from BM into peripheral blood to facilitate easy collection and subsequent transplantation,
15 e.g., G-CSF and G-CSF plus cyclophosphamide.

Further, the system of the present invention enables the identification of Identify the MPC proteins whose expression is pathologically altered in hematopoietic disease states such as: MDS, CML, AML, CLL, ALL and MM by matching the 2-D PAGE protein maps of disease-associated MPCs with the 2-D
20 PAGE database of normal MPCs. If a protein of interest does not exist in the normal MPC proteome, or if it exists in the normal MPC proteome but has not yet been characterized, then such proteins can be identified by MALDI-MS and/or Nano ESI MS/MS.

The system facilitates understanding of the pathogenetic mechanisms
25 by identifying the phosphoproteins involved in cell signaling pathways. The systems immunoblots the whole cell lysate proteins of normal MPCs, untreated and treated with respective cytokines, using antibodies to phosphotyrosine, phosphoserine, and phosphothreonine. The system then locates the corresponding putative phosphoprotein spots on the gel and identifies the proteins by MALDI-MS and/or
30 Nano ESI MS/MS. Similarly, the system can locate the altered phosphoproteins by immunoblotting the whole cell lysate proteins of untreated MPCs derived from leukemic patients. If a protein of interest does not exist in the normal MPC proteome, or if it exists in the normal MPC proteome but has not yet been identified,

then MALDI-MS and/or Nano ESI MS/MS can identify the protein.

Bone marrow MPCs derived from a leukemia background express distinctively different patterns of cell adhesion molecules from normal MPCs.

5 BM stromal cells provide the background required for homing and subsequent proliferation and differentiation of hematopoietic stem cells. BM stromal cells also provide a rich microenvironment for metastases and growth of various leukemias. Based on the hypothesis that homing of normal hematopoietic cells and leukemic cells to marrow utilize the same adhesion mechanisms, it was questioned
10 whether there are fine regulatory distinctions in terms of quantitative differences in the expression of the adhesion molecules in normal vs. leukemic BM microenvironments. In a pilot study 11 cell adhesion molecules (CAMs) and several lineage-associated markers for Northern blot analysis were targeted. Dexter-type cultures were grown under standard stromal cell culture conditions using bone
15 marrow samples from a normal individual and from one patient diagnosed with and treated for acute myelogenous leukemia (AML). Representative cultures were treated with cytokines such as TNF α alone, IL-4 alone, and TNF α plus IL-4. MPCs from unstimulated and cytokine-treated cultures were purified using Percoll gradient techniques disclosed above. Total RNAs were extracted by a standard method and
20 analyzed by Northern blotting. This study demonstrated expression by MPCs of several CAMs, heretofore unsuspected of expression by BM stroma. These include an embryonic endothelial cell protein Dell (developmental endothelial locus 1), galectin-I, human milk fat globule protein (RMFG, lactadherin), and epithelial membrane protein 1 (EMP 1). Secondly, MPCs from the AML patient expressed
25 significantly lower levels of mRNA for three CAMs Del- 1, galectin- 1, and collagen type 1 as well as for the adipocyte marker adipsin, and to a minor degree the muscle-associated protein caldesmon. On the other hand, mRNA for CAMs like TGF beta-inducible BiGH3, HMFG, osteoblast-specific cadherin 11, and VCAM1 were dramatically increased in AML-associated MPCs. CAMs such as integrin beta 5,
30 fibronectin, EMP 1 and the muscle-associated molecule transgelin are variably increased in diseased MPCs and appear to be unaffected by treatment with cytokines tested. ICAM I was undetectable at basal level in either patient or normal samples, but was slightly elevated by TNF α and markedly elevated by TNF α plus

IL-4. VCAM1 was mildly up regulated by TNF α alone or IL-4 alone, but markedly up regulated by TNF α /IL-4 in combination. Also, the MPCs from the patient were much more sensitive to stimulation by these inflammatory cytokines than were the normal MPCs. These studies establish that stromal cells in a leukemic patient are
5 functionally defective.

Role of leptin receptor in hematopoiesis using human marrow stromal cells as a model.

The receptor for the product of the obesity gene, leptin, is widely distributed in tissues ranging from central nervous system to reproductive system to
10 hematopoietic system. Within hematopoietic system, OB-R is reportedly expressed on diverse cell types ranging from early CD 34+ hematopoietic stem cells to circulating monocytes. Leptin acts on monocytes to induce production of TNF α and IL-6, which are powerful regulators of hematopoiesis. However, literature reports on the expression of leptin or its receptor on stromal cells are infrequent. To date, one
15 particular report suggests that leptin acts on the stromal cells to enhance their differentiation into osteoblasts and to inhibit differentiation into adipocytes. Because leptin is an adipocyte-generated hormone and because marrow stromal cells represent a unique pluridifferentiated mesenchymal cell type expressing some adipocytic features, the expression of the leptin receptor by these cells was
20 investigated in the hope of revealing its role in hematopoiesis.

By Northern blotting marrow stromal cells showed abundant expression of OB-R, consistent with their adipocytic nature. In terms of regulation, exposure of the stromal cultures to different cytokines revealed an interesting pattern of OB-R. As shown, G-CSF and TNF α down-regulated OB-R while IL-4 up-
25 regulated OB-R expression by stromal cells. Simultaneous treatment of stromal cultures with TNF α and IL-4 nearly abolished OB-R expression. The expression of OB-R was also analyzed at the protein level by a high-resolution, high capacity 2-D PAGE system, followed by Western blotting.

More specifically, the method provides the identification of leptin
30 receptor in human BM stromal cell membrane protein extracts using 2-D Western blotting. The expression of OB-R was investigated at protein level using 2-D PAGE, followed by Western blotting. Two isoforms differing in molecular weight of 2.2 kDa (60.2; 62) and an isoelectric point of 0.2 pH unit (5.78; 5.98, respectively) have been

identified (the pH was determined by using the values specified by the IPG strip manufacturer). The ability to subsequently stain the same Western blot with gold stain allowed precise localization of the immunoreactive protein spots of interest on the blot. The gold staining of the blot, by revealing other protein spots in addition to the immunoreactive spots, has provided the necessary landmarks in turn facilitating subsequent alignment with the silver-stained gel using an appropriate 2-D analysis software program (Melanie 3).

This technique has identified two OB-R isoforms that differ in molecular mass by 2.2 kDa (60.2; 62.4) and differ in their isoelectric point by 0.2 pH units (5.78; 5.98). The level of macrophage contamination is determined by two macrophage markers, CD68 and cathepsin B. The studies include the determination of OB-R expression in a) unfractionated stromal cells vs. isolated pluri-differentiated mesenchymal progenitor cells; b) unstimulated cultures vs. cultures stimulated with a variety of cytokine/hormones including leptin itself. The studies also include mass spectrometric characterization of the two OB-R isoforms detected by Western blotting in order to establish their exact structural differences.

Proteome analysis of 2-D PAGE separated human BM stromal cell membrane proteins.

BM stromal cells support the growth and development of normal blood cells as well as providing a haven for malignant leukemia/lymphoma cells. Focusing on stromal cell-surface proteins as potentially playing a role in cell-to-cell communication in normal as well as in abnormal hematopoiesis, the mixtures of stromal-cell plasma membrane, and plasma membrane-associated proteins were analyzed by a high-resolution, high-capacity 2-D gel electrophoresis. The 2-D system described utilizes an immobilized pH gradient gel (pH 4-7) in the first dimension and a mini nondenaturing but high-resolution lithium dodecyl sulfate-polyacrylamide gel electrophoresis (LDS-PAGE) in the second dimension. As identified by silver staining, this system has resolved greater than 800 protein spots in a pH interval of 2.5 units (4.25-6.75, the isoelectric pH range for most of plasma membrane proteins to migrate) and a molecular mass range of 10-150 kDa. Equally important, the system is compatible with high sample loads (up to 1.5 — 2.0 mg of total protein in up to 350- μ l sample volume). All the protein species identifiable by a silver stain that is compatible with subsequent mass spectrometric analysis have

been analyzed by a 2-D gel software with respect to isoelectric point, molecular weight and mass abundance. The lectin-binding status of these proteins has also been determined by lectin blotting. Lectin blots and Western blots have subsequently been stained by a gold stain for detection of total proteins on the same PVDF membrane. Although gold-staining of the Western blot is not as sensitive as silver-staining of the gel, gold-staining of the Western blot generates the necessary landmarks for alignment with the silver stained gel, facilitating excision of spots of interest from the gel for identification by MALDI-MS. Representative protein spots were excised from gel and subjected to mass spectrometric profiling (MALDI-MS) and/or sequencing (Nano ESI MS/MS) with subsequent database searching, resulting in a productive identification of ten proteins. The protein digests are then submitted in a near-ready state for mass spectrometry. Upon receiving the MS data the group performs the database searching. MALDI/MS has been used, which identifies a protein on the basis of its characteristic mass sizes, as well as MS/MS studies that provide amino acid sequences of selected masses to identify proteins with enhanced specificity and confidence level. This work represents the first systematic attempt to analyze BM stromal cell proteins by high-resolution 2-D gel electrophoresis and provides the basis for a full-scale proteome mapping of the marrow stromal cells. The present work can facilitate the long-term goal of deciphering the hematopoietic support functions of BM stromal cells.

Modulation of stromal cell plasma membrane protein expression by TNF α /IL-4.

The effects of TNF α /TM on bone marrow stromal cell plasma membrane protein expression has been tested using the described system. TNF α and IL-4 are regarded as negative regulators of hematopoiesis. Notably these cytokines, especially TNF α , are elevated in marrow plasma of patients with myelodysplastic syndromes (MDS), the clinical hallmarks of which are anemia, leukopenia and thrombocytopenia (i.e., pancytopenia). TNF α and IL-4 are thus possible mediators of hematopoietic dysregulation typical of MDS. TNF α /IL-4 treatment of the stromal cultures induced dramatic changes in the protein profile. Initial studies using plasma membrane protein samples show reduced expression of at least 7 proteins and enhanced expression of 13 proteins.

Analyzing the insulin-like growth factor system in human marrow stromal cells

by 2-D PAGE analysis of BM stromal cell culture supernatants.

Proliferation and development of normal and leukemic hematopoietic cells within bone marrow is regulated by interplay of various classes of molecules. These include cell adhesion molecules (CAMs), colony stimulating factors (CSFs), and cytokines as well as growth factors including insulin-like growth factors 1 and 2 (IGF 1 and IGF 2), which are small peptide homologs of prolinsulin. IGF 1 has known erythropoietic activity, whereas the function of IGF 2 is less clear. IGF 1 and 2 exert their activities through two types of receptors. The type I IGF receptor, a tyrosine kinase receptor highly homologous to the insulin receptor, binds to IGF 1 and IGF 2 with high affinity. The type II IGF receptor, a mannose 6-phosphate receptor that lacks intrinsic kinase activity, binds IGF 2 with high affinity and IGF 1 with low affinity. The type and number of receptors expressed on a target cell determine the strength of the IGF signal. One important key to understanding the IGFs' role in hematopoiesis is to appreciate how biological effects of receptors are modulated by larger soluble proteins, the IGF binding proteins (IGFBPs), which share no homology with the IGF receptors. Because IGFs and IGFBPs play important roles in cell growth and proliferation in many tissues, and because marrow stromal cells support hematopoietic growth and development, the patterns of expression of the IGF system components by marrow stromal cells cultured under serum-free conditions is necessary. To this end, unfractionated and purified stromal cells were analyzed, side-by-side, by Northern blotting, under varied stimulatory conditions for expression of IGFs and IGFBPs with surprising results. IGF 2 is constitutively expressed at a high level by macrophages in Dexter cultures; it is down regulated markedly by TNF α alone; moderately by TNF α plus IL-4; and unaffected by IL-4 alone. On the other hand, IGF 2 is minimally expressed by unstimulated MPCs, but is markedly up regulated by TNF α alone or IL-4 alone; and moderately up regulated by combined TNF α and IL-4. IGFBP4 is abundantly expressed both by macrophages and MPCs and is unaffected by cytokine treatment. In contrast, IGFBPs 5, 7, and 10, selectively expressed by MPCs, show no evidence of expression by macrophages and are unaffected by cytokine treatments. IGF 1 and the precursor to IOFBP 3 are not expressed in either macrophages or MPCs, either constitutively or after stimulation with TNF α , IL-4 or both. In initial studies, bone marrow mononuclear cells expressed none of the IGFs or IGFBPs tested. These

results provide important insights into the operation of the IGF system in stromal cells and it is likely that potentially novel IGFBPs can be uncovered by ligand blotting studies.

The present invention provides a large-format 2-D gel electrophoretic system for reproducible separation of MPC proteins and to prepare 2-D PAGE protein maps for normal bone marrow-derived MPCs (untreated and treated with representative cytokines, e.g. TNF α or IL-4) and for MPCs derived from patients with representative pre-leukemic and leukemic conditions. The pre-leukemic conditions include myelodysplastic syndromes (MDS) and the leukemic conditions include chronic myeloid leukemia (CML), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), acute lymphocytic leukemia (ALL), and multiple myeloma (MM). The protein samples can consist of culture supernatants/secreted proteins; extracellular matrix (ECM) proteins; plasma membrane proteins solubilized using a three-step differential extraction protocol employing conditions of progressively increasing solubility; and whole cell lysate proteins similarly solubilized using the three-step differential extraction protocol. This subproteome approach not only simplifies the 2-D PAGE electrophoretic protein patterns but also reveals additional proteins, which would otherwise have gone undetected.

Molecular analysis assay involving the high-resolution 2-D PAGE and mass spectrometric identification of gel-separated proteins.

The completion of human genome project has provided a huge proteome database including the theoretical mass databases generated on the basis of site-specific cleavage employing proteolytic enzymes, such as trypsin and others. The availability of highly sensitive biological mass spectrometers together with the capability of bioinformatics to search extremely large amounts of data and identify the relevant proteins matching the mass spectrometry data provides the basis for the current excitement in proteomics. The focus of the interest is the BM MPC proteome as expressed under varied functional and disease states. The goal of the present invention is to identify BM MPC proteins that have possible functional and/or pathologic significance, that is, those proteins that show altered levels of expression in response to cytokine treatments and various leukemic states.

Until recently, the focus of the laboratory has centered on isolation and characterization of BM stromal cell adhesion molecules using a novel 2-D cell

blotting technique. For this purpose, applicants have established an analytical 2-D mini gel system that separates stromal cell plasma membrane proteins using 18-cm long 4-7 pH range IPG strips in the 1st D (Amersham Pharmacia Biotech). Subsequent to IEF, the IPG strip is cut into appropriately small pieces and subjected to 2 D separation using nondenaturing lithium dodecyl sulfate-polyacrylamide gel electrophoresis (LDSPAGE) and mini gels. The reason for using mini gels in the 2nd D is that they are compatible with a downstream functional assay involving cell adhesion. The stromal cell membrane proteins are blotted on to a PVDF membrane and assayed for hematopoietic cell-binding proteins directly on the blotting membrane. The system can be extended using 17-cm long 3-10 pH range IPG strips (Bio-Rad) for separation of stromal cell culture supernatants, ECM proteins, and whole cell lysates. As detected by silver staining of the gels, and analyzed by appropriate software (GelLab II or Melanie 3) this 2-D system has resolved greater than 800 membrane protein spots within a pH interval of 2.5 units (4.25-6.75) and a MW range of 10-150 kDa. Similarly, the ECM samples showed 475 spots; and conditioned media from BM stromal cell cultures grown under serum free conditions showed 524 spots. Not surprisingly, the total cell lysate of BM stromal cultures showed only 553 spots, most likely representing the abundant housekeeping proteins and masking detection of many functionally relevant proteins. These observations provide the rationale for the proposed subproteome approach involving the use of differential solubilization of sample proteins and multiple large gels. Membrane proteins thus far identified by mass spectrometry followed by database searching; proteins are identified by standard Western blotting. Select IGF binding proteins were identified by ligand Western blotting. The blotting shows the identification of IGF-binding proteins (IGFBPs) using 2-D ligand blotting. The conditioned media from BM stromal cultures grown under serum-free conditions were concentrated using Microcon concentrator, and proteins were fractionated using a high-resolution 2-D PAGE. The separated proteins were electroblotted onto PVDF membrane and subjected to Western ligand-blotting assays using 1-125 labeled IGF-2, resulting in the identification of a series of IGFBPs (up to 30 spots). Notably, TNF α treatment of the cultures down-regulated two IGFBPs and up-regulated IGFBP labeled 6.

By necessity the protein work began on BM stromal cells using a

nondenaturing (LDS-PAGE) mini gel system that contained no reducing/alkylating agents. To preserve the function of 2-D gel separated proteins many otherwise powerful sample preparation methodologies designed for proteomic studies (such as multiple surfactant solution, MSS) were avoided. While mini gels are convenient and
5 allow comparison and information transfer to large-format gels, they are less sensitive.

Subproteomes according to sample prefractionation.

In order to be able to identify the low-abundance proteins implicated in the regulatory and pathologic processes, a number of approaches to prefractionation
10 of the whole cell lysates have been described. Applicant studied the subproteomes of secreted proteins from BM stromal cell culture supernatants as well as ECM proteins. Notably, the ECM protein samples can be a rich source of functionally relevant cytokines and chemokines since the latter are known to mediate function by binding to ECM. In addition, the plasma membrane and whole cell samples were
15 subjected to the 3-step sequential solubilization protocol shown. The solubilizing solutions can be prepared in-house or purchased commercially (Bio-Rad). The first step involves the use of Tris base, which can solubilize the peripheral membrane proteins and cytosolic proteins. These proteins are lyophilized and subsequently solubilized prior to 2-D PAGE in a standard solubilizing medium (the modified
20 O'Farrell cell lysis solution containing urea, CHAPS, DII, Iris, ampholytes and appropriate protease inhibitors). The resulting pellet can also be solubilized in the standard 2-D solubilizing medium and subjected to 2-D PAGE. Because the standard solution cannot solubilize some proteins, the membrane-rich pellet is finally solubilized in a potent multiple surfactant solution (MSS) consisting of urea,
25 thithea, CI-LAPS, zwittergent 3-10 and tributyl phosphine (TBP) in addition to Iris base and ampholytes that is compatible with subsequent IEF. The MSS has been shown to solubilize the hydrophobic proteins with as many as 12 transmembrane regions (TMRs), facilitating their 2-D analysis. Another final step incorporating 1% SDS in boiling sample buffer can be used to test by 1-D SDS-PAGE if any proteins
30 remained unsolubilized after these extractions (notably, SDS extract is unsuitable for 2-D PAGE analysis since SDS interferes with IEF). The prefractionation step clearly reduces the complexity of the sample. Thus, the serial extractions not only simplify the gel images and reduce spot overlapping frequently encountered in single-step

extractions but also correlate closely with the cellular location of specific proteins, providing clues to their function. The prefractionation strategy can be extended to enriching low-abundance proteins in culture supernatants by selective removal of contaminating albumin using an Albumin Depletion Kit (containing Cibachron Blue resins) (Genomic Solutions, mc). Similarly membrane glycoproteins can be enriched
5 by a Glycoprotein Enrichment Kit (containing lectins) prior to 2-D PAGE analysis (Genomic Solutions, Inc.).

Subproteomes according to overlapping pH gradients.

Using a series of medium-range and partially overlapping pH gradients
10 (3-6, 5-8, 7-10, each 17-cm long) (Bio-Rad) can enhance reproducibility and resolution by creating "virtual" gels with up to 40 cm equivalent of PI separation across a pH 3-10 range. Alternatively, a combination of two pH gradients, pH 4-7 and pH 6-11, each 24 cm-long (Amersham Pharmacia Biotech) can be used, also providing a "virtual" separation distance of 40 cm across a pH range of 4-11. These
15 strips accept micropreparative sample loads (1-2 mg). Notably, a given sample of cells yields a total of 8 protein samples. These samples include one protein sample composed of conditioned medium, one protein sample comprising of ECM proteins, three protein samples derived from plasma membrane lysates and three protein samples derived from total cell lysates, following application of a three-step protein
20 extraction protocol to purified plasma membranes and total cells. Eight protein samples can thus translate into 24 large format (18 cm) gels corresponding to three overlapping 1st D gels; or 16 extra large format gels (24 cm) corresponding to two overlapping 1st D gels. Proteomics is no longer considered a single 2-D gel study. Taking advantage of the common spots in the 2nd D corresponding to overlapping
25 regions, PDQUEST software can allow "stitching together" of the constituent gels, creating the so-called "cyber gel" providing a composite map for each protein sample. The data generated can be stored in an internet-accessible 2-D PAGE database in the form of 8 submaps. Three of these submaps correspond to plasma membrane proteins representing 3-step solubilization; one of them corresponds to
30 secreted proteins; one of them corresponds to ECM proteins; and 3 of them correspond to total cell lysate proteins representing 3-step solubilization. These submaps can be linked to a master synthetic gel, a conglomerate of the submaps, representing the so-called "cyberproteome" of MPCs. Given the ability to run up to

12 IPG strips per 1st D gel (using IPGPhor) and 10 to 12 large or extra large SDS-PAGE gels per 2nd D gel run (using Hoefer DALI and Ettan DALI II, respectively), the resulting number of gels can be well within the manageable workload of one person (36). Although not easily accessible now, some innovative technological developments are on the horizon, e.g., development of fluorescence 2-D difference gel electrophoresis (DIGE), which could minimize the tedium. Unlike the current practice of running different protein samples on separate gels, and then staining and comparing the gels, DIGE technology uses matched, spectrally resolvable dyes (e.g., Cy2, Cy3 and Cy5) to label protein samples prior to 2-D separation.

10 Differentially labeled protein samples are mixed and co-separated by 2-D electrophoresis, allowing analysis of at least three samples on a single gel. Gels are scanned and proteins are subjected to image analysis using appropriate software. Alternatively, one can use a highly sensitive silver stain to visualize the proteins after electrophoretic separation. Notably, the silver stain is compatible with subsequent

15 mass spectrometry analysis.

Follow-up strategy for 2-D PAGE using the so-called ultrazoom LPG gels with narrow-range pH gradients.

Commercially available narrow-range IPG strips include pH 3.5-4.5; 4.0-5.0; 4.5-5.5; 5.0-6.0; 5.5-6.7. These are available as 18 cm and 24 cm-long strips, consequently allowing spanning of 1 pH unit over a distance of 18-24 cm and providing extraordinary resolution. By using narrow pH gradients (1pH unit) up to 10mg of protein would be loaded onto a single IPG gel strip, either by repeated sample cup application or by in-gel rehydration without incurring vertical or horizontal streaking. Employing a combination of such narrow-range overlapping IPG strips,

25 one study utilized up to 40 2-D gels for analysis of a single protein sample. The preference is not to follow such extreme approach but rather to use these gradients as a backup in situations where a functionally relevant protein is first detected by the front-end strategy but could not be studied by mass spectrometry for lack of adequate resolution or due to overlapping spots. The 24-cm long narrow IPG strips

30 can be subjected to 2nd D using correspondingly extra large slab gels (the required precast, plastic-backed gels can be purchased from Amersham Pharmacia Biotech). However, the "giant 2-DE" 30 X 40cm size gels are impractical to handle. The situations for the use of narrow range pH gradients include situations like detection

of proteins by Western blotting using anti-phosphotyrosine antibodies or Western ligand blotting using labeled IGF 1 or 2, which are probably more sensitive than silver staining. Consequently, these assays identify the functionally relevant proteins but without providing the actual identity of the individual proteins. Because the front-end strategy can at least provide the range of the phosphoprotein or the IGF-binding protein identified, on the basis of this information samples can be subjected 2-D PAGE using the appropriate ultrazoom IPG strip, which as indicated above can permit loading of several mg of protein sample. Extra large precast slab gels (26x20 cm) with plastic backing suitable for running the 24-cm long ultrazoom IPG strips and the appropriate electrophoretic system (Ettan DALI II 2 dimension electrophoresis system) that runs up to 12 of these gels are commercially available (Amersham Pharmacia Biotech).

Summary of subproteome strategy.

The subproteome approach involves: 1) Cellular fractionation involving isolation of purified MPCs. 2) Subcellular fractionation involving preparation of functionally relevant protein sets. These include: 2a) secreted proteins such as colony stimulating factors (CSFs), cytokines, etc in the conditioned media; 2b) ECM proteins such as cell adhesion molecules (CAMs), etc; 2c) plasma membrane proteins such as various receptor molecules, CAMs and components of cell signaling systems, etc; 2d) finally, whole cell lysate proteins that include some of these proteins plus cytosolic and nuclear proteins. The cytosolic and nuclear proteins can be a rich source of target proteins for phosphorylation with a regulatory function.

2-D PAGE data capture and analysis

2-D PAGE data capture and analysis can be performed using standard equipment and protocols. Silver-stained gels can be scanned using an imaging densitometer and processed with QuantOne software (Bio-Rad) whereas gels stained with fluorescent Sypro Ruby (with 450 nm in the excitation range) can be scanned using a STORM 860 gel and blot imaging system and processed with ImageQuant Solutions software (Amersham Pharmacia Biotech). A number of factors, including differences in sample preparation and loading, staining and image acquisition can influence the reproducibility of 2-D gel protein separation. Quantitative data are reported as spot volumes (integrated spot densities). In

experiments comparing replicate 2-DE patterns of the same sample or 2-DE patterns of samples from different individuals, the spot volumes in each pattern are scaled to correct for differences in the total amount of protein loaded onto each gel. These variations are compensated by accurately comparing the quantity of any spot across multiple gels. These operations can be performed using a dedicated 2-D gel analysis software, Melanie 3. This program can analyze such variations by scatter analysis and can compensate for varying staining absorption across proteins by normalizing protein expression change. Varying stain intensities and sample sizes can be compensated for by relative spots quantification. The Melanie 3 software also has the capability to merge several gel electrophoretic patterns from the same sample into a composite gel, providing fine control over the included proteins. Finally, the software can compensate for gel distortions caused by variations in protein migration through alignment of the gels.

Mass spectrometric instrumentation.

Examples of such mass spectrometers include, but are not limited to, Voyager DE Pro (Applied Biosystems, formerly Perceptive Biosystems, Inc.) and QSTAR (Applied Biosystems). Voyager DE Pro is a matrix-assisted laser desorption time-of-flight mass spectrometer (MALDI-TOF) that can be operated in a linear mode for the analysis of large biomolecules or in a reflector mode for high-resolution analysis of smaller molecules, i.e., peptides. The MALDI-TOF instrument also utilizes delayed extraction technology that results in greatly increased resolution, sensitivity and mass accuracy. This is the instrument of choice for high throughput analysis, with a capacity of up to 100 samples per sample plate. On the other hand, the QSTAR is a hybrid quadrupole-quadrupole-time-of-flight mass spectrometer. Samples are introduced in solution and are ionized by electrospray. For samples requiring the highest sensitivity, Dr. Jackson utilizes a low flow rate (25 nl min⁻¹) electrospray called nanoelectrospray, typically requiring only 1-2 μ l of a solution for sample analysis. The QSTAR instrument yields data quite similar to those obtained from the MALDI-TOF instrument, except that the QSTAR data analysis is somewhat more complex due to the multiple charging of peptides by the electrospray process compared to the single charging applied to peptides on the MALDI-TOF instrument. One important additional characteristic of the QSTAR is its ability to determine structural information from sample molecules by tandem MS/MS. This is achieved by

effectively "purifying" selected molecules within the mass spectrometer's first quadrupole section. For analysis of peptides produced by tryptic digestion, a single MS experiment is initially performed to determine the masses of components present in the mixture. Next, MS/MS experiments are carried out to select specific peptides for *de novo* amino acid sequence determination. Typically 2 µl of peptide mixture is sufficient for determining the sequences of ten to twelve peptides.

Mass spectrometric analysis by MALDI

The scheme for mass spectrometric analysis of in-gel tryptic digests of proteins for the purpose of protein identification consists of several steps. First, the peptides extracted from the gel must be cleaned and concentrated. The cleanup is necessary to remove residual detergent and other non-peptide materials that can interfere with the analysis of the tryptic peptides. This step involves binding of the peptides to a Microcon-SCX adsorptive microconcentrator. This is a cation exchange membrane held within a microcentrifuge device. At low pH, the peptides bind to the negatively charged membrane, while uncharged or negatively charged molecules pass through. After a brief wash, the peptides are eluted from the membrane in two 25-µl steps of 1.5 N ammonium hydroxide in 1:1 methanol/water. The samples are then speed-vac dried for 10 minutes, and fresh solvent is added for additional treatment to concentrate the sample prior to MS analysis. Initially, all samples can be analyzed by MALDI-TOF MS. For this analysis, the sample from the Microcon-SCX elution can be dissolved in 0.1% trifluoroacetic acid (TFA) in water and loaded on a ZipTipC 18 Pipette tip. The tip is then washed with the same solution and the peptides are then eluted directly onto the MALDI-TOF sample plate with 2 µl matrix solution (cyano-4-hydroxy-cinnamic acid, 10 mg/ml in 0.1% TFA in 1:1 acetonitrile/water). The spotted sample is dried at room temperature for at least five minutes before the sample plate is loaded in the instrument. The instrument calibration is performed externally by the addition of a calibration mixture to the sample plate. Samples are calibrated internally if the known tryptic autodigestion peptides are observed in the sample. This can be used as long as the specific type of trypsin used in the proteolytic digestion step is known. After data collection, the data can be further processed in two ways. First, the data can be treated by noise reduction software and second, it can be deisotoped. Software for both operations of these programs are standard features of the Data Explorer system provided with the

Voyager DE Pro mass spectrometer. The obtained peptide mass data can be subjected to peptide fingerprint analysis utilizing one of the protein database search sites on the Internet, such as Mascot or MS-Fit. While each of these search sites has access to several databases, one can initially select either OWL or NCBI nr. One
5 can search the database with a standard set of criteria without using a species filter. The practice is to select three variable modifications to allow for conversion of peptide N-terminal glutamine to pyroglutamate, and oxidation of methionine residues; allowing for up to one missed cleavage. Neither the protein MW nor the PI can be used as a search parameter (these, however, can be used for subsequent
10 validation of the matched protein). Also important is that expected peptide masses of known potential "contaminants" such as keratin and trypsin can be excluded from analysis. Finally, the peptide mass tolerance can be set to ± 0.15 Da relative to the monoisotopic MW of the singly charged peptide ion. Positive database hits are scored with a MOWSE number. The higher the number of hits the greater the
15 confidence level. The database search algorithm relates the significance level for a given search. If a high MOWSE score is obtained indicating an unambiguous match, one can consider the protein positively identified, otherwise the sample can be subjected to analysis by use of the QSTAR mass spectrometer.

Mass spectrometric analysis by Nano ESI MS/MS.

20 Samples that require analysis utilizing the QSTAR, following cleanup by Microcon-SCX adsorptive microconcentrator, can be concentrated by binding the peptide mix to a small amount of POROS R12 reversed-phase C18 chromatographic support packed into a nanopurification capillary. The packed capillary column volume is ~ 10-15 nl. The sample, dissolved in 10- μ l of 5% acetic acid in water, is
25 applied to the capillary by use of a ten- μ l gel loading pipette tip. A brief centrifugation forces the liquid down the capillary so that the peptides can bind to the support. The support is then washed with 10-15 μ l of 0.5% acetic acid in 1:50 methanol/water. The peptides are eluted from the purification capillary into a nanospray capillary by the addition of 2 μ l of 0.5% act id in 1:1 methanol/water followed by brief
30 centrifugation with the nanospray capillary stacked just below the purification capillary in a micropurification holder (MDS Protana). Initially, data for a single MS run is collected. The peak masses are labeled and peptides are selected for potential MS/MS sequencing by locating those that appear to be doubly charged.

Most peptides resulting from a tryptic digest can have a significant doubly charged form, which is ideal for MS/MS sequencing. The first quadrupole of the QSTAR is tuned to pass a 2 Dalton window for the pre-selected doubly charged peptide ions, one at a time, for fragmentation by collision with low-pressure argon gas in the second quadrupole. Collision energy is adjusted for each peptide to obtain the best possible MS/MS spectra. Data are collected long enough to get good quality spectra. After MS/MS spectra are collected for all selected peptides, the data are manually interpreted. Internet protein database searches are performed similar to that for MALDI-TOF peptide fingerprint, except that the search is a partial amino acid sequence search with mass information (i.e., Mascot, employing Sequence Query format). The search criteria cannot screen for a species or a protein MW or PI (which, however, can be used for subsequent validation of the protein matched). Also important is that expected peptide masses of known potential "contaminants" such as keratin and trypsin can be excluded from MS/MS analysis. One missed cleavage can be allowed and two variable modifications can be selected, carbamidomethylation of cysteine and oxidation of methionine. The tolerance of the peptide monoisotopic mass can be set to $\pm 1-0.3$ and the MS/MS tolerance can be set at $\pm 1-0.2$. This type of search generally requires only two or three peptide sequences consisting of three of the amino acids per peptide to obtain a statistically significant match (a high MOWSE score). Once a match is identified, a list of the matched peptide's theoretical MS/MS fragments can be generated to compare with the observed fragments to further confirm the correctness of the match.

Establishment of large-format 2-D PAGE protein maps for MPCs derived from normal BM.

The normal cell samples include, A) Untreated normal MPCs; B) Normal MPCs treated with TNF α ; C) Normal MPCs treated with TNF- α and IL-4. Each cell sample can generate a total of 8 protein samples, 1) culture supernatants/secreted proteins (1 protein sample); 2) extracellular matrix (ECM) proteins (1 protein sample); 3) plasma membrane proteins solubilized using a three-step differential extraction protocol employing conditions of progressively increasing solubility (3 protein samples); 4) whole cell lysate proteins similarly solubilized using a 3-step differential extraction protocol (3 protein samples). Each protein sample can generate 3 large format 2 D gels (corresponding to 3 medium-range, overlapping

IPG gradient gels, pH 3-6; 5-8; 7-10). This means each cell sample can generate 24 large format 2 D gels, leading to generation of at least 72 large format gels for analysis of normal MPCs. To account for duplicate or triplicate samples, the gel number falls in the range of 200-300.

5 **Establishment of large-format 2-D PAGE protein maps for MPCs derived from BM involved with representative pre-leukemic and leukemic conditions.**

The disease-associated MPCs include those from MDS, CML, AML, CLL, ALL, and MM. As above, each MPC sample can generate 24 large-format 2 D gels. With 6 such diseases being studied, the gel number can reach 144. To account
10 for duplicate or triplicate samples, the gel number falls within the range of 400-500. The use of IPGPhor, together with ready-made IPG strips, permits sample in-gel re-hydration and performance of unattended IEF overnight by adding automation to the 2-D procedure.

Using high-resolution proteomics and with the added power of high-
15 throughput robotics, identify on a larger (semi-comprehensive) scale the MPC proteins that are differentially expressed in conditions that simulate pre-leukemic bone marrow (following stimulation with different cytokines); and in actual pre-leukemic disorders (MDS) as well as in overt leukemias (CML, AML, CLL, ALL, MM).

20 A robotically guided system facilitates excision of protein spots (by a spot cutter or picker) from 2-D PAGE gels, transfer of protein samples to 96-well microplates, and automated protein digestion in the microwells. Such a system reduces the time and labor relative to manual procedures and provides high throughput while minimizing keratin contamination from human skin, a frequent
25 problem in proteomics research. The preferred method is to excise all spots from a gel but to process only the spots of interest, storing the remaining excised proteins frozen at -70°C for a later use. The robotic components can include MALDI slide spotter in addition to an automated protein spot picker and digestion station.

Example 8

30 **Methods**

The present study involved microarray analysis of 23 samples and a corresponding number of chips. The samples were obtained from 4 normal healthy adult human subjects, consisting of mixtures of unfractionated stromal cells

(collective USCs or cUSCs, 8 samples), Percoll gradient-purified MPCs (collective MPCs or cMPCs, 5 samples) and single-cell MPCs (sMPCs, 10 samples) obtained by laser-capture microdissection (LCM). The study design allowed for adequate controls and replicates appropriate for a comprehensive gene expression profiling of normal BM stromal cells. The isolated single stromal cells were selected on the basis of morphology. Wright-Giemsa stained cytopsin preparation revealed characteristically large cells with a relatively irregular nucleus and cytoplasm compartmentalized into ectoplasm and endoplasm. Subsequently, applicant identified a hematoxylin stain as a substitute for Wright-Giemsa stain. The hematoxylin stain is simpler to use and provides morphologic detail sufficient to allow recognition and isolation of these cells by laser capture microdissection and does not interfere with the downstream microarray testing (see details under Materials & Methods). The photomicrographs of 10 stromal cells that have been subjected to microarray testing are shown in Figure 15. To serve as controls and facilitate comparison, applicant analyzed side-by-side 8 samples of unfractionated stromal cells that are "contaminated" by up to 35% macrophages and 5% hematopoietic cells (referred to collective USC, or cUSC), and 5 samples of Percoll-gradient purified stromal cells, up to 95% pure (referred to collective MPC, or cMPC to distinguish from sMPC). RNA isolated from sMPC samples was subjected to 2 rounds of amplification using RiboAmp kit (Arcturus, Inc) prior to *in vitro* transcription (IVT). In contrast, RNA samples isolated from cUSCs and cMPCs were used without amplification for IVT. The subsequent steps of microarray testing were standard for all 3 types of samples and are schematized as follows: Preparation of total RNA → generation of cDNA → preparation of ds cDNA → *in vitro* transcription into cRNA → fragmentation of cRNA → hybridization of target RNA to a microarray of known genes (Affymetrix U95Av2 oligonucleotide microarray, with 12,625 probe sets) → Signal quantification and first-tier analysis using the microarray quantification software, Microarray Suite (MAS v. 5, Affymetrix, Inc). The presence of a gene within a given a sample was determined at a detection p-value of <0.05, according to the statistical expression analysis algorithm employed by MAS v.5, and was graded absent (A), marginal (M) or present/ positive (P).

Assessment of RNA amplification method

Since single-cell microarrays are relatively novel, applicant critically reviewed the

data with respect to two important statistics that would reflect on the reliability of RNA amplification assay procedure employed before analysis involving data-mining techniques. **a) 3': 5' ratios of housekeeping control genes:** As shown in Table 9, these ratios were close to 1 in the standard unamplified samples, whereas, they were increased in the amplified samples. Although this is to be expected due to preferential amplification toward 3' end, since amplification may not proceed all the way up to 5' end, applicant wanted to exclude possible sample degradation. For reasons unclear, in the case of ACTB (beta actin), the 3': 5' ratios were highly variable across single cell MPC samples. In any event, the 3': 5' ratios in case of GAPD (glyceraldehyde 3-phosphate dehydrogenase) were relatively tight, suggesting no evidence of sample degradation. Furthermore, both GAPD and ACTB gene probes that were employed as part of the standard gene probe set yielded relatively stable signals across replicates in each sample type, which is further evidence of intactness of RNA samples targeted for microarray analysis. **b)**

Number of genes present or detected: As outlined in Table 9, the amplified single cell MPC RNA samples expectedly showed significantly lower number of genes compared to the standard RNA samples (on average 34% vs. 46% of the genes etched on the array). The fact that the number is relatively constant across single cell replicate samples is further indication of the reliability of the data.

Notwithstanding the shortcomings of the amplification procedure, it is important to bear in mind that the conclusions are based only on those stromal cell genes that are detected commonly across unamplified cMPCs and cUSCs as well as in amplified sMPCs (but do not include the genes undetected or the genes selectively detected in sMPCs).

25 Data mining and reproducibility of overall procedures

The thrust of the present invention is to identify genes that are relatively uniformly expressed across normal untreated bone marrow stromal cell samples, regardless whether they are of single cell type or collective cell samples, purified or unpurified. As detailed under Materials & Methods, GeneSpring was used to achieve the following data-analysis objectives: a) Filtering for genes reliably detected in each sample group by eliminating the genes with weak expressions that are statistically close to the background estimate. b) Filtering for genes that are active or "present" across replicates in each sample group. c) Exclusion of genes

with weak expressions from genes "present" in each sample group. d) Preparation of master stromal cell gene list by intersecting gene lists from step (c) (as shown in Figure 16). These steps have led to identification of a list of 2755 genes that are detected in at least 7 of 8 cUSC samples AND 4 of 5 cMPC samples AND 9 of 10 sMPC samples, i.e., in at least 20 of 23 stromal cell samples investigated. The main conclusions of the present report are based on this "stromal cell gene list" that is broadly representative of all 3 types of stromal cell samples investigated, and not on a gene list that is selective to sMPCs. A hallmark of the quality of microarray data can be discerned from hierarchical cluster analysis of replicates, which involves the principles of vector algebra. An array of numbers representing expression levels of a particular gene in terms of normalized signal intensity in a group of samples is considered a gene expression vector. Likewise, an array of numbers showing expression levels of a group of genes by a particular tissue sample is considered a tissue expression vector. In the case, applicants have 2755 gene expression vectors and 23 tissue or sample expression vectors. These vectors are amenable to algebraic treatment, facilitating calculation of similarity between any two gene- or tissue-expression vectors on the basis of a correlative metric or a similarity-measure employed, e.g., Euclidean angle. Grouping together of two samples on the basis of these principles signifies that they are most closely related out of all the samples in terms of their overall pattern of gene expression. Construction of a bone marrow stromal cell hierarchical tree has enabled visualization of global gene expression patterns across replicates and conditions. As shown in Figure 17, stromal cell genes that are expressed at a relatively lower level in amplified samples (sMPCs) are clustered to the left of gene tree, genes that are more strongly expressed in sMPCs are prominently figured in the middle of gene tree, and genes that are expressed approximately at same level as in unamplified samples (cMPCs and cUSCs) are clustered to right of gene tree. Even more important as noticeable on the sample or experiment tree, hierarchical clustering segregated the members of each sample type into a separate group (cMPC, cUSC and sMPC). Note within each sample type, corresponding subject replicates clustered together with minor exceptions. This is a reflection on the reproducibility of the overall assay-procedures employed, which encompass a variety of stages and steps in addition to target RNA amplification prior to *in vitro* transcription (see Materials & Methods for details).

Finally, it is important to keep in mind that the measured level of a transcript following amplification does not necessarily provide a quantitative estimate of gene expression, but only provides a qualitative indication that the gene is transcriptionally active, which by itself is sufficient grounds for the conclusions arrived at in the present report. As shown in Figure 18, the expression of genes within the stromal cell gene list ranges from 0.2 to 6 (on the log scale) in unamplified samples (cMPC and cUSC) and from 0.02 to 36 in amplified samples (sMPC), thus showing much greater variability in the amplified samples. For illustration purpose, the coloring of gene expression curves (following the linear color bar shown on the right) was based on the gene expression pattern of a particular single-cell sample, SCA1. Note that the genes that are detected at a low level in this sample (as indicated in blue) are not necessarily expressed at a low level in unamplified samples (as read by the log scale on Y-axis). In fact, a significant number of them are expressed at a high level in the unamplified samples. This finding together with the observation that amplified samples detected about 34% of genes as opposed to unamplified samples detecting about 46% of genes tested (Table 9), strikes a cautious note that some genes do not amplify at all by the method used, and other genes amplify to a sufficient degree to be detectable (shown in blue), while some other genes amplify to a degree equal to (in yellow) or surpassing (in red) the amounts in the collective samples. (The curve shown in white is the housekeeping gene, GAPD.) The statistical algorithm as implemented in the latest version of Microarray Analysis Suite (MAS v.5) determined that a gene within a given sample as positive, regardless of grading. To overcome the limitations of the amplification procedure employed, applicant focused only on genes that were positive in at least 20 of the 23 stromal cell samples investigated.

A stromal cell gene list is expected to be representative of typical stromal cell gene expression profile. Such master gene list forms the basis for derivation of all other stromal cell gene lists, organized in accordance with lineage or functional categories. As depicted in Figure 19A & 19B, and listed in Tables 10 through Table 17, that were prepared according to lineage/ functional assignment, the findings show that isolated single cells simultaneously express genes associated with diverse mesenchymal cell lineages, namely osteoblasts, muscle cells, fibroblasts, adipocytes, epithelial cells, endothelial cells, nerve cells and glial cells,

providing confirmation of the existence of a pluridifferentiated progenitor cell type. By definition the stromal cell genes are present in at least 4 of 5 collective MPC samples AND 7 of 8 collective USC samples AND 9 of 10 single cell MPC samples; consequently, they are active in at least 20 of 23 samples tested, representing a
5 typical genomic profile of stromal cells. The following gene lists are sub-lists of the master stromal cell gene list consisting of 2,755 genes. The stromal cell gene list contains a number of genes that are capable of causing endothelial differentiation and vasculogenesis within the marrow microenvironment; however, these genes themselves are not necessarily endothelial cell markers. In fact, stromal cells
10 express a gene, EDF1, the expression of which inversely correlates with endothelial cell differentiation within the stromal cells. Of the 67AFFX control genes present on the U95A v2 chip, 22 genes are detected in at least 7 of 8 cUSC samples, 24 genes are detected in 4 of 5 cMPC samples and 19 genes are detected in at least in 9 of 10 sMPC samples. Thirteen of these genes are present in the stromal cell gene list,
15 i.e., in 20 of the 23 samples investigated.

As evident from these gene lists, note that an isolated single stromal cell simultaneously expresses transcripts for epithelial and neuroectodermal cell types as well. Departing even further from the initial thinking, the findings add to the evidence that the MPCs within the Dexter system might represent a form or stage of
20 the progenitor cell that is common to nonhematopoietic and hematopoietic cells. As depicted in Figure 20, and listed in Table 18 through Table 21, the isolated single stromal cells express transcripts that are typical of hematopoietic cells, in particular precursor B cells. That BM stromal cells express CD10 (CALLA) is not novel since BM stromal cells as well as endometrial stromal cells and normal breast
25 myoepithelial cells are known to express CD10. However, the expression of CD19, CD79A and immunoglobulin enhancer binding factors E12/E47 (proto-oncogene TCF3) by BM stromal cells is unforeseen, and forms the basis for postulating the existence of a common progenitor with B cell lineage. B-cell progenitors typically display the phenotype, (CD45 +/-, CD34 +/-, CD20 +/-), (CD10 +, CD19 +, CD79A +,
30 HLA-Dr +), which as reported here is also displayed by isolated single stromal cells at least at the transcriptome level.

CD45 positivity by cMPC and cUSC samples is attributable to coexisting or contaminating hematopoietic cells in these samples as evidenced by

concurrent positivity for myelomonocytic markers CD13, CD33 and CD14 (Table 21). However, a similar explanation cannot hold true in case of isolated single stromal cells. The protein products or transcripts for CD45 and CD19 are most likely present in stromal cells at a basal level that is beyond the detection limits of conventional techniques, e.g., immunocytochemistry and Northern blotting, respectively. Conceivably, two rounds of amplification prior to IVT sufficiently increased their transcript levels to be detected by microarray analysis. In fact, the CD45 levels were several-fold lower in cMPC and cUSC compared to CD45 levels in sMPC, and CD19 was undetectable in unamplified samples. Finally, note that CD45 and CD19 are not isolated examples in this regard since applicant has identified at least 200 other genes that are uniquely present across sMPC samples but undetectable in cMPC and cUSC (Figure 16).

The issue of stromal cell – B cell connection

Although no anlage of Bursa of Fabricius exists in mammals, bone marrow is generally regarded as the site of B-cell generation. While the Dexter type stromal cell culture system was devised for investigation of hematopoiesis, specifically myelopoiesis (see Introduction), Whitlock and Witte developed another system for the study of B-lymphopoiesis. Whitlock-Witte cultures, like Friedenstein cultures, are grown in the absence of hydrocortisone and horse serum. When stromal cell layers in W-W cultures are seeded with fresh bone marrow as a source of B cell precursors or with purified B cell precursors, the latter then differentiate into mature B cells. On the other hand, although Dexter cultures do not promote B cell maturation, Dexter cultures do contain B cell precursors, which upon switching of culture conditions from those of Dexter to Whitlock-Witte, differentiate into mature B cells. While BM stromal cells in one form or another are definitely known to support B-lymphopoiesis, it has not been so clear as to whether stromal cells actually give rise to B-cell precursors. Evidence for a progenitor cell common to stromal cells and hematopoietic cells has been coming to light piecemeal in the form of isolated reports. 1) Singer JW et al in 1984 in the course of investigating bone marrow cultures from human patients with clonal myeloproliferative disorders showed that the nonhematopoietic stromal cells were derived from the same clonal progenitors that were involved by the hematopoietic neoplasm, as revealed by G6PD marker analysis. 2) Huss R et al in 1995 in the course of investigating a canine BM stromal

cell line showed that the adherent stromal cells had "turned" into nonadherent hematopoietic cells, especially when the latter were cultured in presence of stem cell factor. 3) Pessina et al in 1997 showed that a particular murine stromal cell line upon stimulation with bFGF, expressed a B-cell phenotype, including CD45R and surface immunoglobulin. Although not by design, applicant shows for the first time that isolated single stromal cells express transcripts that are typically associated with hematopoietic lineage, namely, CD45 and CD19, as well as relevant proto-oncogenes and transcription factors. These results are strongly supportive of the existence of a progenitor cell common to bone marrow stromal cells and hematopoietic cells, particularly the bone marrow-derived (B) lymphocytes. Note that the study involves no feeder cells, no embryonic stem cells, no cell lines and no colonies of cells. Contrasting with the existing literature, the present study embarks on a new path of investigation entailing gene expression analysis of single, primary, normal human stromal cells that suggest a broad capacity for multilineage differentiation. On this model, progenitor cells express genes that are characteristic of any of the lineage fates that these cells are capable of adopting.

Perspective on pluripotentiality vs. pluridifferentiation

The present investigation involves isolated single stromal cells, consisting of 10 cells from 4 different individuals (Figure 15). The cell culture system has been earlier characterized at light microscopic level, ultrastructural level and by karyotypic analysis, showing no evidence to suggest the artifacts discussed. Spontaneous cell fusion most likely involves monocytes/macrophages, forming multinucleated giant cells; however applicant observed no expression of myelomonocytic marker genes by isolated single stromal cells (Table 12). Keep in mind that the readout of *in vivo* transdifferentiation studies involves localization of different lineage cells in different tissues or organs; such a situation only requires fusion between two cell types (one donor cell and one recipient cell) for the investigators to believe the artifact as transdifferentiation. In contrast, applicant shows here presence of genes for a variety of cell-lineages simultaneously within the same cell. The probability of an array of different cell types fusing into one cell which then masquerading as a pluridifferentiated cell, and that too happening with 10 of 10 cells investigated, is in the opinion close to zero. There has never before been an opportunity to assess the extent of differentiation within these multipotential

progenitor cells in molecular terms at the single-cell level. Theoretically, a) A stem cell can directly become a terminally differentiated cell, or b) A stem cell can enter a phase of multilineage differentiation prior to becoming a single-lineage, mature cell. To the knowledge, this study is the first systematic attempt to answer these questions at the single cell level by using the marrow stromal cells as a model. Although numerous forward-looking reviews exist on the topic of single-cell genomics, only a rare report is available on the actual application of this technology. Applicant has applied this frontier technology to show that a phase of multilineage differentiation indeed exists at least in Dexter-type stromal cells. Pluripotentiality of the bone marrow mesenchymal stromal cells in terms of their ability to become muscle cells, bone cells, fat cells and fibroblasts under select culture conditions has been described by other investigators. Instead of documenting another example of the phenomenon per se, the results provide an independent validation of the studies on transdifferentiation by casting light at the molecular basis of cellular plasticity. Finally, to borrow a concept from the clinical practice setting, a morphologically "poorly" differentiated neoplasm expressing hematopoietic markers is classified as a leukemia/ lymphoma and treated as such. Similarly, a morphologically "undifferentiated" neoplasm marking for epithelial gene expression is diagnosed as a carcinoma and treated according to the protocols designed for a carcinoma. It is in this sense that applicant uses the term "pluridifferentiated" as opposed to "pluripotent" to characterize the BM stromal cells. Notwithstanding the semantics, applicant shows that the pluripotent stromal cells are pluridifferentiated, at least at the molecular level.

Conclusions

The findings of the present study clarify the on-going controversy as to the co-existence of multiple stromal cell types vs. one stromal cell type with co-expression of multiple phenotypes within the Dexter system of BM stromal cell cultures. An isolated single stromal cell from these cultures simultaneously expresses an array of phenotypes, i.e., osteoblasts, fibroblasts, muscle cells, adipocytes, epithelial cells, endothelial cells, neural cells/glia cells and even hematopoietic cells, in particular, B-lymphoid progenitors, thus documenting its wide differentiation repertoire. The significance of the findings is three-fold, 1st) They validate the hypothesis that the BM stromal cells express a pluridifferentiated

progenitor cell phenotype, providing insight into the molecular basis of cellular plasticity as well as establishing the utility of single-cell genomics, 2nd) They provide evidence for a common progenitor for mesenchymal progenitors and BM-derived (B) lymphoid progenitors, 3rd) By establishing a comprehensive phenotype of cultured
5 bone marrow stromal cells at single cell level for the first time, the findings pave the road for ultimate identification and investigation of these cells in fresh samples of marrow, normal as well as diseased, in which they occur at a low frequency.

Materials & Methods

Second-tier data-analysis/ data mining

10 The microarray data outputted by MAS v.5 (in the form of tab delimited text files) were imported into GeneSpringTM software version 4.2.1 (Silicon Genetics, Redwood City, CA). Following instructions accompanying GeneSpring, each gene was normalized to itself (per-gene normalization) by using the median of the gene's expression values over all the samples of an experimental group (or groups) and
15 dividing each measurement for that gene by the corresponding median value, assuming that it was at least 0.01. The ratios were then log transformed to base e. No per-sample normalization was performed in GeneSpring since it was already accomplished as part of MAS v.5 analysis. The purpose of the above data transformations, including scaling and normalization, was to remove systematic error
20 within and across conditions or experimental groups prior to further analysis. GeneSpring was used to achieve the following data-analysis objectives. **a) Filtering for reliably present genes by eliminating the genes with weak expressions that are statistically close to the background estimate.** As per the instructions accompanying GeneSpring, random error was estimated from control strength or
25 median measurement level using the two-component global error model of Rocke-Lorenzato that assumes variability between replicates as being similar for all genes showing similar measurement level. The formula for the error model of normalized expression levels can be written as follows:

$$S(norm)^2 = a^2/C^2 + b^2$$

30 Where, S = standard error of normalized expression data, a & b are the two error components, a = an absolute or fixed error component impacting at lower measurement values, b = a relative or proportional error component impacting at higher measurement levels, and C = control strength. According to the

manufacturer, a curve is fitted for each group of replicates, with standard error of normalized data on Y-axis vs. control strength on X-axis. At lower end of control strength, the normalized standard error would be high and as the control strength increases, the standard error would decrease reaching a point where the curve flattens and data become more reliable. Control strength for each condition or sample group at which the above-referred two error components contribute equally, was calculated as follows, for collective MPCs, $C = 128.68$; collective USCs, $C = 253.52$; single-cell MPCs, $C = 348.32$. Each condition was filtered for genes expressing signals greater than the respective control strength, thus eliminating the genes with weak expressions from each group. Note 7,196 genes (out of 12,625 gene probes tested) passed the restriction in case of cMPCs, 7,287 genes in case of cUSCs and 5,937 in case of sMPCs. Corresponding gene lists were created. ***b) Filtering for genes "present" across replicates in each sample group.*** GeneSpring's "Add data file restriction" feature was used to prepare the respective lists of genes that were present (or expressed or active) in a least 7 of 8 cUSC samples, 4 of 5 cMPC samples, and 9 of 10 sMPC samples. Note 5,204 genes (out of 12,625 gene probes tested) passed the restriction in case of cMPCs, 4,763 genes in case of cUSCs, and 3,124 genes in case of sMPCs. Corresponding gene lists were created. ***c) Exclusion of genes with weak expressions from genes "present" in each sample group.*** Respective gene-lists for each sample group from steps (a) and (b), were intersected via Venn diagrams. Note 5,204 genes passed the restriction in case of cMPCs, 4,761 genes in case of cUSCs, and 3,124 genes in case of sMPCs, which are almost identical to the numbers obtained as under step (b), except for a difference of 2 genes in case of cUSCs, thus providing no significant improvement in restricting the data beyond under step (b). This is a reflection of the high stringency of the criterion employed under step (b). The 2 genes in case of cUSCs that passed the restriction under step (b) but failed the combined restriction under step (c) did show weak expressions (raw signals ranging, 142-331). Corresponding gene lists were created. ***d) Preparation of master stromal cell gene list.*** Respective gene lists for the three sample groups from step (c) were intersected via Venn diagrams, resulting in identification of a list of 2,755 genes that are uniformly present or expressed in at least 20 of 23 stromal cell samples investigated. The stromal cell gene list thus arrived at contained genes that

are representative of diverse mesenchymal lineages. Parenthetically, intersecting of gene lists corresponding to the three sample groups from step (b) resulted in a stromal cell gene list consisting of 2,756 genes, thus differing by 1 gene from the "official" master stromal cell gene list. **e) Two-way hierarchical clustering of 2755 stromal cell genes based on expression profiles in 23 stromal cell samples.**

Only the data that were "cleaned up" of genes with weak expressions as outlined under step (a) were used for hierarchical clustering. This necessitated further processing of data in Microsoft Access prior to analysis by GeneSpring. Note that the data for each individual sample as outputted by MAS v.5 contained probe IDs, quantitative and qualitative data, as well as other information such as annotations and are readily recognizable by GeneSpring. In contrast, the gene list, resulting from step (a), contained only probe IDs and could not contain the data associated with each individual sample and was not recognizable by GeneSpring for inputting as part of an Experiment. Therefore, the microarray data for each group of individual samples (in Excel format) as well as the corresponding gene list for that group from step (a) (also in Excel format) were imported into an Access database. The genes that did not pass the test under step (a) were deleted from the microarray data for each individual sample by querying and intersecting with the appropriate post-clean-up gene list. The resulting data files were saved first as Excel files, then re-saved as tab delimited text files and then imported into GeneSpring. Per-gene normalization and log transformation were applied as described above. "Gene Tree" and "Experiment Tree" were constructed by applying a method similar to that of Eisen et al as implemented in GeneSpring and by using the stromal cell gene list and the following parameters: standard correlation as similarity measure; a minimum distance of 0.001; and a separation ratio of 0.5 in case of Gene Tree and 1.0 in case of Experiment Tree. **f) Preparation of stromal cell gene lists as relevant to different cellular phenotypes and/ or functions.** The gene lists associated with distinct mesenchymal cell lineages or phenotypes, i.e., osteoblasts, fibroblasts, muscle cells and adipocytes, etc, were prepared using a combination of methods. These include 1) Visually inspecting the entire stromal-cell gene list for relevant key words. 2) Directly searching the stromal cell gene list by using key words of interest via "Advanced Find Genes" feature under Edit menu in GeneSpring and by selecting "Search Only Current Gene List". 3) Intersecting the stromal cell gene list with gene

lists of interest from Gene Ontology lists, e.g., list of oncogenes, via Venn diagrams.

g) Visualization of gene-expression plots. The expression pattern of a gene across a given group (or groups) of samples of interest was pictured via Gene Inspector window, utilizing desired display options.

5 Throughout this application, various publications, are referenced by author and year. Full citations for the publications are listed below. The disclosures of these publications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art to which this invention pertains.

10 The invention has been described in an illustrative manner, and it is to be understood that the terminology which has been used is intended to be in the nature of words of description rather than of limitation.

 The preceding descriptions of the invention are merely illustrative and should not be considered as limiting the scope of the invention in any way. From the
15 foregoing description, one of ordinary skill in the art can easily ascertain the essential characteristics of the instant invention, and without departing from the spirit and scope thereof, can make various changes and/or modifications of the inventions to adapt it to various usages and conditions. As such, these changes and/or modifications are properly, equitably, and intended to be, within the full range of
20 equivalence of the following claims.

Tables

Table 5

Summary of bone marrow stromal cell samples targeted for microarray analysis with an outline of the corresponding indicators of assay quality performance

| | Unfractionated stromal cells (Collective USC, 8 replicates) | Percoll gradient-purified stromal cells (Collective MPC, 5 replicates) | LCM-dissected single cell samples (Single Cell MPC, 10 replicates) |
|--|--|--|---|
| Subject A | UNFR A | MPC A | SCA1, SCA2, SCA3 |
| Subject B | UNFR B, UNFR B R1, UNFR B R2 | MPC B R2 | SCB1, SCB3 |
| Subject C | UNFR C R1, UNFR C R2 | MPC C R2 | SCC1, SCC3 |
| Subject D | UNFR D R1, UNFR D R2 | MPC D R1, MPC D R2 | SCD1, SCD2, SCD3 |
| Amplification of RNA before IVT | No | No | Two rounds |
| Number of genes present (% of 12,625) | Mean: 46.63 SD: 5.95 | Mean: 46.54 SD: 3.66 | Mean: 33.93 SD: 3.94 |
| 3':5' ratio, GAPD M33197 (Probe used as part of housekeeping control gene probe set) | Mean: 0.89 SD: 0.33 | Mean: 1.23 SD: 0.53 | Mean: 6.76 SD: 2.97 |
| GAPD signal 35905_s_at (Probe used as part of standard gene probe set) | Mean: 130,723 SD: 36,990 | Mean: 164,593 SD: 40,204 (See Figure 5B.) | Mean: 43,235 SD: 14,413 (See Figure 5B.) |
| 3':5' ratio, ACTB X00351 (Probe used as part of housekeeping control gene probe set) | Mean: 1.44 SD: 0.60 | Mean: 2.29 SD: 1.57 | Mean: 57.92 SD: 67.82 |
| ACTB signal 32318_s_at (Probe used as part of standard gene probe set) | Mean: 86,104 SD: 18,458 | Mean: 100,383 SD: 28,427 (See Figure 5B.) | ♦ Mean: 4,445 ♦ SD: 884 (See Figure 5B.) |

Footnote to Table 5

Replicate samples shown under each sample type as indicated correspond to each subject. The replicates of collective USC and collective MPC represent cell-culture or biological replicates of stromal cells grown in parallel flasks (instead of technical replicates). We started with 27 samples of which 2 collective MPC samples and 2 single cell MPC samples failed either at the test chip stage or produced unusual results in terms of the number of genes present and/or 3':5' ratios and were therefore excluded as outliers. Only those samples that were targeted for the data mining analysis are represented in this table. The statistics shown (means and SDs) were based on the number of sample replicates indicated in the top row of the table except for ACTB-signal for single cell MPCs (noted in the table by ♦), which were based on 9 replicates instead of 10.

Table 6: Osteoblast/ bone cell/ bone disorders (Seshi, B)

| Systematic | Common | Genbank | Description | Phenotype/ Function |
|------------|--------|----------|---|--|
| 38112_g_at | CSPG2 | X15998 | chondroitin sulfate proteoglycan 2 (versican) | OMIM Notes: c-fos restricted to perichondrial growth regions of the cartilaginous skeleton. |
| 38111_at | CSPG2 | X15998 | chondroitin sulfate proteoglycan 2 (versican) | |
| 38126_at | BGN | J04599 | biglycan | |
| 36976_at | CDH11 | D21255 | cadherin 11, type 2, OB-cadherin (osteoblast) | |
| 37315_f_at | BM036 | AI057607 | uncharacterized bone marrow protein BM036 | |
| 36996_at | OS-9 | U41635 | amplified in osteosarcoma | |
| 41202_s_at | OS4 | AF000152 | conserved gene amplified in osteosarcoma | |
| 671_at | SPARC | J03040 | secreted protein, acidic, cysteine-rich (osteonectin) | |
| 2087_s_at | CDH11 | D21254 | cadherin 11, type 2, OB-cadherin (osteoblast) | |
| 1916_s_at | c-fos | V01512 | Human cellular oncogene c-fos (complete sequence). | |
| 1915_s_at | c-fos | V01512 | Human cellular oncogene c-fos (complete sequence). | ?Osteoporosis, involutional; Rickets, vitamin D-resistant |
| 1388_g_at | VDR | J03258 | vitamin D (1,25- dihydroxyvitamin D3) receptor | |
| 1451_s_at | OSF-2 | D13666 | osteoblast specific factor 2 (fasciclin I-like) | |
| 32094_at | CHST3 | AB017915 | carbohydrate (chondroitin 6) sulfotransferase 3 | Ehlers-Danlos syndrome, type VIIA2; Marfan syndrome, atypical; Osteogenesis imperfecta, 3 clinical forms, 166200, 166210; Osteoporosis, idiopathic |
| 32307_s_at | COL1A2 | V00503 | collagen, type I, alpha 2 | |
| 32306_g_at | COL1A2 | J03464 | collagen, type I, alpha 2 | |

| | | | | |
|------------|--------|----------|---|--|
| 32305_at | COL1A2 | J03464 | collagen, type I, alpha 2 | Ehlers-Danlos syndrome, type VIIA2; Marfan syndrome, atypical; Osteogenesis imperfecta, 3 clinical forms, 166200, 166210; Osteoporosis, idiopathic |
| 34321_i_at | GS3786 | D87120 | predicted osteoblast protein | |
| 34342_s_at | SPP1 | AF052124 | secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1) | |
| 34763_at | CSPG6 | AF020043 | chondroitin sulfate proteoglycan 6 (bamacan) | |
| 222_at | EXT1 | S79639 | exostoses (multiple) 1 | Chondrosarcoma; Exostoses, multiple, type 1 |
| 36822_at | WAC | U51334 | WW domain-containing adapter with a coiled-coil region | Chondrosarcoma, extraskeletal myxoid |
| 41202_s_at | OS4 | AF000152 | conserved gene amplified in osteosarcoma | |
| 40790_at | BHLHB2 | AB004066 | basic helix-loop-helix domain containing, / transcription factor class B, 2; OMIM Notes: Alternative title, DEC1, expressed primarily in differentiated chondrocytes. | |

Table 7: Muscle/ muscle disorders (Seshi, B)

| Systematic | Common | Genbank | Description | Phenotype/ Function |
|----------------------|----------------|--------------------|---|---|
| 38251_at 38923_at | MLC1SA FRG1 | AI127424 L76159 | myosin light chain 1 slow a FSHD (Facioscapulohumoral muscular dystrophy) region gene 1 | |
| 37012_at | CAPZB | U03271 | capping protein (actin filament) muscle Z-line, beta | |
| 37279_at | GEM | U10550 | GTP binding protein overexpressed / GTPase in skeletal muscle | |
| 36791_g_at | TPM1 | M19267 | tropomyosin 1 (alpha) | Cardiomyopathy, familial hypertrophic, 3 |
| 36790_at | TPM1 | M19267 | tropomyosin 1 (alpha) | Cardiomyopathy, familial hypertrophic, 3 |
| 36792_at | TPM1 | Z24727 | tropomyosin 1 (alpha) | |
| 36678_at | TAGLN2 | D21261 | transgelin 2 | |
| 36641_at | CAPZA2 | U03851 | capping protein (actin filament) muscle Z-line, alpha 2 | |
| 36931_at | TAGLN | M95787 | transgelin | |
| 37631_at | MYO1E | U14391 | myosin IE | |
| 41439_at | MYO1B | AJ001381 | myosin IB | |
| 40910_at | CAPZA1 | U56637 | capping protein (actin filament) muscle Z-line, alpha 1 | / binds barbed ends of actin filaments |
| 41187_at | MLC-B | U26162 | myosin regulatory light chain | |
| 41747_s_at | MEF2A | U49020 | Human myocyte-specific enhancer factor 2A (MEF2A) gene, last coding exon, and complete cds. | |
| 41738_at | CALD1 | M64110 | caldesmon 1 | |
| 41739_s_at | CALD1 | M83216 | caldesmon 1 | |
| 39791_at | ATP2A2 | M23114 | ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 | Darier disease |
| 39790_at | ATP2A2 | M23115 | ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 | Darier disease |
| 39378_at | BECN1 | U17999 | beclin 1 (coiled-coil, myosin-like BCL2 interacting protein) | |
| 40488_at | DMD | M18533 | dystrophin (muscular dystrophy, Duchenne and Becker types) | Becker muscular dystrophy; Cardiomyopathy, dilated, X-linked; Duchenne muscular dystrophy |
| 40438_at | PPP1R12A | D87930 | protein (myosin) phosphatase 1, regulatory (inhibitor) subunit 12A | OMIM Notes: Regulates the interaction of actin and myosin downstream of the guanosine triphosphatase Rho. |

| | | | | |
|------------|---|----------|--|---|
| 32838_at | smooth muscle myosin heavy chain isoform SMem | S67247 | Homo sapiens cDNA: FLJ23324 fis, clone HEP12482, highly similar to HUMMYOHC Human nonmuscle myosin heavy chain-B (MYH10) mRNA | |
| 32755_at | ACTA2 | X13839 | actin, alpha 2, smooth muscle, aorta | |
| 33994_g_at | MLC | M22919 | Human nonmuscle/smooth muscle alkali myosin light chain gene, complete cds. | |
| 33447_at | MLCB | X54304 | myosin, light polypeptide, regulatory, non-sarcomeric (20kD) | |
| 32313_at | TPM2 | M12125 | tropomyosin 2 (beta) | OMIM Notes: Fibroblast and muscle isoforms result from alternative splicing on exons 6 and 9. |
| 35362_at | MYO10 | AB018342 | myosin X | |
| 34306_at | MBNL | AB007888 | muscleblind-like (Drosophila) | |
| 36989_at | DAG1 | L19711 | dystroglycan 1 (dystrophin-associated glycoprotein 1) | |
| 40022_at | FCMD | AB008226 | Fukuyama type congenital muscular dystrophy (fukutin) | ?Walker-Warburg syndrome; Muscular dystrophy, Fukuyama congenital |
| 39031_at | COX7A1 | AA152406 | cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) | |
| 35729_at | MYO1D | AB018270 | myosin ID | |
| 32378_at | PKM2 | M26252 | pyruvate kinase, muscle | |
| 40375_at | EGR3 | X63741 | early growth response 3; OMIM Notes: Expressed in developing muscle spindles. | |
| 1637_at | MAPKAPK3 | U09578 | mitogen-activated protein kinase-activated protein kinase 3; OMIM Notes: Expressed especially high in heart and skeletal muscle. | |
| 40399_r_at | MEOX2 | A1743406 | mesenchyme homeobox 2 (growth arrest-specific homeobox). OMIM Notes: Important regulator of myogenesis. | |
| 39565_at | BMPR1A | Z22535 | bone morphogenetic protein receptor, type IA. OMIM Notes: Alternative title, activin receptor-like kinase 3; ALK3. Expressed almost exclusively in skeletal muscle with weak expression in heart and placenta. | Polyposis, juvenile intestinal |
| 41449_at | SGCE | AJ000534 | sarcoglycan, epsilon | Dystonia, myoclonic |

Table 8: Fibroblast (Seshi, B)

| Systematic | Common | Genbank | Description | Phenotype/ Function |
|------------|---------|----------|---|---|
| 39333_at | COL4A1 | M26576 | Human alpha-1 collagen type IV gene, exon 52. | |
| 37037_at | P4HA1 | M24486 | procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I | |
| 36666_at | P4HB | M22806 | precursor; Human prolyl 4-hydroxylase beta-subunit and disulfide isomerase (P4HB) gene, exon 11, clones 6B-(1,3,5,6). | |
| 41504_s_at | MAF | AF055376 | v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) | |
| 39757_at | SDC2 | J04621 | syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan) | |
| 39945_at | FAP | U09278 | fibroblast activation protein, alpha | OMIM Notes: Expressed in fetal normal mesenchymal tissues and stromal fibroblasts within common types of epithelial tumors. |
| 32835_at | MAFF | AA725102 | v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian) | |
| 32535_at | FBN1 | X63556 | fibrillin 1 (Marfan syndrome) | Ectopia lentis, familial; Marfan syndrome; MASS syndrome; Shprintzen-Goldberg syndrome |
| 2057_g_at | FGFR1 | M34641 | fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome) | Jackson-Weiss syndrome; Pfeiffer syndrome |
| 1380_at | FGF7 | M60828 | fibroblast growth factor 7 (keratinocyte growth factor) | OMIM Notes: May play a role in mesenchymal stimulation of epithelial cell proliferation. |
| 32313_at | TPM2 | M12125 | tropomyosin 2 (beta) | OMIM Notes: Fibroblast and muscle isoforms result from alternative splicing on exons 6 and 9. |
| 31720_s_at | FN1 | M10905 | fibronectin 1 | |
| 31719_at | FN1 | X02761 | fibronectin 1 | |
| 35835_at | PDL-108 | AB019409 | periodontal ligament fibroblast protein | |
| 34390_at | P4HA2 | U90441 | procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II | |

Table 9: Adipocyte (Seshi, B, et al)

| Probe ID | Gene Name | Genbank ID | Description | OMIM Notes |
|------------|-----------|------------|---|---|
| 34378_at | ADRP | X97324 | adipose differentiation-related protein (adipophilin) / lipid-droplet binding/ adipocyte-specific | mRNA levels are induced rapidly and maximally after triggering adipocyte differentiation. |
| 40282_s_at | DF | M84526 | D component of complement (adipsin) | High level of expression in fat. |
| 33337_at | DEGS | AF002668 | degenerative spermatocyte homolog, lipid desaturase (Drosophila) | |
| 39673_i_at | ECM2 | AB011792 | extracellular matrix protein 2, female organ and adipocyte specific | |
| 39674_r_at | ECM2 | AB011792 | extracellular matrix protein 2, female organ and adipocyte specific | |
| 31504_at | HDLBP | M64098 | high density lipoprotein binding protein (vigilin) | |
| 37542_at | LHFPL2 | D86961 | lipoma HMGIC fusion partner-like 2 | |
| 36073_at | NDN | U35139 | necdin homolog (mouse)/ Prader-Willi syndrome | |
| 37122_at | PLIN | AB005293 | Perilipin (Did not meet the criteria to be included in stromal cell gene list because it was positive in 5 of 5 cMPC and 9 of 10 sMPCs, but only 6 of 8 cUSc instead of 7 of 8 cUSC samples). | Plays an important role in adipocyte metabolism. Has significant sequence relationship with ADRP. |

Table 10: Epithelial cell/ carcinoma (Seshi, B)

| Systematic | Common | Genbank | Description | Phenotype/ Function |
|------------|-----------------------|----------|---|---|
| 38590_r_at | PTMA | M14630 | prothymosin, alpha (gene sequence 28) | |
| 38589_i_at | PTMA | M14630 | prothymosin, alpha (gene sequence 28) | |
| 38610_s_at | KRT10; KPP | X14487 | unnamed protein product; Human gene for acidic (type I) cytokeratin 10. | Epidermolytic hyperkeratosis |
| 37326_at | A4 | U93305 | integral membrane protein; swiss-prot accession: O04901; may play role in cell differentiation in intestinal epithelium | |
| 36812_at | BCAR3 | U92715 | breast cancer anti-estrogen resistance 3 | |
| 36953_at | MADH4 | U44378 | MAD, mothers against decapentaplegic homolog 4 (Drosophila) | Pancreatic cancer; Polyposis, juvenile intestinal |
| 36852_at | N33 | U42349 | Putative prostate cancer tumor suppressor | |
| 36851_g_at | N33 | U42360 | 39 kDa protein; Human N33 protein form 2 (N33) gene, exon 11 and complete cds. | ?Prostate cancer, susceptibility to |
| 37762_at | EMP1 | Y07909 | epithelial membrane protein 1 | / receptor |
| 37731_at | EPS15 | Z29064 | epidermal growth factor receptor pathway substrate 15 | |
| 40856_at | SERPINF1; PEDF; EPC-1 | U29953 | PEDF; Human pigment epithelium-derived factor gene, complete cds. | |
| 41431_at | ICK | AB023153 | intestinal cell kinase | |
| 39363_at | BC-2 | AF042384 | putative breast adenocarcinoma marker (32kD) | |
| 39631_at | EMP2 | U52100 | epithelial membrane protein 2 | |
| 39542_at | ENC1 | AF059611 | ectodermal-neural cortex (with BTB-like domain) | / associates with p110(RB) |
| 40454_at | FAT | X87241 | FAT tumor suppressor homolog 1 (Drosophila) | |
| 32781_f_at | BPAG1 | AA058762 | bullous pemphigoid antigen 1 (230/240kD) | |
| 32780_at | BPAG1 | AB018271 | bullous pemphigoid antigen 1 (230/240kD) | |
| 32329_at | KRTHB6 | X99142 | keratin, hair, basic, 6 (monilethrix) | Monilethrix |
| 34005_at | PIGR | X73079 | polymeric immunoglobulin receptor, expressed in glomerular epithelial cells. | / Binds and transports polymeric immunoglobulin |
| 1846_at | LGALS8 | L78132 | lectin, galactoside-binding, soluble, 8 (galectin 8); OMIM Notes: Expressed in prostate carcinoma cells but only rarely in prostatic hypertrophy. | |

Table 11: Endothelial cell (Seshi, B)

| Systematic | Common | Genbank | Description | Phenotype/ Function |
|------------|--------------|----------|--|---|
| 32755_at | ACTA2 | X13839 | actin, alpha 2, smooth muscle, aorta | |
| 39315_at | ANGPT1 | D13628 | angiopoietin 1 | / ligand for the TIE2 receptor |
| 1929_at | ANGPT1 | U83508 | angiopoietin 1 | |
| 40387_at | EDG2 | U80811 | endothelial differentiation, lysophosphatidic acid (LPA) G-protein-coupled receptor, 2 | |
| 40874_at | EDF1 | AJ005259 | endothelial differentiation-related factor 1; OMIM Notes: EDF1 level inversely correlates with the level of endothelial differentiation. Inhibition of EDF1 expression promotes endothelial cell differentiation. It is postulated that EDF1 may function as a bridging molecule that interconnects regulatory proteins and the basal transcriptional machinery, thus modulating the transcription of the genes involved in endothelial differentiation. | |
| 37907_at | F8A; DXS522E | M34677 | Factor VIII-associated gene 1; CpG island protein; Human nested gene protein gene, complete cds. | |
| 41433_at | VCAM1 | M73255 | Human vascular cell adhesion molecule-1 (VCAM1) gene, complete CDS. | |
| 36988_at | TNFAIP1 | M80783 | tumor necrosis factor, alpha-induced protein 1 (endothelial); OMIM Notes: Involved in the primary response of the endothelium to TNF. | |
| 583_s_at | VCAM1 | M30257 | vascular cell adhesion molecule 1 | |
| 1953_at | VEGF | AF024710 | vascular endothelial growth factor | |
| 36100_at | VEGF | AF022375 | vascular endothelial growth factor | |
| 37268_at | VEGFB | U43368 | vascular endothelial growth factor B | |
| 159_at | VEGFC | U43142 | vascular endothelial growth factor C | / ligand and activator of the receptor tyrosine kinase Flt4 |

Table 12: Nerve cell/ neuroendocrine/ neurologic disorders (Seshi, B)

| Systematic | Common | Genbank | Description | Phenotype/ Function |
|------------|-----------|----------|--|---|
| 37298_at | GABARAP | AF044671 | GABA(A) receptor-associated protein | |
| 37692_at | DBI | AI557240 | diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein) | |
| 35767_at | GABARAPL2 | AI565760 | GABA(A) receptor-associated protein-like 2 | |
| 35785_at | GABARAPL1 | W28281 | GABA(A) receptor-associated protein like 1 | |
| 38406_f_at | PTGDS | AI207842 | prostaglandin D2 synthase (21kD, brain) | |
| 38657_s_at | CLTA | M20471 | clathrin, light polypeptide (Lca), brain-specific insertion sequences | |
| 38653_at | PMP22 | D11428 | peripheral myelin protein 22 | Charcot-Marie-Tooth disease with deafness; Charcot-Marie-Tooth neuropathy-1A; Dejerine-Sottas disease; Neuropathy, recurrent, with pressure palsies |
| 38291_at | PENK | J00123 | preproenkephalin (; Human enkephalin gene: exon 3 and 3'flank. | |
| 39072_at | MXI1 | L07648 | MAX interacting protein 1 | Neurofibrosarcoma; Prostate cancer, susceptibility to/ transcription factor; forms heterodimers with Max protein |
| 38841_at | GDBR1 | AF068195 | putative glioblastoma cell differentiation-related | |
| 38818_at | SPTLC1 | Y08685 | serine palmitoyltransferase, long chain base subunit 1 | Neuropathy, hereditary sensory and autonomic, type 1 |
| 36990_at | UCHL1 | X04741 | ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase), neuron-specific. OMIM Notes: Highly specific to neurons and to cells of the diffuse neuroendocrine system and their tumors. | Parkinson disease, familial |
| 37005_at | NBL1 | D28124 | neuroblastoma, suppression of tumorigenicity 1 | |
| 37286_at | NRCAM | AB002341 | neuronal cell adhesion molecule | |
| 36667_at | PYGB | U47025 | phosphorylase, glycogen; brain | |
| 36965_at | ANK3 | U13616 | ankyrin 3, node of Ranvier (ankyrin G) | / peripheral proteins believed to act as membrane-cytoskeleton linker molecules |

| | | | | |
|------------|-------|----------|---|---|
| 38040_at | SPF30 | AF107463 | splicing factor 30, survival of motor neuron-related | |
| 37958_at | BCMP1 | AL049257 | brain cell membrane protein 1 | |
| 41221_at | PGAM1 | J04173 | phosphoglycerate mutase 1 (brain) | |
| 40936_at | CRIM1 | AI651806 | cysteine-rich motor neuron 1 | |
| 41091_at | FALZ | U05237 | fetal Alzheimer antigen. OMIM Notes: Abnormally expressed in fetal brain. The corresponding antibody ALZ50 recognizes neurofibrillary pathology associated with Alzheimer's disease. | |
| 41136_s_at | APP | Y00264 | amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) | Alzheimer disease-1, APP-related; Amyloidosis, cerebroarterial, Dutch type; Schizophrenia, chronic |
| 763_at | GMFB | AB001106 | glia maturation factor, beta | |
| 641_at | PSEN1 | L76517 | presenilin 1 (Alzheimer disease 3) | Alzheimer disease, familial, with spastic paraparesis and unusual plaques; Alzheimer disease-3 |
| 39793_at | GBAS | AF029786 | glioblastoma amplified sequence | |
| 40023_at | BDNF | X60201 | brain-derived neurotrophic factor | |
| 39687_at | E46L | AI524873 | like mouse brain protein E46 | |
| 39686_g_at | E46L | AL050282 | like mouse brain protein E46 | |
| 39542_at | ENC1 | AF059611 | ectodermal-neural cortex (with BTB-like domain) | / associates with p110(RB). OMIM Notes: Expressed highest in brain. |
| 40193_at | ENO2 | X51956 | Human ENO2 gene for neuron specific (gamma) enolase. | |
| 40121_at | HIP2 | U58522 | huntingtin interacting protein 2 | |
| 40467_at | SDHD | AB006202 | succinate dehydrogenase complex, subunit D, integral membrane protein | Paragangliomas, familial central nervous system; Paragangliomas, familial nonchromaffin, 1, with and without deafness; Pheochromocytoma |
| 40281_at | NEDD5 | D63878 | neural precursor cell expressed, developmentally down-regulated 5 | |
| 32824_at | CLN2 | AF039704 | deficient in late-infantile neuronal ceroid lipofuscinosis; Homo sapiens lysosomal pepstatin insensitive protease (CLN2) gene, complete cds. | Ceroid-lipofuscinosis, neuronal 2, classic late infantile |
| 32607_at | BASP1 | AF039656 | brain abundant, membrane attached signal protein 1 | |

| | | | | |
|------------|---------|----------|---|---|
| 33817_at | D10S102 | S63912 | FBRNP; heterogeneous ribonucleoprotein homolog; This sequence comes from Fig. 3; D10S102=FBRNP [human, fetal brain, mRNA, 3043 nt]. | |
| 33942_s_at | STXBP1 | AF004563 | syntaxin binding protein 1 | / implicated in vesicle trafficking and neurotransmitter release |
| 1659_s_at | RHEB2 | D78132 | Ras homolog enriched in brain 2 | |
| 1695_at | NEDD8 | D23662 | neural precursor cell expressed, developmentally down-regulated 8 | |
| 2053_at | CDH2 | M34064 | cadherin 2, type 1, N-cadherin (neuronal) | |
| 216_at | PTGDS | M98539 | Human prostaglandin D2 synthase gene, exon 7, brain | |
| 32102_at | SACS | AB018273 | spastic ataxia of Charlevoix-Saguenay (sacsin) | Spastic ataxia, Charlevoix-Saguenay type |
| 31896_at | NAG | AL050281 | neuroblastoma-amplified protein | |
| 35681_r_at | ZFH1B | AB011141 | zinc finger homeobox 1b. OMIM Notes: SMAD-interacting protein 1 (SMADIP1) appears to be essential to embryonic neural and neural crest development. | Hirschsprung disease-mental retardation syndrome; Hirschsprung disease-mental retardation syndrome without Hirschsprung disease |
| 35268_at | AXOT | AL050171 | axotrophin | |
| 36190_at | CDR2 | M63256 | cerebellar degeneration-related protein (62kD) | |
| 36609_at | SLC1A3 | D26443 | solute carrier family 1 (glial high affinity glutamate transporter), member 3 | |
| 35973_at | HYPH | AB023163 | Huntingtin interacting protein H | |
| 36142_at | SCA1 | X79204 | spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1) | Spinocerebellar ataxia-1 |
| 34817_s_at | A2LP | U70671 | ataxin 2 related protein | |
| 34777_at | ADM | D14874 | adrenomedullin | |
| 34394_at | ADNP | AB018327 | activity-dependent neuroprotector | |
| 32606_at | BASP1 | AA135683 | brain abundant, membrane attached signal protein 1 | |
| 38233_at | HOMER-3 | AF093265 | Homer, neuronal immediate early gene, 3 | |
| 36998_s_at | SCA2 | Y08262 | spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant, ataxin 2) | Spinocerebellar ataxia-2 |
| 35150_at | TNFRSF5 | X60592 | tumor necrosis factor receptor superfamily, member 5 | Immunodeficiency with hyper-IgM, type 3 |
| 34166_at | SLC6A7 | S80071 | solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 | |

| | | | | |
|----------|--------|----------|---|---|
| 34265_at | SGNE1 | Y00757 | secretory granule, neuroendocrine protein 1 (7B2 protein) | |
| 654_at | MXI1 | L07648 | MAX interacting protein 1 | Neurofibrosarcoma; Prostate cancer, susceptibility to/ transcription factor; forms heterodimers with Max protein |
| 37945_at | BACH | U91316 | brain acyl-CoA hydrolase | |
| 39685_at | E46L | AL050282 | like mouse brain protein E46 | |
| 33769_at | MPZL1 | AF087020 | myelin protein zero-like 1 | |
| 39356_at | NEDD4L | AB007899 | neural precursor cell expressed, developmentally down-regulated 4-like | |
| 38800_at | STMN2 | D45352 | stathmin-like 2; OMIM Notes: Neuronal growth-associated protein SCG10. | |
| 36933_at | NDRG1 | D87953 | N-myc downstream regulated gene 1 | Neuropathy, hereditary motor and sensory, Lom type |
| 40140_at | ZFP103 | D76444 | zinc finger protein 103 homolog (mouse); OMIM Notes: Alternative title, KF1, expressed in normal cerebellum and Alzheimer disease cerebral cortex, but not in normal cerebral cortex. | |
| 1452_at | LMO4 | U24576 | LIM domain only 4 | OMIM Notes: is highly expressed in the cranial neural crest cells, somite, dorsal limb bud mesenchyme, motor neurons, Schwann cell progenitors, and T-lymphocyte lineage. |
| 1058_at | WASF3 | S69790 | WAS protein family, member 3 | |

Table 13: Drosophila and/ or homeotic genes (Seshi, B)

| Systematic | Common | Genbank | Description | Phenotype/ Function |
|------------|--------|----------|--|---|
| 38288_at | SNAI2 | U69196 | snail homolog 2 (Drosophila). OMIM Notes: Neural crest transcription factor SLUG. A zinc finger protein that plays an important role in the transition of epithelial to mesenchymal characteristics within the neural crest. | |
| 39037_at | MLLT2 | L13773 | myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2 | |
| 39070_at | SNL | U03057 | singed-like (fascin homolog, sea urchin) (Drosophila). OMIM Notes: Positive in dendritic cells of lymph nodes and Reed-Sternberg cells. | |
| 39164_at | ARIH2 | AF099149 | ariadne homolog 2 (Drosophila). OMIM Notes: Upregulated during retinoic acid-induced granulocytic differentiation of APL cells. | |
| 38750_at | NOTCH3 | U97669 | Notch homolog 3 (Drosophila). OMIM Notes: Promotes the differentiation of astroglia from multipotent progenitors. | Cerebral (autosomal dominant) arteriopathy with subcortical infarcts and leukoencephalopathy (CADASIL) |
| 38944_at | MADH3 | U68019 | MAD, mothers against decapentaplegic homolog 3 (Drosophila) | OMIM Notes: SMAD3 signal transduction important in the regulation of muscle-specific genes. |
| 37693_at | NUMB | L40393 | numb homolog (Drosophila) | OMIM Notes: Numb directs neuronal cell fate decisions. |
| 40004_at | SIX1 | X91868 | sine oculis homeobox homolog 1 (Drosophila) | OMIM Notes: Expressed in adult skeletal muscle, and in multiple tumors including mammary carcinoma. |
| 39610_at | HOXB2 | X16665 | homeo box B2 | OMIM Notes: Essential for motor neuron development. Within the hematopoietic compartment, expressed specifically in erythromegakaryocytic cell lines. |

| | | | | |
|-----------|--------|----------|---|---|
| 40575_at | DLG5 | AB011155 | discs, large (Drosophila) homolog 5 | OMIM Notes: Expressed in prostate gland epithelial cells. |
| 40570_at | FOXO1A | AF032885 | forkhead box O1A (rhabdomyosarcoma) | Rhabdomyosarcoma, alveolar. OMIM Notes: Activates myogenic transcription program. |
| 40127_at | PMX1 | M95929 | paired mesoderm homeo box 1 | OMIM Notes: Expressed in cardiac, skeletal and smooth muscle tissues. |
| 40454_at | FAT | X87241 | FAT tumor suppressor homolog 1 (Drosophila) | OMIM Notes: Expressed in many epithelial, some endothelial and smooth muscle cells. |
| 40328_at | TWIST | X99268 | twist homolog (acrocephalosyndactyly 3; Saethre-Chotzen syndrome) (Drosophila) | Saethre-Chotzen syndrome. OMIM Notes: Required for cranial neural tube morphogenesis. |
| 33222_at | FZD7 | AB017365 | frizzled homolog 7 (Drosophila) | OMIM Notes: Highest expression adult skeletal muscle and fetal kidney. FZD7 dependent PKC signaling controls cell sorting behaviour in the mesoderm. |
| 32696_at | PBX3 | X59841 | pre-B-cell leukemia transcription factor 3 | |
| 33337_at | DEGS | AF002668 | degenerative spermatocyte homolog, lipid desaturase (Drosophila); adipocyte associated. | |
| 1857_at | MADH7 | AF010193 | MAD, mothers against decapentaplegic homolog 7 (Drosophila) | OMIM Notes: MAD proteins were originally defined in Drosophila as essential components of the signaling pathways of the TGF-beta receptor family (e.g., TGFBR1). MADH7 and MADH6 as shown by IHC and ISH are predominantly expressed in vascular endothelium. |
| 1955_s_at | MADH6 | AF035528 | MAD, mothers against decapentaplegic homolog 6 (Drosophila) | / inhibitor of BMP signaling |

| | | | | |
|------------|--------|----------|---|---|
| 1013_at | MADH5 | U59913 | MAD, mothers against decapentaplegic homolog 5 (Drosophila) | OMIM Notes: SMAD5 plays a critical role in the signaling pathway by which TGF-beta inhibits the proliferation of human hematopoietic progenitor cells. |
| 1453_at | MADH2 | U68018 | MAD, mothers against decapentaplegic homolog 2 (Drosophila) | OMIM Notes: SMAD2/ SMAD3 signal transduction appears to be important in the regulation of muscle-specific genes. |
| 1433_g_at | MADH3 | U68019 | MAD, mothers against decapentaplegic homolog 3 (Drosophila) | |
| 35681_r_at | ZFHX1B | AB011141 | zinc finger homeobox 1b. OMIM Notes: SMAD-interacting protein 1 (SMADIP1) appears to be essential to embryonic neural and neural crest development. | Hirschsprung disease-mental retardation syndrome; Hirschsprung disease-mental retardation syndrome without Hirschsprung disease |
| 35226_at | EYA2 | U71207 | eyes absent homolog 2 (Drosophila) | OMIM Notes: Expressed in extensor tendons, and in lens fibers and participates in connective tissue patterning. |
| 36308_at | ZIC1 | D76435 | Zic family member 1 (odd-paired homolog, Drosophila) | OMIM Notes: Specifically expressed in nervous tissue and in particular cerebellar granule cells, potential biomarker for cerebellar granule cell lineage and medulloblastoma. |
| 34306_at | MBNL | AB007888 | muscleblind-like (Drosophila) | OMIM Notes: Expressed in skeletal muscle myoblasts, also in lymphoblastoid cell lines. |
| 33710_at | C3F | U72515 | putative protein similar to nessy (Drosophila) | OMIM Notes: Expressed in fibroblasts and hepatocytes. |

Table 14: B-cell/ B-cell neoplasms (Seshi, B)

| Systematic | Common | Genbank | Description | Phenotype/ Function |
|------------|--------|----------|---|--|
| 41562_at | BMI1 | L13689 | B lymphoma Mo-MLV insertion region (mouse) | / proto-oncogene |
| 37294_at | BTG1 | X61123 | B-cell translocation gene 1, anti-proliferative | |
| 38418_at | CCND1 | X59798 | cyclin D1 (PRAD1: parathyroid adenomatosis 1) | Centrocytic lymphoma; Leukemia/lymphoma, B-cell, 1; Multiple myeloma; Parathyroid adenomatosis 1 |
| 37730_at | p100 | U22055 | EBNA-2 co-activator (100kD); OMIM Notes: EBNA-2 activates transcription of specific genes and is essential for EBV-mediated B-lymphocyte transformation. | / associates with the EBV nuclear protein 2 acidic domain |
| 466_at | GTF2I | U77948 | general transcription factor II, I; OMIM Notes: Alternative title, BTK-associated protein, 135kD (BAP135). Bruton's tyrosine kinase (BTK) is essential for B-cell activation and phosphorylates BAP135 in B cells. | |
| 36875_at | IBTK | AL050018 | inhibitor of Bruton's tyrosine kinase | |
| 38438_at | NFKB1 | M58603 | nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) | |
| 39730_at | ABL1 | X16416 | v-abl Abelson murine leukemia viral oncogene homolog 1 | Leukemia, chronic myeloid |
| 38743_f_at | RAF1 | X06409 | v-raf-1 murine leukemia viral oncogene homolog-1 | |
| 36645_at | RELA | L19067 | v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian) | |
| 41436_at | ZNF198 | AJ224901 | zinc finger protein 198; OMIM Notes: ZNF198 involves T- or B-cell lymphoblastic lymphoma, myeloid hyperplasia, and eosinophilia and evolves toward AML. This multilineage involvement suggests the malignant transformation of primitive hematopoietic stem cell. | Stem-cell leukemia/lymphoma syndrome |
| 40091_at | BCL6 | U00115 | B-cell CLL/lymphoma 6 (zinc finger protein 51); OMIM Notes: BCL6 is predominantly expressed in the B-cell lineage, especially mature B cells (centrocytes and centroblasts). | Lymphoma, B-cell, Diffuse Large |
| 32776_at | RALB | M35416 | v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein) | |
| 32696_at | PBX3 | X59841 | pre-B-cell leukemia transcription factor 3 | |
| 33791_at | DLEU1 | Y15227 | deleted in lymphocytic leukemia, 1 | |

| | | | | |
|-----------|---------------|----------|--|--|
| 34005_at | PIGR | X73079 | polymeric immunoglobulin receptor | / Binds and transports polymeric immunoglobulin |
| 1636_g_at | ABL | U07563 | ABL is the cellular homolog proto-oncogene of Abelson's murine leukemia virus and is associated with the t9:22 chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia. | Leukemia, chronic myeloid |
| 1728_at | BMI1 | L13689 | B lymphoma Mo-MLV insertion region (mouse) | / proto-oncogene |
| 2020_at | CCND1 | M73554 | cyclin D1 (PRAD1: parathyroid adenomatosis 1) | Centrocytic lymphoma; Leukemia/lymphoma, B-cell, 1; Multiple myeloma; Parathyroid adenomatosis 1 |
| 1295_at | RELA | L19067 | v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian) | |
| 1377_at | NFKB1 | M58603 | nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) | |
| 1461_at | NFKBIA | M69043 | nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha | / Ikb-like activity |
| 1389_at | MME | J03779 | membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) | |
| 35350_at | GALNAC4 S-6ST | AB011170 | B cell RAG associated protein | |
| 35992_at | MSC | AF087036 | musculin (activated B-cell factor-1, ABF1); OMIM Notes: Downstream target of B-cell receptor signal transduction pathway. Also expressed in proliferating undifferentiated myeloblasts. | / basic helix-loop-helix transcription factor |
| 34344_at | IKBKAP | AF044195 | inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein | Dysautonomia, familial |
| 34350_at | RSN | X64838 | restin (Reed-Sternberg cell-expressed intermediate filament-associated protein); Note R-S cell is a form of B-cell. | |
| 36204_at | PTPRF | Y00815 | protein tyrosine phosphatase, receptor type, F; OMIM Notes: Alternative title, Leukocyte antigen-related tyrosine phosphatase (LAR). Both LAR and LCA (CD45) map to chromosome 1. LCA is protein-tyrosine phosphatase, receptor-type C, PTPRC, whereas LAR is PTPRF. | |
| 34391_at | IGBP1 | Y08915 | immunoglobulin (CD79A) binding protein 1. | IGBP1, a marker for early B-cells |

| | | | | |
|----------|---------|----------|---|---|
| 1373_at | TCF3 | M31523 | proto-oncogene or transcription factor 3 TCF3 (E2A immunoglobulin enhancer binding factors E12/E47); OMIM Notes: E2A mutant mice will have selective failure to develop B cells, all other hematopoietic cell lineages being intact. The block to B cell development occurs before immunoglobulin D(H)-J(H) rearrangement. | Leukemia, acute lymphoblastic. A homeobox gene contributing the DNA binding domain of the t(1:19) translocation protein in precursor B-cell ALL. |
| 35150_at | TNFRSF5 | X60592 | tumor necrosis factor receptor superfamily, member 5; OMIM notes: Alternative title, B- cell associated molecule CD40; expressed on the surface of all mature B cells, most mature B-cell malignancies and some early B-cell ALL. | Immunodeficiency with hyper-IgM, type 3 |
| 38740_at | ZFP36L1 | X79067 | zinc finger protein 36, C3H type-like 1; OMIM Notes: Alternative title, BERG36 (B- cell early response gene encoding a 36 kD protein). | |
| 37026_at | COPEB | AF001461 | core promoter element binding protein; OMIM Notes: Alternative title, B-cell-derived 1, BCD1. The expression of BCD1 was limited to two tissues, CD19+ B-cells and testis of normal individuals. B-cell maturation is associated with BCD1 expression. | / transcription factor involved in hepatic wound healing |
| 38050_at | BTF | D79986 | Bcl-2-associated transcription factor | |
| 32696_at | PBX3 | X59841 | pre-B-cell leukemia transcription factor 3 | |

Table 15: Myeloid cell/ myeloid leukemia (Seshi, B)

| Systematic | Common | Genbank | Description | Phenotype/ Function |
|------------|--------|----------|---|--|
| 39037_at | MLLT2 | L13773 | myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2 | Leukemia, acute myeloid; Leukemia, acute T-cell lymphoblastic |
| 37486_f_at | MEIS3 | U68385 | Meis1, myeloid ecotropic viral integration site 1 homolog 3 (mouse) | |
| 37685_at | PICALM | U45976 | phosphatidylinositol binding clathrin assembly protein | |
| 41220_at | MSF | AB023208 | MLL septin-like fusion; a fusion partner gene of MLL | Leukemia, acute myeloid, therapy-related; Ovarian carcinoma |
| 41175_at | CBFB | L20298 | core-binding factor, beta subunit | Myeloid leukemia, acute, M4Eo subtype |
| 943_at | RUNX1 | D43968 | runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) | Leukemia, acute myeloid; Platelet disorder, familial, with associated myeloid malignancy |
| 39730_at | ABL1 | X16416 | v-abl Abelson murine leukemia viral oncogene homolog 1 | Leukemia, chronic myeloid |
| 33146_at | MCL1 | L08246 | myeloid cell leukemia sequence 1 (BCL2-related) | Leukemia, chronic myeloid |
| 1636_g_at | ABL | U07563 | ABL is the cellular homolog proto-oncogene of Abelson's murine leukemia virus and is associated with the t9:22 chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia. | |
| 277_at | MCL1 | L08246 | myeloid cell leukemia sequence 1 (BCL2-related) | |
| 41388_at | MEIS2 | AF017418 | Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) | Leukemia, acute nonlymphocytic |
| 40189_at | SET | M93651 | SET translocation (myeloid leukemia-associated, M2/M4 AML); SET stands for suppressor of variegation, enhancer of zeste and trithorax. | |
| 38992_at | DEK | X64229 | DEK oncogene (DNA binding) | |
| 36941_at | AF1Q | U16954 | ALL1-fused gene from chromosome 1q | Leukemia, acute myelomonocytic |

Table 16: T cell/ NK cell (Seshi, B)

| Systematic | Common | Genbank | Description | Phenotype/ Function |
|------------|----------|----------|---|--|
| 37685_at | PICALM | U45976 | phosphatidylinositol binding clathrin assembly protein | Leukemia, acute myeloid; Leukemia, acute T-cell lymphoblastic |
| 498_at | TAX1BP1 | U33821 | Tax1 (human T-cell leukemia virus type I) binding protein 1 | |
| 40822_at | NFATC3 | L41067 | nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 | |
| 34003_at | CD4 | U47924 | major receptor for HIV-1; member of immunoglobulin supergene family; T cell surface glycoprotein T4 | / T-cell coreceptor; involved in antigen recognition; participant in signal transduction pathway |
| 32602_at | RAP1GDS1 | X63465 | RAP1, GTP-GDP dissociation stimulator 1 | Lymphocytic leukemia, acute T-cell (T-ALL) |
| 35279_at | TAX1BP1 | U33821 | Tax1 (human T-cell leukemia virus type I) binding protein 1 | |
| 34234_f_at | NKTR | AI688640 | natural killer-tumor recognition sequence; OMIM Notes: The protein product of the NKTR gene is present on the surface of LGLs and facilitates their binding to tumor targets. | |
| 39426_at | TCERG1 | AF017789 | transcription elongation regulator 1 (CA150) | / HIV-1 Tat transcriptional coactivator |
| 32602_at | RAP1GDS1 | X63465 | RAP1, GTP-GDP dissociation stimulator 1 | Lymphocytic leukemia, acute T-cell |

Table 17

Stromal cells showing expression of genes that are typically affiliated with B-cell progenitors

| Gene | Probe ID | GenBank ID | cMPC | cUSC | sMPC |
|---|----------|------------|----------------------------|----------------------------|-----------------------------|
| CD45 | 40518_at | | Positive in 4/5 samples | Positive in 8/8 samples | Positive in 6/10 samples |
| CD34 | 538_at | | 4/5 | 5/8 | 4/10 |
| CD19 | 1116_at | | 0/5 | 0/8 | 10/10 |
| CD20 | 619_at | | 1/5 | 0/8 | 3/10 |
| CD22 | 38521_at | | 0/5 | 2/8 | 1/10 |
| *CD10 (CALLA) Common acute lymphoblastic leukemia antigen. | 1389_at | | 5/5 | 8/8 | 10/10 |
| *Transcription factor 3 (E2A) Immunoglobulin enhancer binding factors E12/E47 | 1373_at | | 5/5 | 8/8 | 9/10 |
| *CD79A (IGBP1) Immunoglobulin binding protein 1, a marker for early B- cells | 34391_at | | 5/5 | 8/8 | 9/10 |
| *HLA class II, Dr alpha | 37039_at | | 5/5 | 8/8 | 9/10 |

| | | | | | |
|---------------------------------|----------|--|-----|-----|-------|
| *HLA class II, Dr beta 1 | 33261_at | | 5/5 | 8/8 | 10/10 |
| *B2M Beta-2 microglobulin | 34644_at | | 5/5 | 8/8 | 10/10 |
| CD2 | 40738_at | | 1/5 | 2/8 | 2/10 |
| CD5 | 32953_at | | 0/5 | 0/8 | 0/10 |
| CD7 | 771_s_at | | 0/5 | 0/8 | 0/10 |
| CD13 | 39385_at | | 5/5 | 8/8 | 0/10 |
| CD33 | 36802_at | | 2/5 | 4/8 | 0/10 |
| CD14 | 36661_at | | 3/5 | 8/8 | 0/10 |

Footnote to Table 17

Genes marked with asterisk (*) have met the criteria for inclusion in stromal cell gene list.

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CLAIMS

What is claimed is:

1. Isolated mesenchymal progenitor cells that are pluri-differentiated.
2. A therapeutic composition comprising an isolated pluri-differentiated
5 mesenchymal progenitor cells and a pharmaceutically acceptable carrier,
wherein said isolated pluri-differentiated mesenchymal progenitor cells are
present in an amount effective for treating a disease state in a mammal in need
thereof.
3. A therapeutic composition comprising isolated pluri-differentiated
10 mesenchymal progenitor cells and a pharmaceutically acceptable carrier,
wherein said isolated pluri-differentiated mesenchymal progenitor cells are
present in an amount effective to enhance hematopoietic progenitor cell
engraftment in a mammal in need thereof.
4. A therapeutic composition comprising isolated pluri-differentiated
15 mesenchymal progenitor cells and a pharmaceutically acceptable carrier,
wherein said pluri-differentiated mesenchymal progenitor cells are present in an
amount effective to treat GvHD in a mammal about to undergo bone marrow or
organ transplantation or suffering from GvHD caused by bone marrow or organ
transplantation.
- 20 5. A method for purifying pluri-differentiated mesenchymal progenitor
cells comprising the steps of:
 - a) providing a cell culture preparation by the Dexter method;
 - b) treating the cells to obtain a cell suspension;
 - c) removing macrophages;
 - 25 d) fractionating the cells; and
 - e) collecting the fraction of pluri-differentiated mesenchymal progenitor
cells.
6. A method for enhancing bone marrow engraftment in a mammal in
need thereof which comprises administering to the mammal (i) isolated pluri-
30 differentiated mesenchymal progenitor cells and (ii) a bone marrow graft, wherein
the isolated pluri-differentiated mesenchymal progenitor cells are administered in
an amount effective to promote engraftment of the bone marrow in the mammal.

7. The method according to claim 6, wherein said administrating step includes intravenously injecting or directly injecting the isolated pluri-differentiated mesenchymal progenitor cells to the site of intended activity.

5 8. A gene in an MPC for detecting the presence of cancer or pre-cancer in a cell population.

9. A pharmaceutical for modulating the gene of claim 10.

10 10. A method for enhancing engraftment of cells in a mammal in need thereof which comprises administering to the mammal isolated pluri-differentiated mesenchymal progenitor cells wherein the isolated pluri-differentiated mesenchymal progenitor cells are administered in an amount effective to promote engraftment of the cells in the mammal.

11. The method of claim 10, wherein the isolated pluri-differentiated mesenchymal progenitor cells are administered by intravenous injection or by injecting directly to the site of intended activity.

15 12. The method of claim 10, wherein the isolated pluri-differentiated mesenchymal progenitor cells are administered prior to administration of the hematopoietic progenitor cells.

20 13. The method of claim 10, wherein the isolated pluri-differentiated mesenchymal progenitor cells are introduced in a cell suspension also containing hematopoietic progenitor cells.

14. A SCID mouse model for investigating MPC function.

15. Phenotypic cultured bone marrow stromal cells capable of being analyzed at single cell level.

25 16. A diagnostic test for screening for abnormalities of bone marrow stromal cells.

17. The diagnostic test according to claim 16, wherein said test can be used for screening for various hematologic diseases and other diseases effecting stromal cells

30 18. The diagnostic test according to claim 16, wherein said abnormalities are phenotypic abnormalities that can be discerned at a single cell level.

19. Stromal cells for use in combination with engraftment or other similar procedures for enhancing the effectiveness of the treatment.

20. A method for treating graft-versus-host disease (GvHD) in a mammal about to undergo bone marrow or organ transplantation or suffering from GvHD caused by bone marrow or organ transplantation, by administering to the mammal an effective amount of isolated pluri-differentiated mesenchymal progenitor cells.

- 5 21. A method for diagnosing a disease state comprising the steps of:
- a) establishing gene expression patterns of normal state bone marrow derived isolated pluri-differentiated mesenchymal progenitor cells;
 - b) establishing gene expression patterns of various leukemic state bone marrow derived isolated pluri-differentiated mesenchymal progenitor cells;
 - 10 c) identifying gene sets that are unique to a given state; and
 - d) comparing a profile of bone marrow derived isolated mesenchymal progenitor cell of unknown state to said gene sets.

22. A method for identifying therapeutic targets for treatment of
- 15 hematopoietic function comprising the steps of:
- a) determining the median gene expression profile of bone marrow isolated pluri-differentiated mesenchymal progenitor cells associated with each disease state of interest;
 - b) identifying gene groups that are up-regulated, down regulated, and
 - 20 common to each disease state; and
 - c) identifying gene sets that are unique to a given state.

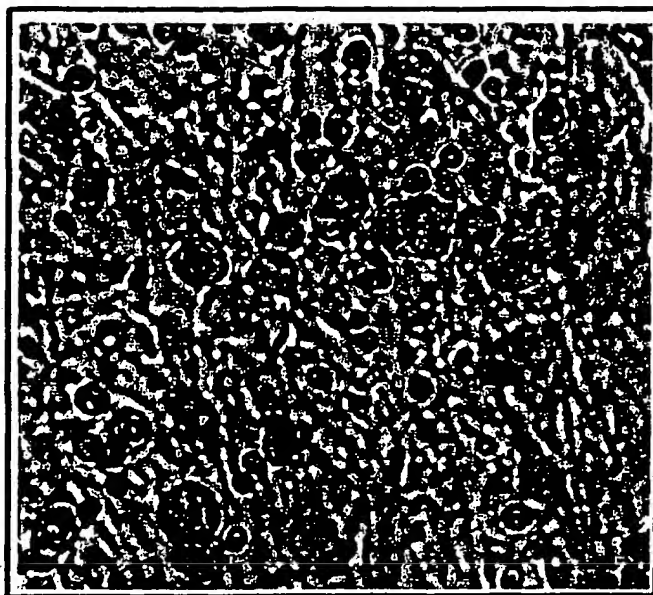
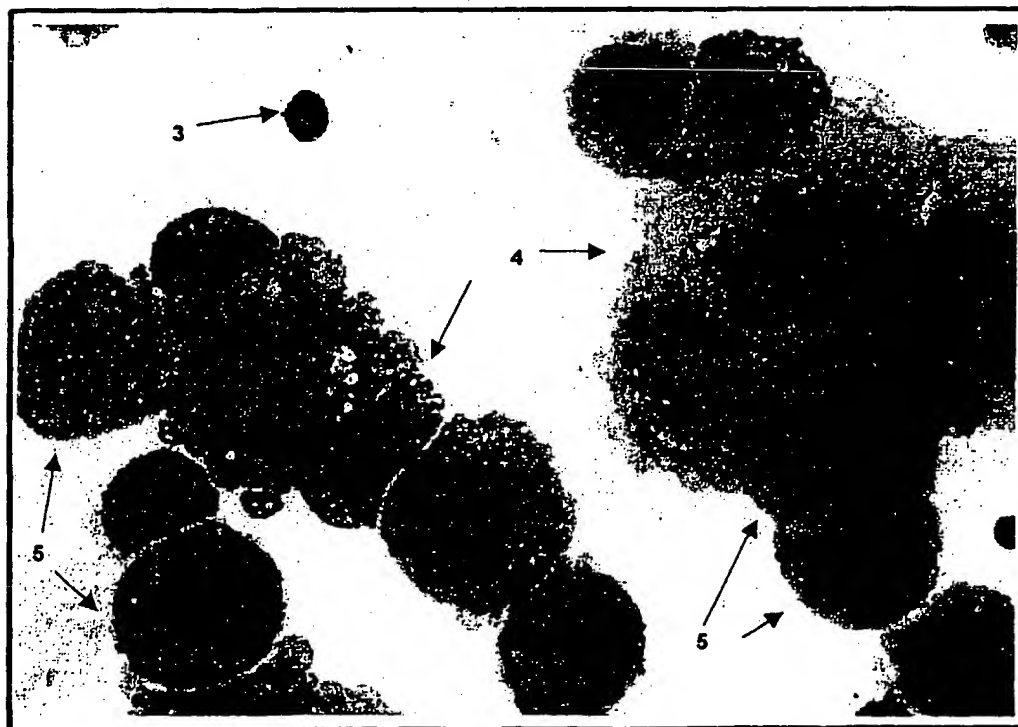
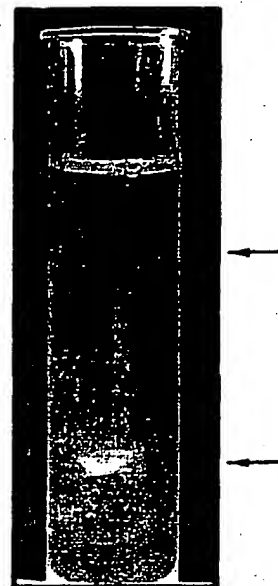
Figure - 1Figure - 2Figure - 3

Figure - 4A



Figure - 4B

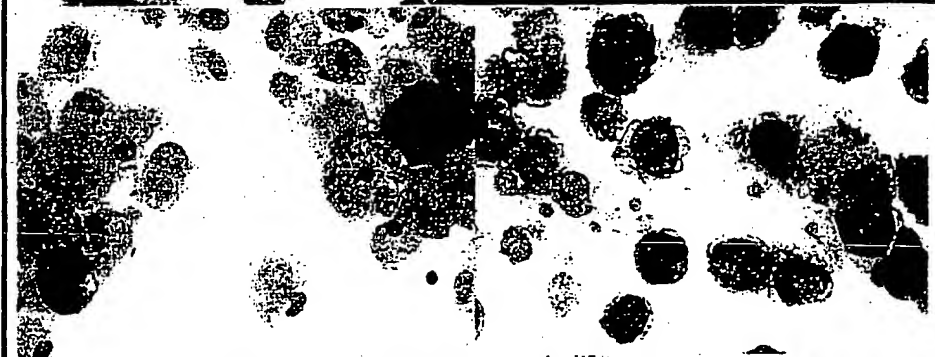


Figure - 4C

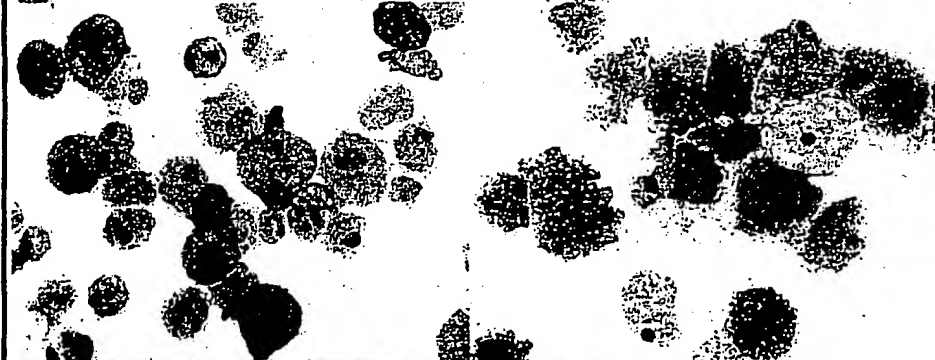


Figure - 4D

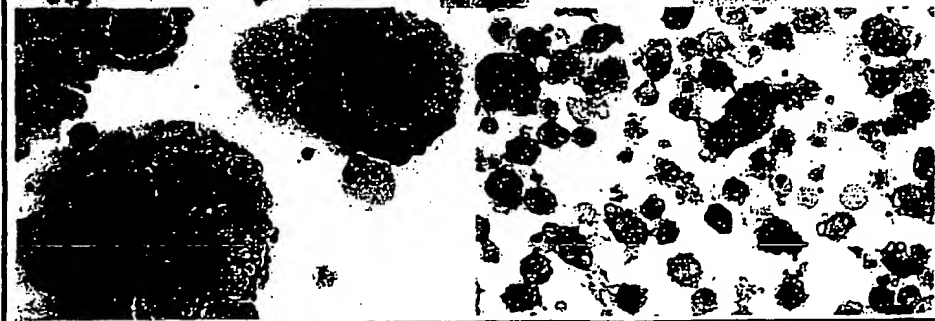


Figure - 4E

Figure - 4F

Figure - 4G

Figure - 4H

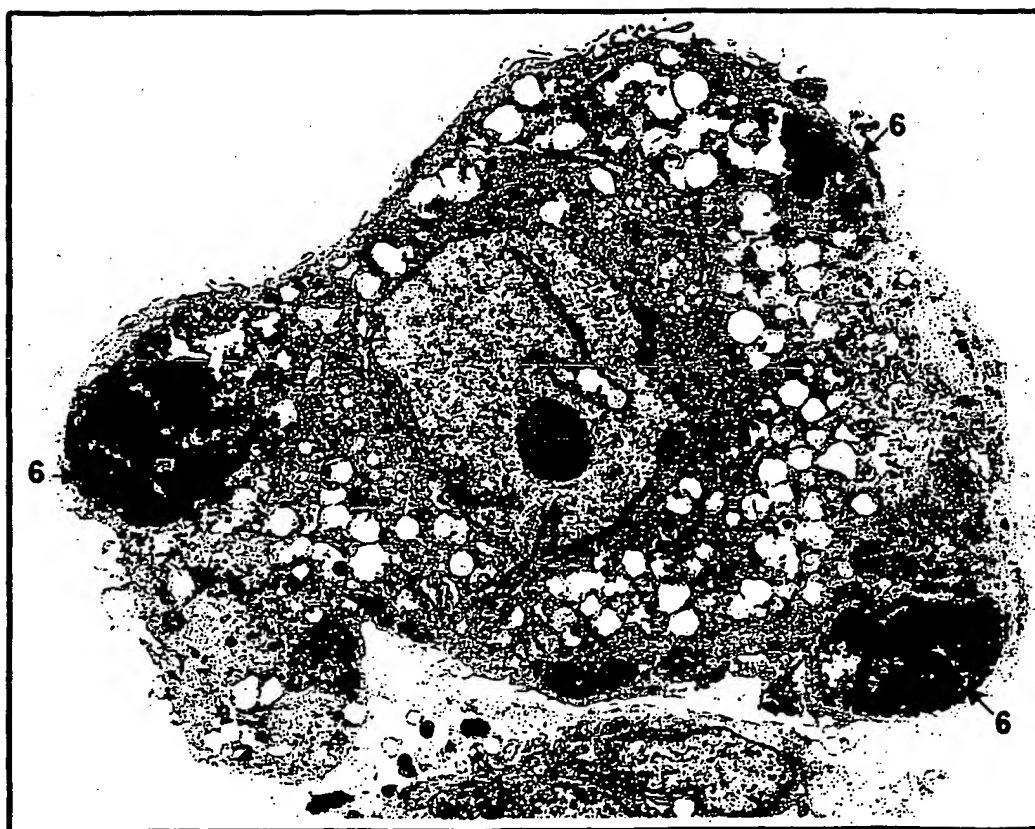
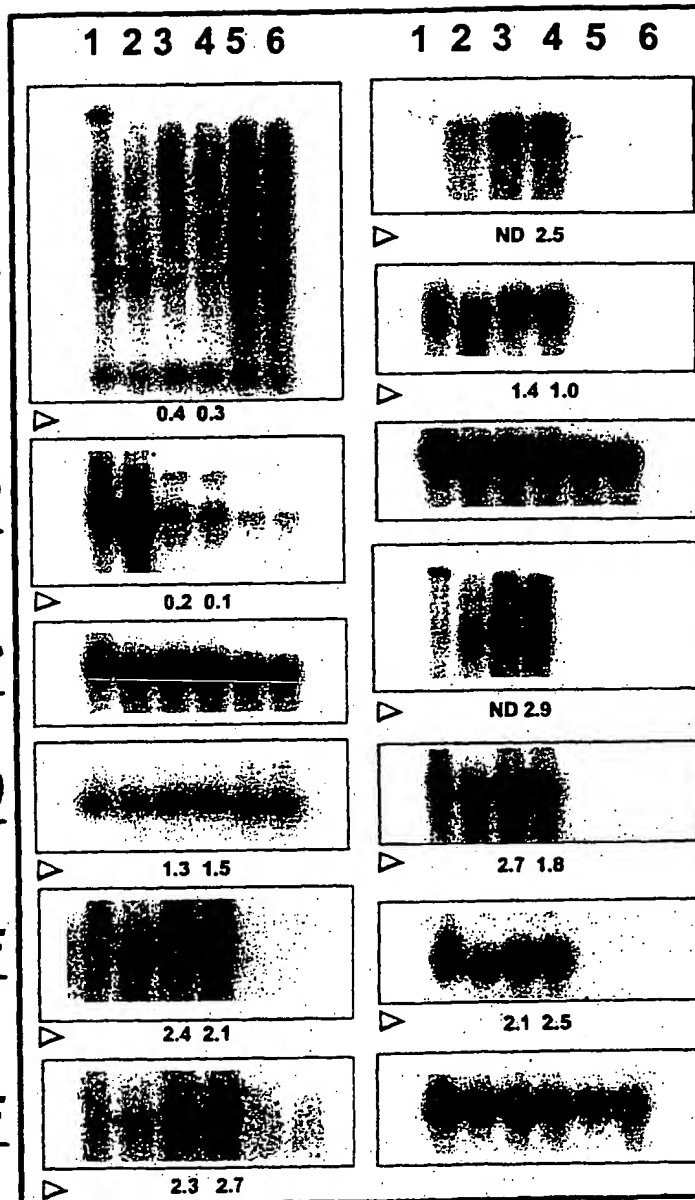


Figure - 5

Figure - 6AFigure - 6GFigure - 6HFigure - 6IFigure - 6JFigure - 6KFigure - 6LFigure - 6M

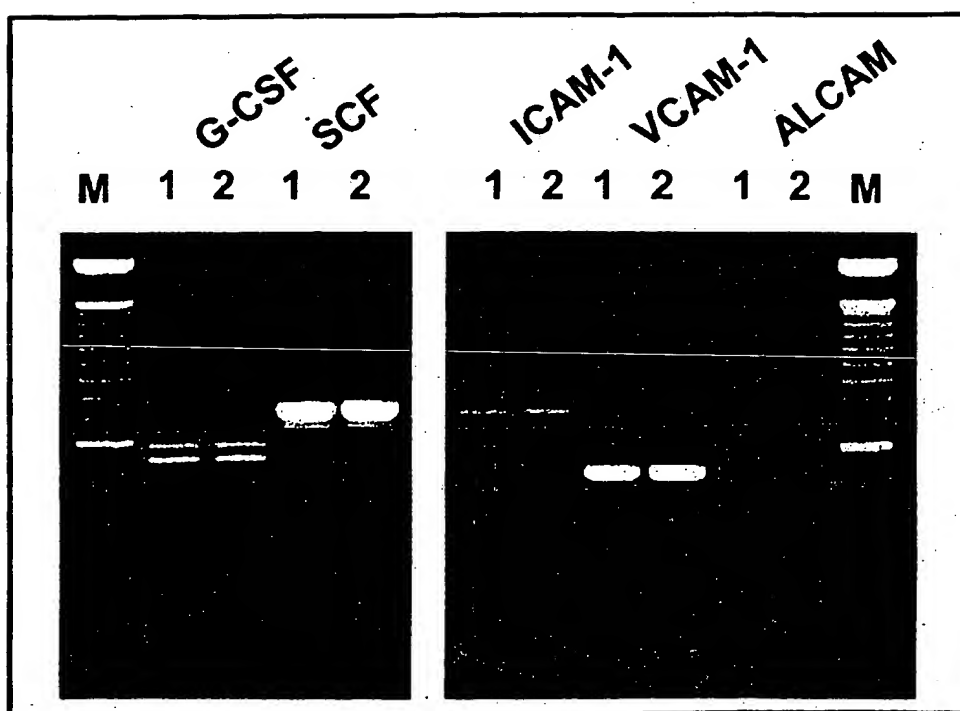


Figure - 7

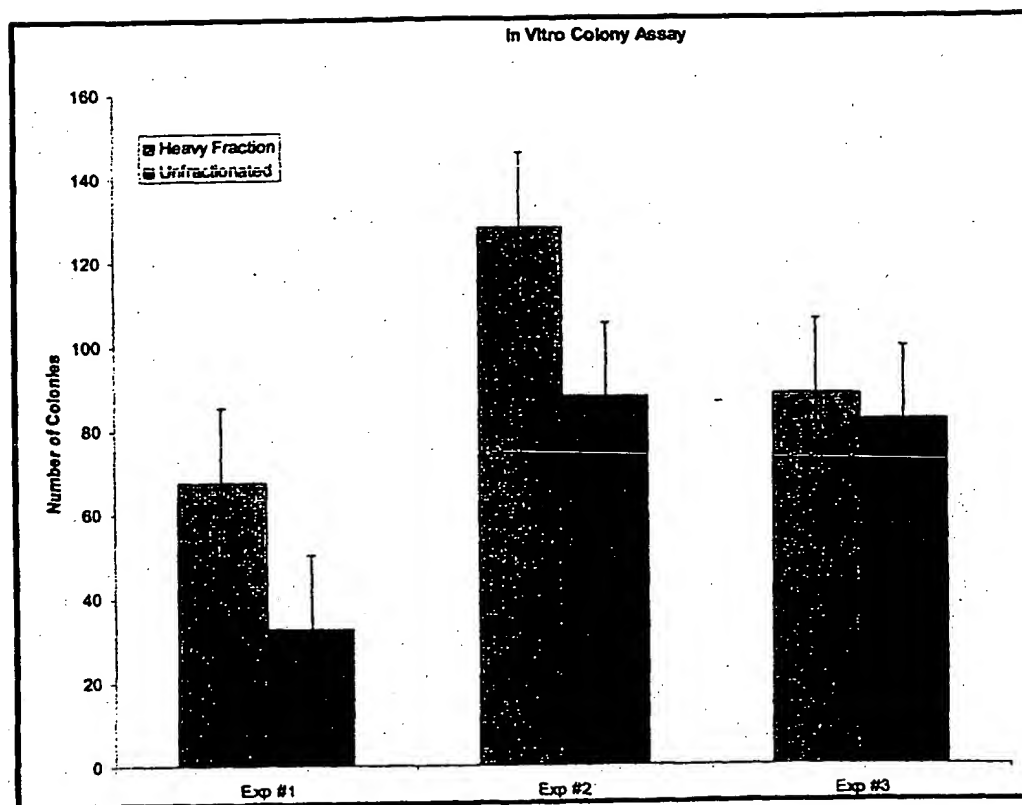


Figure - 8

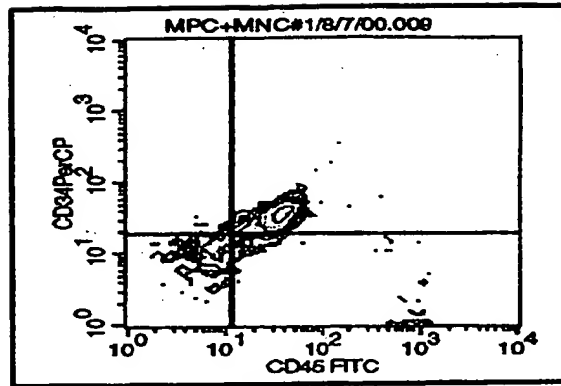


Figure - 9A

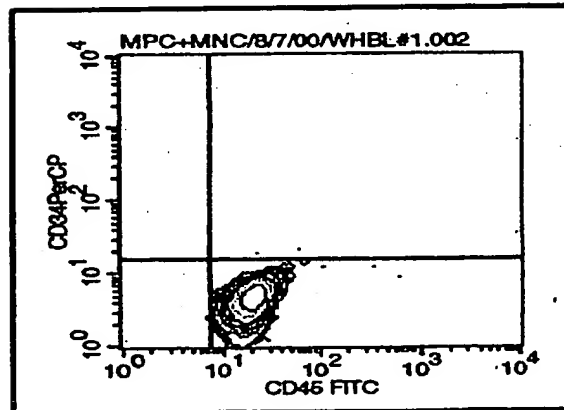


Figure - 9B

Figure - 10A

Figure - 10B

Figure - 10C

Figure - 10D

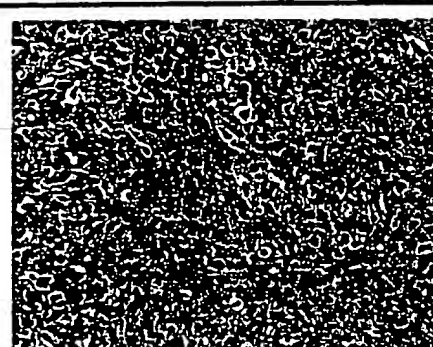
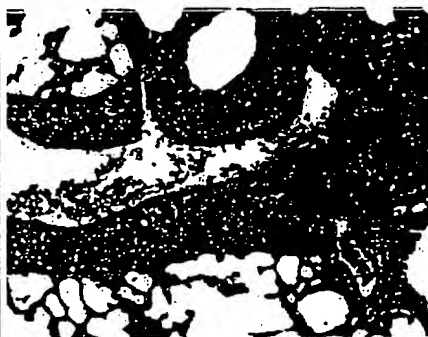
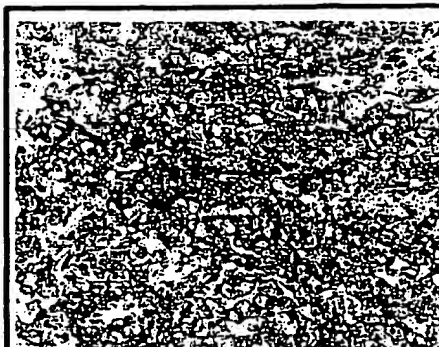


Figure - 10E

Figure - 10F

Figure - 10G

Figure - 10H

Figure - 11A

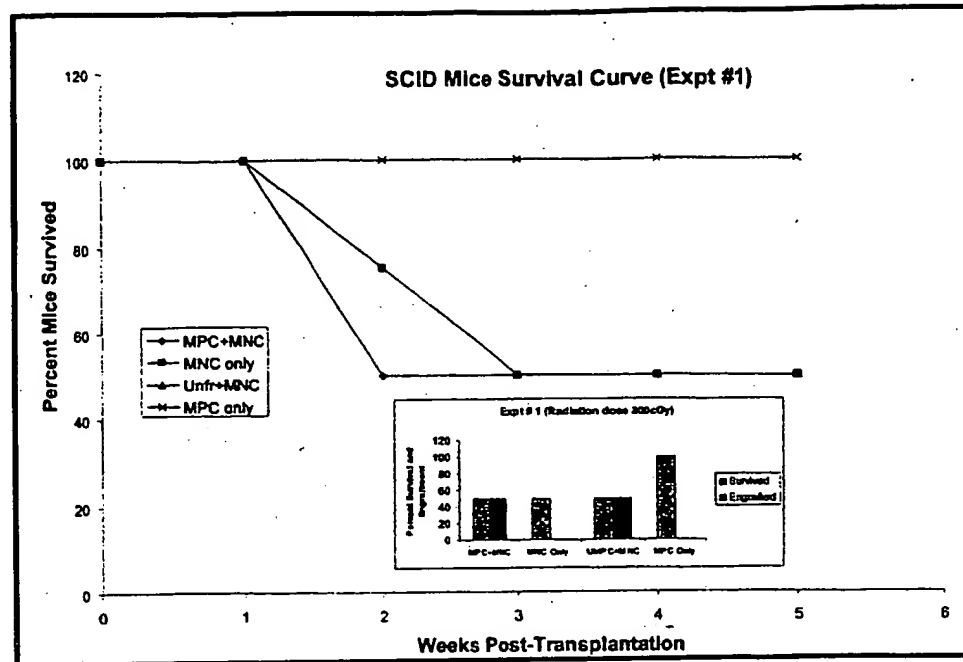
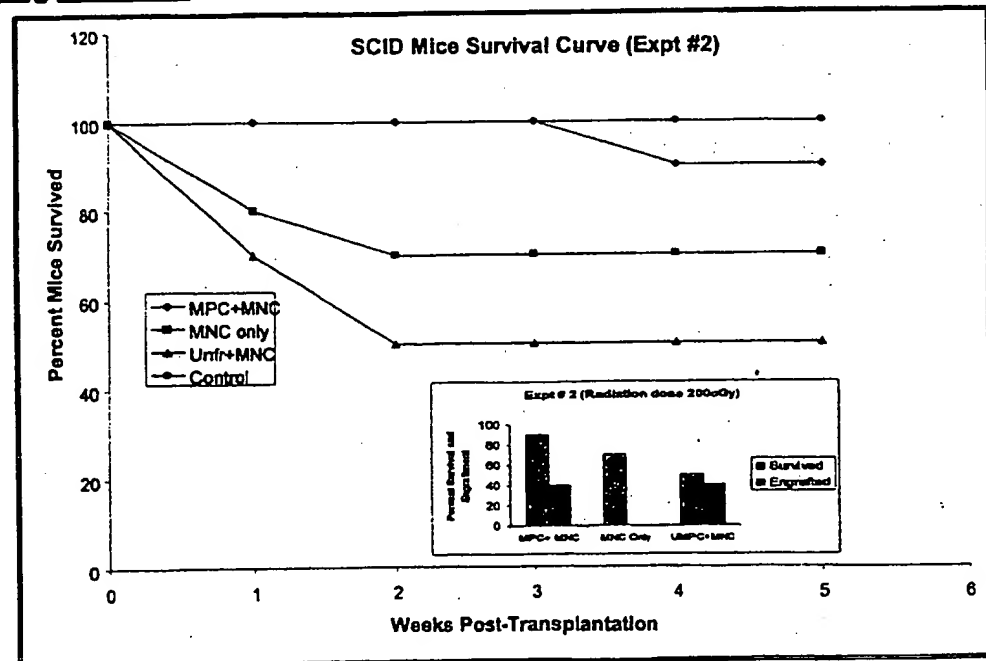


Figure - 11B



Figure - 11C



Figure - 13A**Figure - 13B**

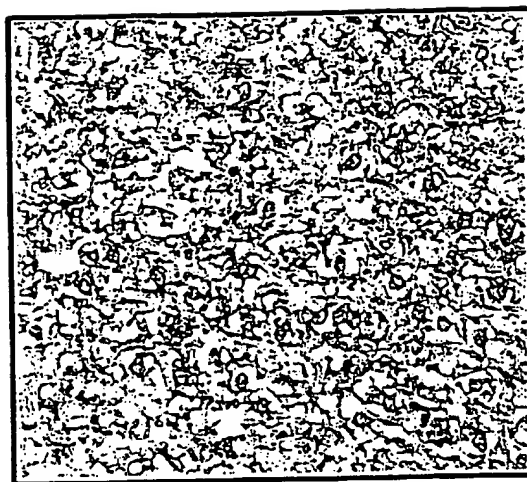


Figure - 14A

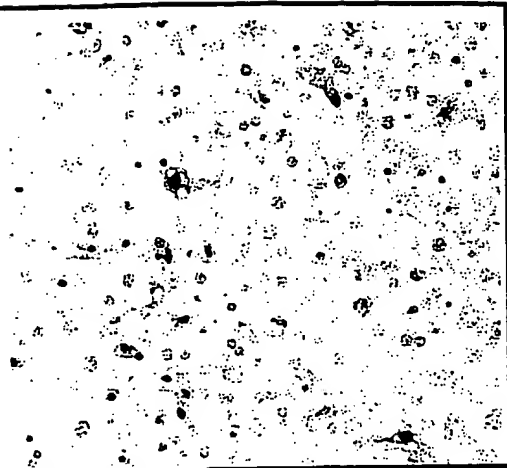


Figure - 14B

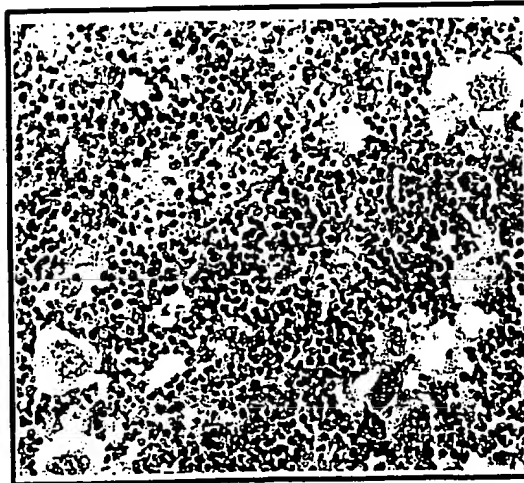


Figure - 14C



Figure - 14D

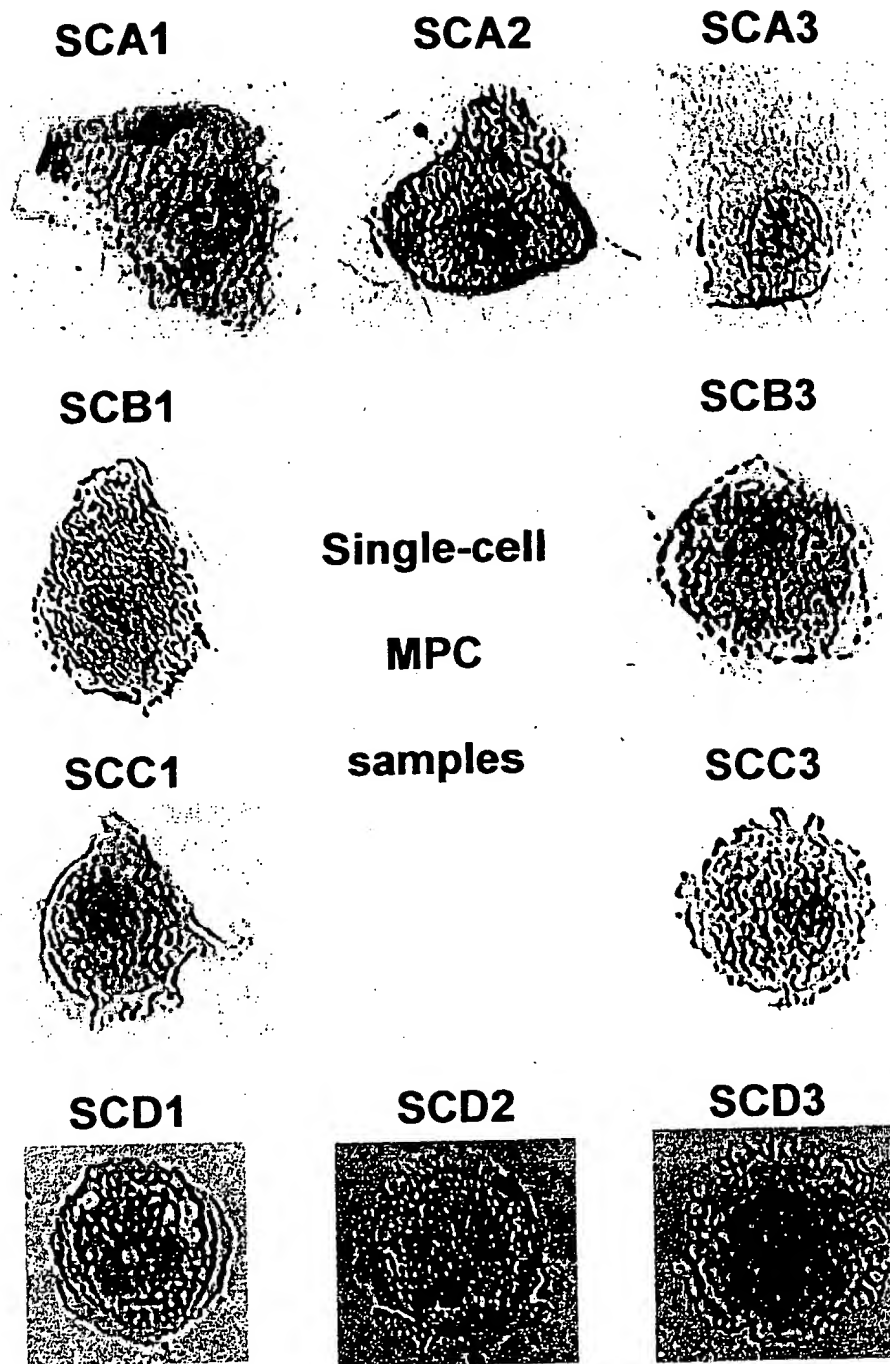


Figure - 15

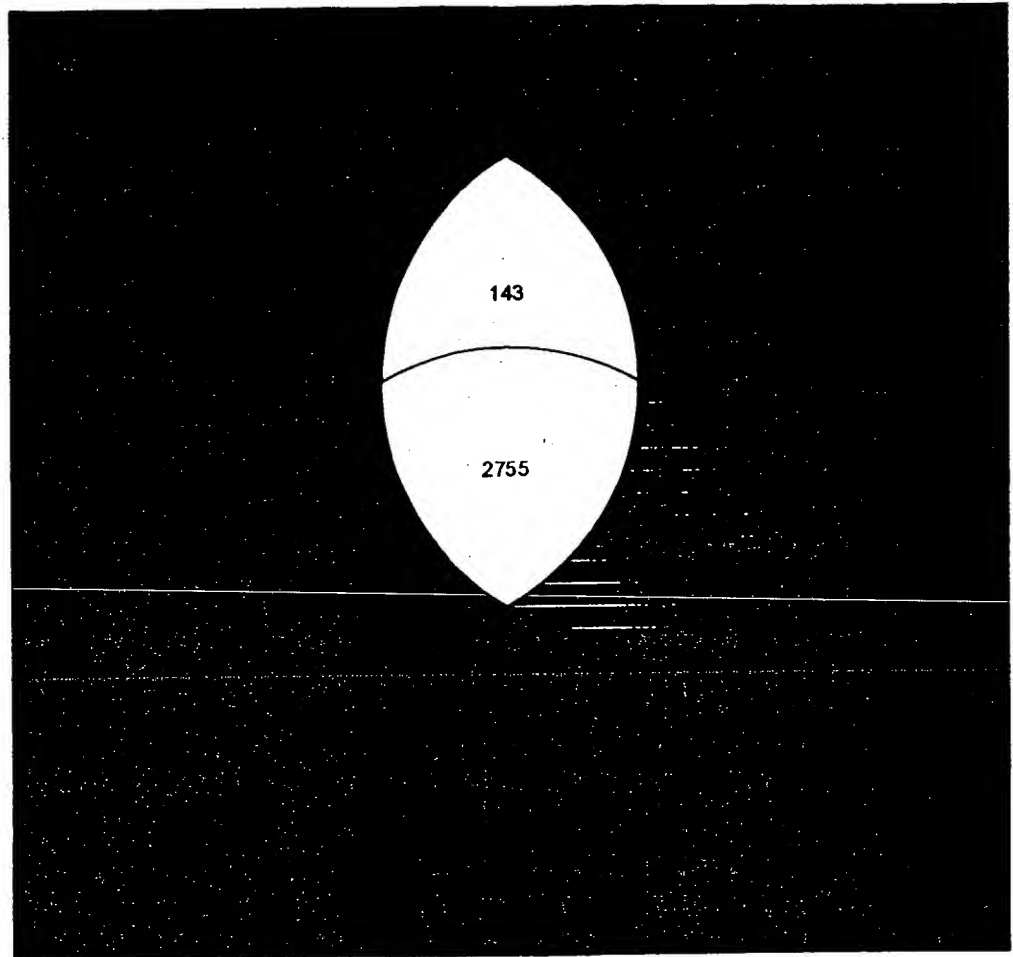


Figure - 16

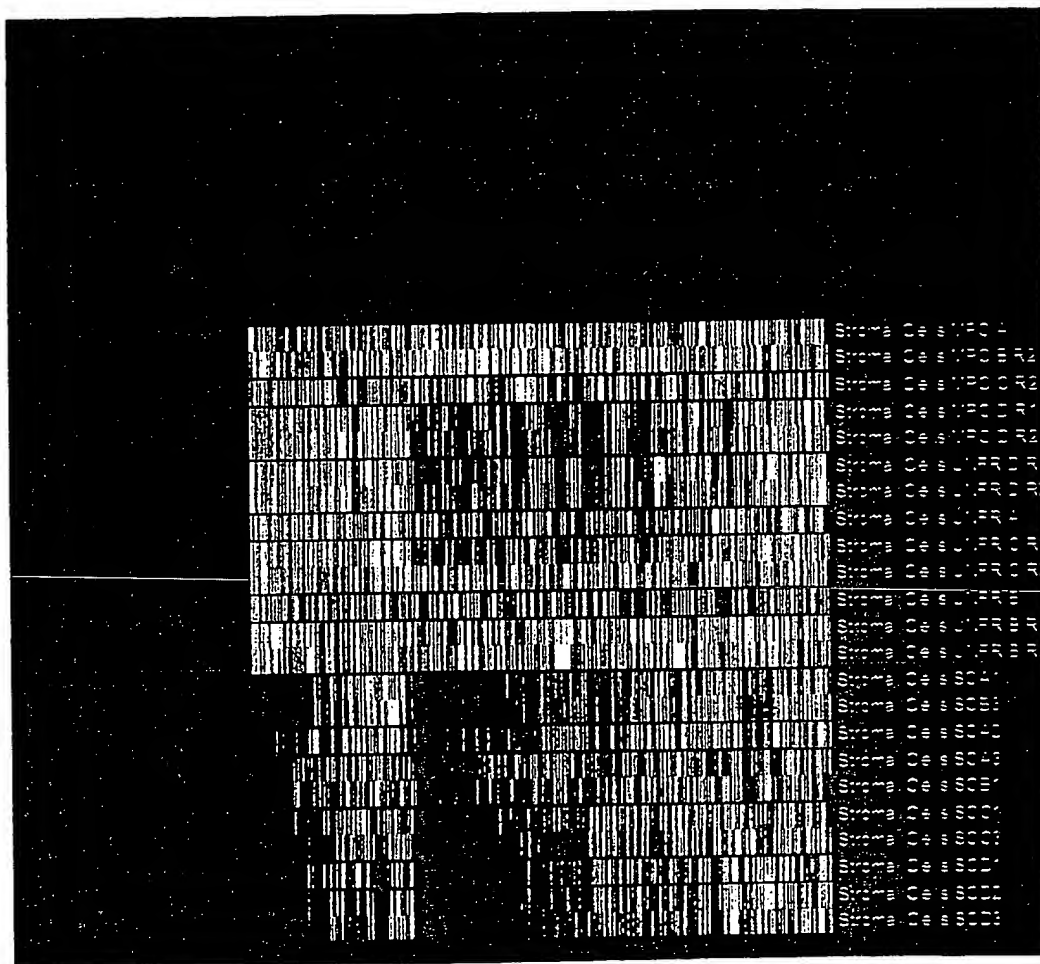


Figure - 17

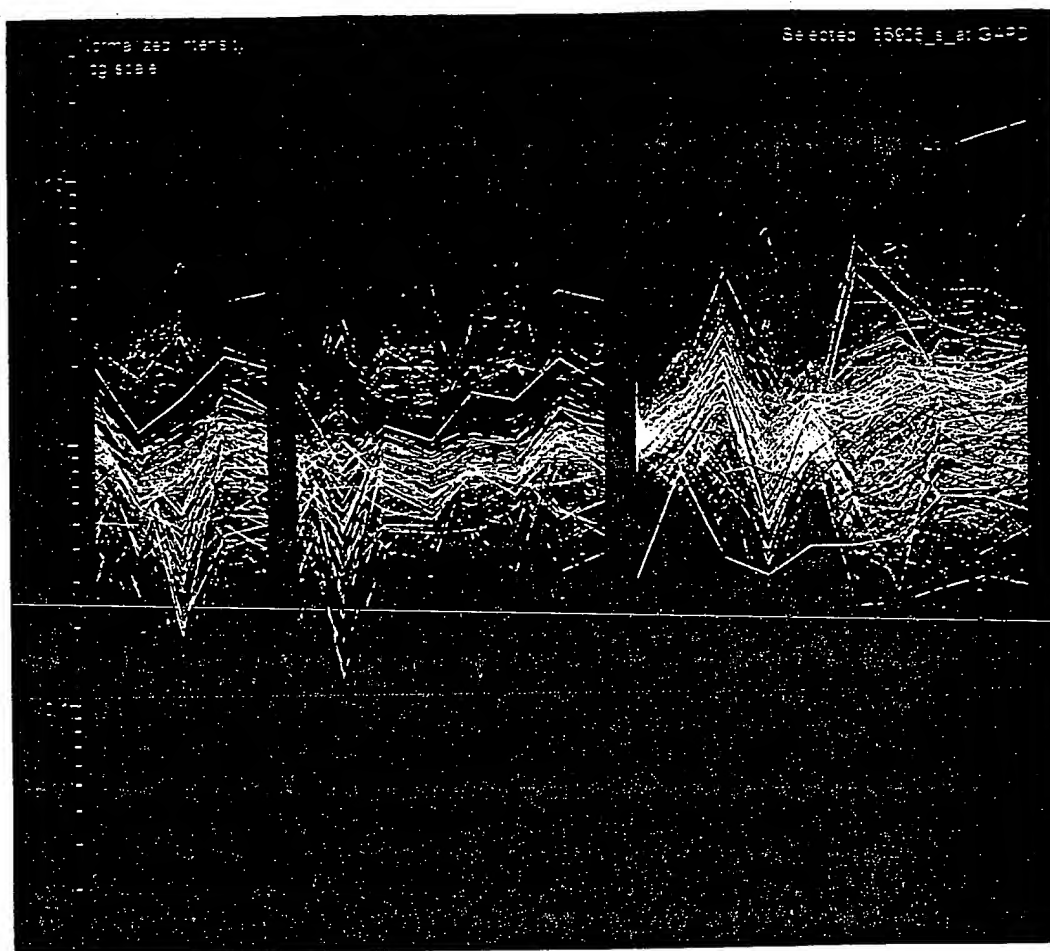


Figure - 18

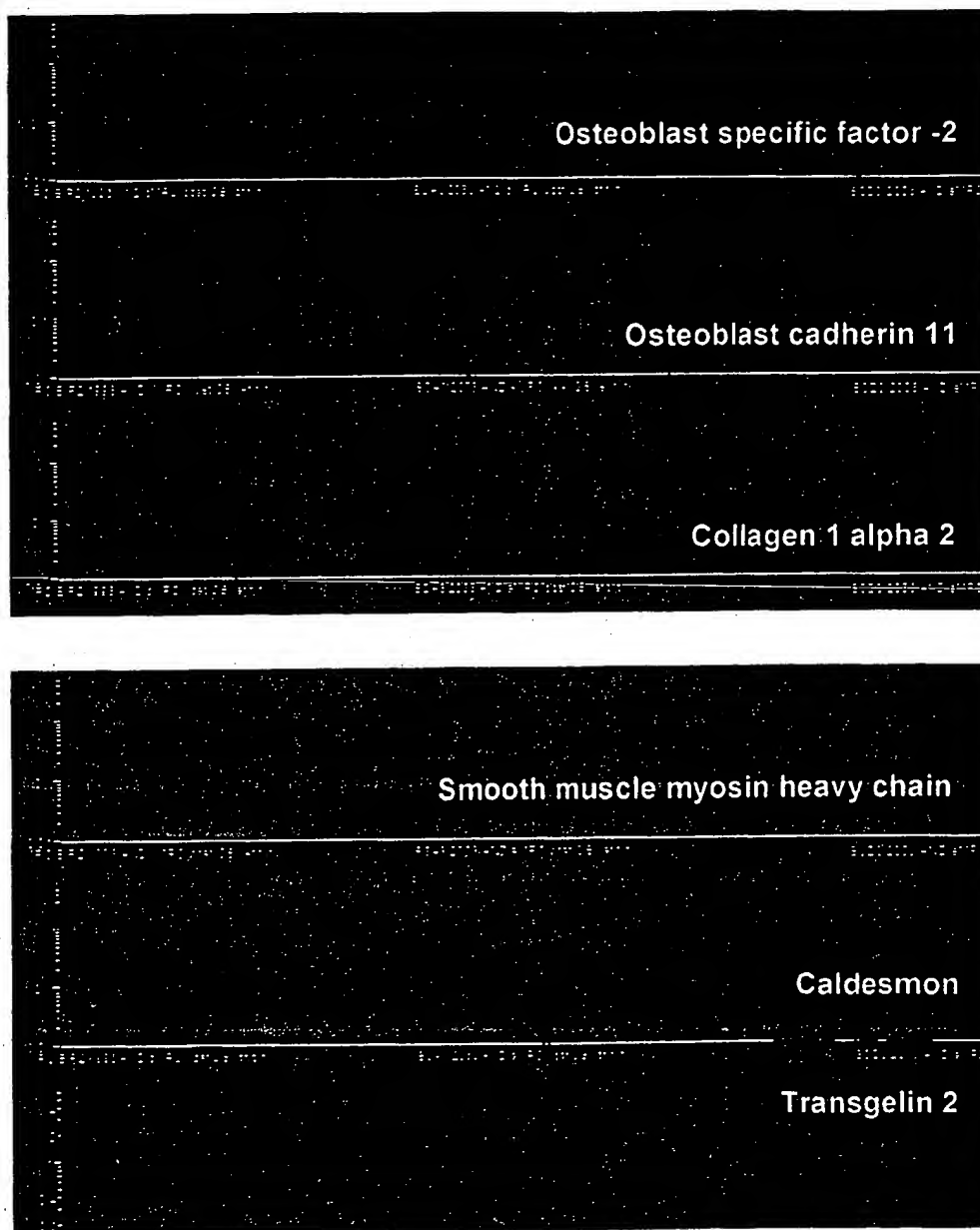
**Collective MPCs
(Samples 1-5)****Single cell MPCs
(Samples 6-15)**

Figure - 19

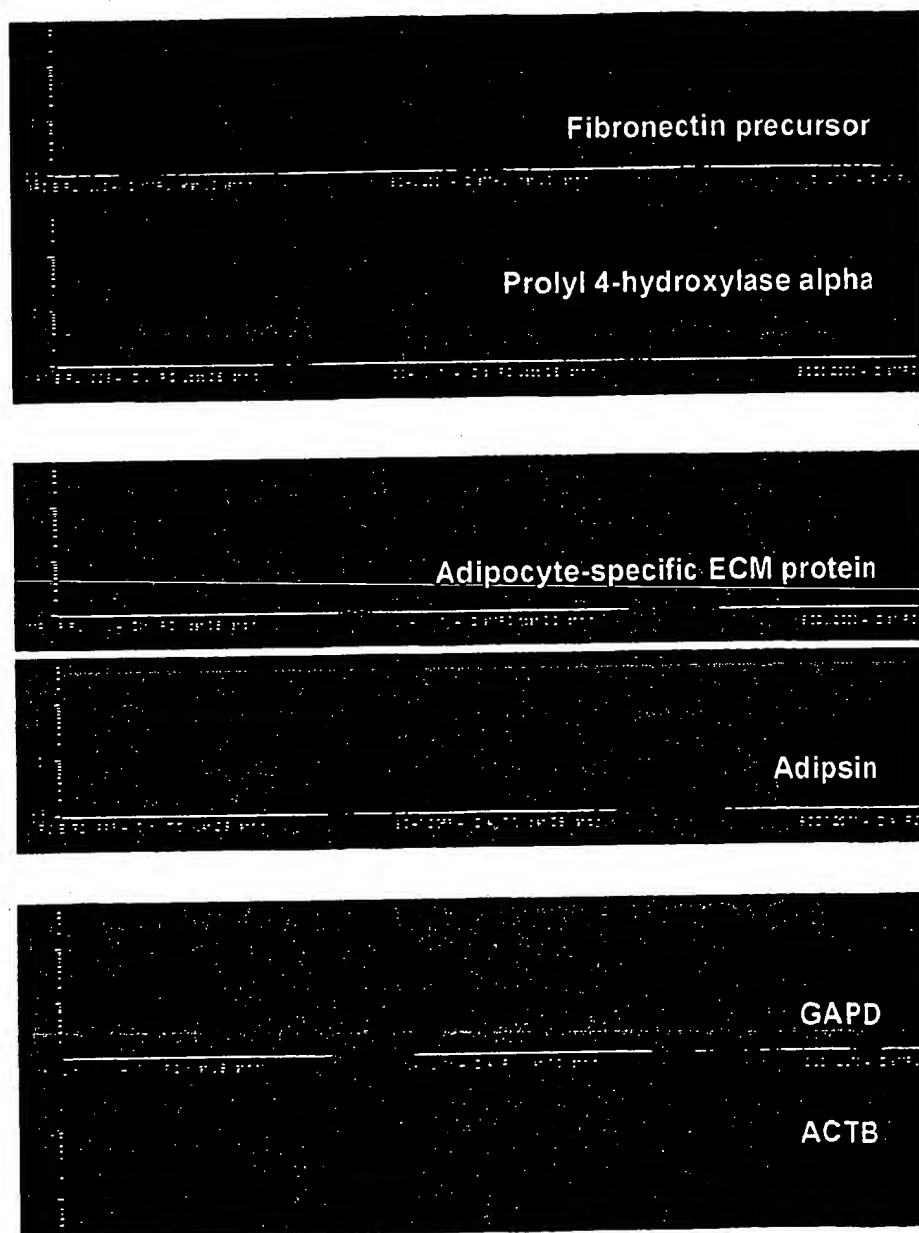
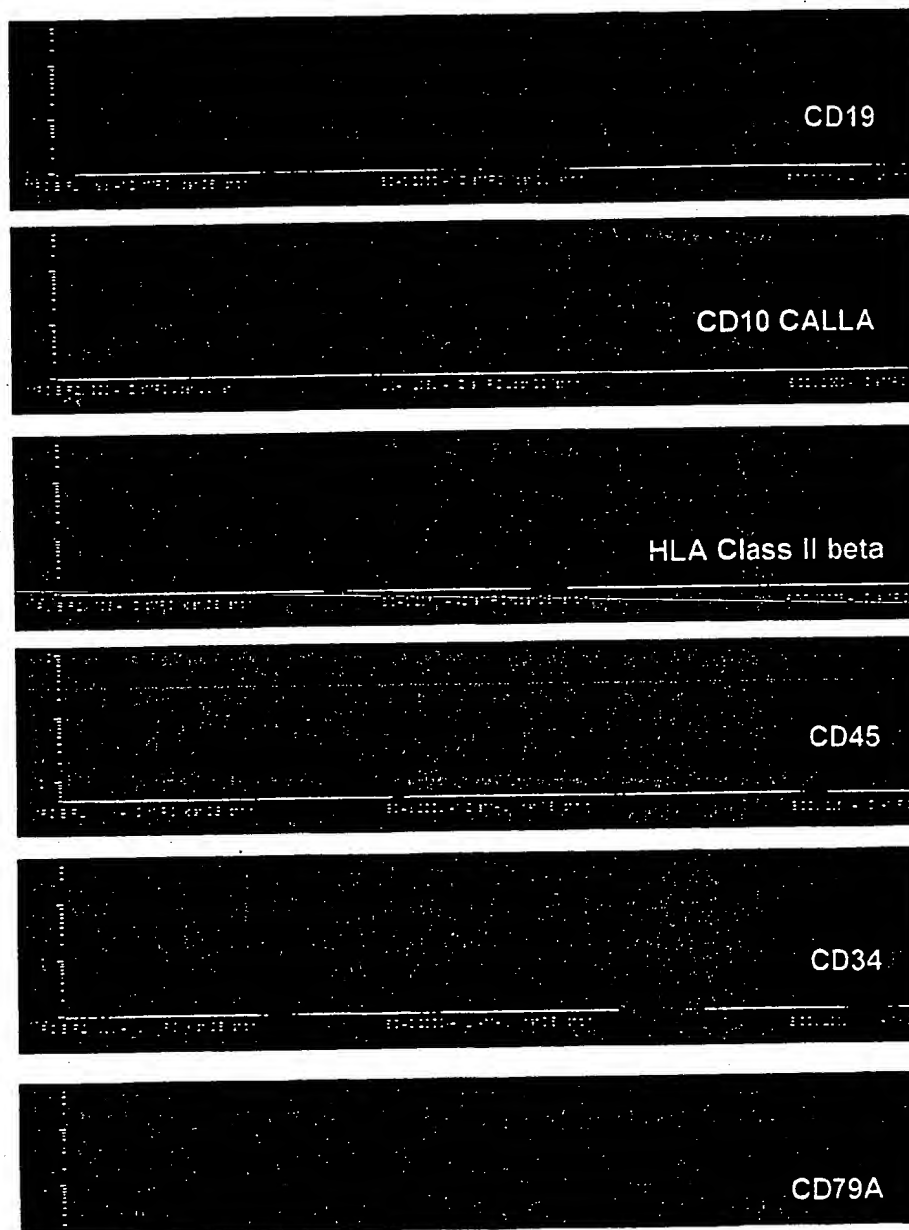
**Collective MPCs
(Samples 1-5)****Single cell MPCs
(Samples 6-15)**

Figure - 20

**Collective MPCs
(Samples 1-5)****Single cell MPCs
(Samples 6-15)****Figure - 21**

| A | | B | | C | | D | | E | |
|----|-----------------|----------|--|----------|--|--|--|---|--|
| 1 | Systematic | Common | | Genbank | | Description | | Product | |
| 2 | AFFX-hum_alu_at | | | U14573 | | ***ALU WARNING: Human Alu-Sq subfamily consensus sequence. | | | |
| 3 | 38820_at | 15-Sep | | AF051894 | | 15 kDa selenoprotein | | 15 kDa selenoprotein | |
| 4 | 33247_at | POH1 | | U86782 | | 26S proteasome-associated pad1 homolog | | 26S proteasome-associated pad1 homolog | |
| 5 | 32165_at | SFRS7 | | L41887 | | 35 kDa protein; Homo sapiens splicing factor, arginine/serine-rich 7 (SFRS7) gene, complete cds. | | splicing factor, arginine/serine-rich 7 | |
| 6 | 36851_g_at | N33 | | U42360 | | 39 kDa protein; Human N33 protein form 2 (N33) gene, exon 11 and complete cds. | | N33 protein form 2 | |
| 7 | 39328_at | HMGCR | | M11058 | | 3-hydroxy-3-methylglutaryl-Coenzyme A reductase | | 3-hydroxy-3-methylglutaryl-Coenzyme A reductase | |
| 8 | 41142_at | OXCT | | U62961 | | 3-oxoacid CoA transferase | | succinyl CoA:3-oxoacid CoA transferase precursor | |
| 9 | 34411_at | PAPSS1 | | Y10387 | | 3'-phosphoadenosine 5'-phosphosulfate synthase 1 | | PAPS synthetase | |
| 10 | 738_at | NT5C2 | | D38524 | | 5'-nucleotidase, cytosolic II | | 5'-nucleotidase | |
| 11 | 31794_at | NT5C2 | | D38524 | | 5'-nucleotidase, cytosolic II | | 5'-nucleotidase | |
| 12 | 38811_at | ATIC | | D82348 | | 5-aminimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase | | 5-aminimidazole-4-carboxamide-1-beta-D-ribo-nucl eotide transferase/inosinase | |
| 13 | 38383_at | MTR | | U73338 | | 5-methyltetrahydrofolate-homocysteine methyltransferase | | methionine synthase | |
| 14 | 39025_at | LOC54543 | | A1557912 | | 6.2 kd protein | | | |

Fig 21

| A | B | C | D | E |
|---------------|-------------|----------|--|--|
| | | | 60S Ribosomal Protein L35A LIKE pseudogene match: proteins P04646 P02434 P18077 P05744 P41056 CE04362 match: cDNAs Y16430 X52966 X03475 V01440 X55030 J00995 match: ESTs AA554649 AA747384 AA572868 AA329139 AA745138 AA330809 AA483371 AA507788 AA483213 D55111 N90267 N91909 AA662153 AA720551 AA836920 AA501529 AA526745 AA608598 AA649846 AA654164 match: genomic DNAs Z32550 X05705 X05706 X05704 I23465 I45758 | |
| 15 40446_at | cICK0721Q.1 | AL021366 | | divalent cation tolerant protein CUTA |
| 16 39059_at | DHCR7 | AF034544 | 7-dehydrocholesterol reductase | delta 7-sterol reductase |
| 17 40797_at | ADAM10 | AF009615 | a disintegrin and metalloproteinase domain 10 | ADAM10 |
| 18 41601_at | ADAM17 | AA142964 | a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme) | |
| 19 34761_r_at | ADAM9 | U41766 | a disintegrin and metalloproteinase domain 9 (meltrin gamma) | metalloproteinase/disintegrin/cysteine-rich protein precursor |
| 20 37680_at | AKAP12 | U81607 | A kinase (PRKA) anchor protein (gravin) 12 | gravin |
| 21 36633_at | AKAP10 | AA114830 | A kinase (PRKA) anchor protein 10 | |
| 22 34657_at | AKAP11 | AB014529 | A kinase (PRKA) anchor protein 11 | KIAA0629 protein |
| 23 35985_at | AKAP2 | AB023137 | A kinase (PRKA) anchor protein 2 | KIAA0920 protein |

Fig 21

| | A | B | C | D | E |
|----|-----------|----------|----------|---|---|
| 24 | 1636_g_at | ABL | U07563 | <p>ABL is the cellular homolog proto-oncogene of Abelson's murine leukemia virus and is associated with the t(9;22) chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia; alternative splicing using alternative first exon 1b; ABL is the cellular homolog proto-oncogene of Abelson's murine leukemia virus and is associated with the t(9;22) chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia; alternative splicing using exon 1a; Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.</p> | <p>proto-oncogene tyrosine-protein kinase</p> |
| 25 | 41724_at | DXS1357E | X81817 | | |
| | | | | | |
| 26 | 41530_at | ACAA2 | D16294 | | |
| 27 | 34668_at | ACATN | D88152 | | |
| | | | | <p>accessory proteins BAP31/BAP29</p> | <p>accessory proteins BAP31/BAP29</p> |
| 28 | 36553_at | ASMTL | AA669799 | <p>acetyl-Coenzyme A thiolase</p> | <p>mitochondrial 3-oxoacyl-CoA thiolase</p> |
| 29 | 37034_at | ANP32A | U73477 | <p>acetyl-Coenzyme A transporter</p> | <p>acetyl-Coenzyme A transporter</p> |
| 30 | 38479_at | ANP32B | Y07969 | <p>acetylserotonin O-methyltransferase-like</p> | |
| 31 | 34397_at | OA48-18 | AF069250 | <p>acidic (leucine-rich) nuclear phosphoprotein 32 family, member A</p> | <p>acidic nuclear phosphoprotein pp32</p> |
| 32 | 39168_at | ALTE | AB018328 | <p>acidic (leucine-rich) nuclear phosphoprotein 32 family, member B</p> | <p>APRIL</p> |
| 33 | 40077_at | ACO1 | Z11559 | <p>acid-inducible phosphoprotein</p> | <p>okadaic acid-inducible phosphoprotein</p> |
| 34 | 37578_at | AFAP | D25248 | <p>Ac-like transposable element</p> | <p>KIAA0785 protein</p> |
| | | | | <p>aconitase 1, soluble</p> | <p>iron regulatory factor</p> |
| 35 | 1718_at | ARPC2 | U50523 | <p>actin filament associated protein</p> | <p>actin filament associated protein</p> |
| | | | | <p>actin related protein 2/3 complex, subunit 2</p> | <p>actin related protein 2/3 complex, subunit 2 (34 kD)</p> |

Fig 21

| | A | B | C | D | E |
|----|--------------|--------|----------|--|---|
| 36 | 34692_r_at | ARPC4 | AF006087 | actin related protein 2/3 complex, subunit 4 (20 kD) | p20-Arc |
| 37 | 38392_at | ARPC5 | AF006088 | actin related protein 2/3 complex, subunit 5 (16 kD) | p16-Arc |
| 38 | 32755_at | ACTA2 | X13839 | actin, alpha 2, smooth muscle, aorta | alpha 2 actin |
| 39 | AFFX-HSAC07X | ACTB | X00351 | actin, beta | beta actin |
| 40 | AFFX-HSAC07X | ACTB | X00351 | actin, beta | beta actin |
| 41 | 32318_s_at | ACTB | X63432 | actin, beta | mutant beta-actin (beta'-actin) |
| 42 | 34160_at | ACTG1 | X04098 | actin, gamma 1 | gamma-actin |
| 43 | 39329_at | ACTN1 | X15804 | actinin, alpha 1 | actinin, alpha 1 |
| 44 | 41753_at | ACTN4 | U48734 | actinin, alpha 4 | alpha actinin |
| 45 | 38642_at | ALCAM | Y10183 | activated leucocyte cell adhesion molecule | MEIMD protein |
| 46 | 36171_at | PC4 | AI521453 | activated RNA polymerase II transcription cofactor 4 | |
| 47 | 39764_at | ACVR1 | Z22534 | activin A receptor, type I | ALK-2 |
| 48 | 35162_s_at | ACVR2 | D31770 | activin A receptor, type II | activin type II A receptor precursor |
| 49 | 34394_at | ADNP | AB018327 | activity-dependent neuroprotector | KIAA0784 protein |
| 50 | 40673_at | ACADSB | U12778 | acyl-Coenzyme A dehydrogenase, short/branched chain | acyl-CoA dehydrogenase |
| 51 | 40459_at | ACOX1 | S69189 | acyl-Coenzyme A oxidase 1, palmitoyl | peroxisomal acyl-coenzyme A oxidase |
| 52 | 40745_at | AP1B1 | L13939 | adaptor-related protein complex 1, beta 1 subunit | beta-prime-adaptin |
| 53 | 35275_at | AP1G1 | AL050025 | adaptor-related protein complex 1, gamma 1 subunit | hypothetical protein |
| 54 | 39795_at | AP2M1 | D63475 | adaptor-related protein complex 2, mu 1 subunit | adaptor-related protein complex 2, mu 1 subunit |
| 55 | 39347_at | AP2S1 | X97074 | adaptor-related protein complex 2, sigma 1 subunit | clathrin-associated protein |
| 56 | 32039_at | AP3B1 | U81504 | adaptor-related protein complex 3, beta 1 subunit | beta-3A-adaptin subunit of the AP-3 complex |
| 57 | 36172_s_at | AP3D1 | AF002163 | adaptor-related protein complex 3, delta 1 subunit | delta-adaptin |
| 58 | 38074_at | AP3S1 | U91932 | adaptor-related protein complex 3, sigma 1 subunit | AP-3 complex sigma3A subunit |
| 59 | 33102_at | ADD3 | D67031 | adducin 3 (gamma) | adducin-like protein |

Fig 21

| | A | B | C | D | E |
|----|------------|---------------|----------|---|---|
| 60 | 38014_at | ADAR | X79448 | adenosine deaminase, RNA-specific | adenosine deaminase, RNA-specific, isoform ADAR-a; adenosine deaminase, RNA-specific, isoform ADAR-b; adenosine deaminase, RNA-specific, isoform ADAR-c |
| 61 | 38748_at | ADARB1 | U76421 | adenosine deaminase, RNA-specific, B1 (RED1 homolog rat) | dsRNA adenosine deaminase DRADA2b |
| 62 | 168_at | ADK | U50196 | adenosine kinase | adenosine kinase |
| 63 | 33865_at | BS69 | AA127624 | adenovirus 5 E1A binding protein | |
| 64 | 33134_at | ADCY3 | AB011083 | adenylate cyclase 3 | KIAA0511 protein |
| 65 | 40585_at | ADCY7 | D25538 | adenylate cyclase 7 | adenylate cyclase 7 |
| 66 | 33800_at | ADCY9 | AF036927 | adenylate cyclase 9 | adenylate cyclase type IX |
| 67 | 40788_at | AK2 | U84371 | adenylate kinase 2 | adenylate kinase 2A |
| 68 | 36639_at | ADSL | AF067853 | adenylosuccinate lyase | adenylosuccinate lyase |
| 69 | 935_at | CAP | L12168 | adenylyl cyclase-associated protein | adenylyl cyclase-associated protein |
| 70 | 33405_at | CAP2 | N90755 | adenylyl cyclase-associated protein 2 | |
| 71 | 34378_at | ADFP | X97324 | adipose differentiation-related protein | adipophillin |
| 72 | 36861_at | DKFZp564I1922 | AL049946 | adican | hypothetical protein |
| 73 | 33987_at | ARF1 | M36340 | ADP-ribosylation factor 1 | ADP-ribosylation factor 1 |
| 74 | 39336_at | ARF3 | M74491 | ADP-ribosylation factor 3 | ADP-ribosylation factor 3 |
| 75 | 36585_at | ARF4 | M36341 | ADP-ribosylation factor 4 | ADP-ribosylation factor 4 |
| 76 | 37537_at | ARFD1 | L04510 | ADP-ribosylation factor domain protein 1, 64kD | nucleotide binding protein |
| 77 | 39905_i_at | ARFGAP1 | AA402332 | ADP-ribosylation factor GTPase activating protein 1 | |
| 78 | 37296_at | ARL1 | L28997 | ADP-ribosylation factor-like 1 | ADP-ribosylation factor-like 1 |
| 79 | 36572_r_at | ARL6IP | D31885 | ADP-ribosylation factor-like 6 interacting protein | |
| 80 | 41146_at | ADPRT | J03473 | ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase) | poly(ADP-ribose)transferase |
| 81 | 1287_at | ADPRT | J03473 | ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase) | poly(ADP-ribose)transferase |
| 82 | 34777_at | ADM | D14874 | adrenomedullin | adrenomedullin precursor |
| 83 | 32218_at | | AF034176 | AF034176 Human mRNA (Tripodis and Ragoussis) Homo sapiens cDNA clone ntcon5 contig. | |

Fig 21

| | A | B | C | D | E |
|-----|------------|----------|----------|---|---|
| 84 | 34315_at | AFG3L2 | Y18314 | AFG3 ATPase family gene 3-like 2 (yeast) | paraplegin-like protein |
| 85 | 33454_at | AGRN | AF016903 | agnin | agnin precursor |
| 86 | 37027_at | AHNAK | M80899 | AHNAK nucleoprotein (desmoyokin) | |
| 87 | 36185_at | AARS | D32050 | alanyl-tRNA synthetase | alanyl-tRNA synthetase |
| 88 | 36686_at | ALDH1A3 | U07919 | aldehyde dehydrogenase 1 family, member A3 | aldehyde dehydrogenase 6 |
| 89 | 32747_at | ALDH2 | X05409 | aldehyde dehydrogenase 2 family (mitochondrial) | aldehyde dehydrogenase 2 family (mitochondrial) |
| 90 | 40409_at | ALDH3A2 | U46689 | aldehyde dehydrogenase 3 family, member A2 | aldehyde dehydrogenase |
| 91 | 37331_g_at | ALDH4A1 | U24266 | aldehyde dehydrogenase 4 family, member A1 | pyrroline-5-carboxylate dehydrogenase |
| 92 | 36132_at | ALDH7A1 | S74728 | aldehyde dehydrogenase 7 family, member A1 | antiquitin |
| 93 | 33899_at | ALDH9A1 | U34252 | aldehyde dehydrogenase 9 family, member A1 | gamma-aminobutyraldehyde dehydrogenase |
| 94 | 38780_at | AKR1A1 | J04794 | aldo-keto reductase family 1, member A1 (aldehyde reductase) | aldo-keto reductase family 1, member A1 (aldehyde reductase) |
| 95 | 36589_at | AKR1B1 | X15414 | aldo-keto reductase family 1, member B1 (aldose reductase) | aldo-keto reductase family 1, member B1 (aldose reductase) |
| 96 | 37399_at | AKR1C3 | D17793 | aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II) | aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II) |
| 97 | 32510_at | AKR7A2 | AF026947 | aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase) | aflatoxin aldehyde reductase AFAR |
| 98 | 39225_at | AGPS | Y09443 | alkylglycerone phosphate synthase | alkyl-dihydroxyacetonephosphate synthase precursor |
| 99 | 36941_at | AF1Q | U16954 | ALL1-fused gene from chromosome 1q | AF1Q protein |
| 100 | 37040_at | G2AN | D42041 | alpha glucosidase II alpha subunit | alpha glucosidase II alpha subunit |
| 101 | 35223_at | KIAA1017 | AB023234 | alpha integrin binding protein 63 | KIAA1017 protein |
| 102 | 39147_g_at | ATRX | U72936 | alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae) | putative DNA dependent ATPase and helicase |

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| | A | B | C | D | E |
|-----|------------|----------|----------|--|--|
| 103 | 818_s_at | ATRX | U72936 | alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae) | putative DNA dependent ATPase and helicase |
| 104 | 34327_at | HLTF | Z46606 | alternative translation initiation; H.sapiens HLTF gene for helicase-like transcription factor. | helicase-like transcription factor |
| 105 | 35761_at | AASDHPPT | AL050073 | aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase | hypothetical protein |
| 106 | 39431_at | NPEPPS | AJ132583 | aminopeptidase puromycin sensitive | puromycin sensitive aminopeptidase |
| 107 | 41338_at | AES | AI951946 | amino-terminal enhancer of split | OS-9 precursor |
| 108 | 36996_at | OS-9 | U41635 | amplified in osteosarcoma | |
| 109 | 38253_at | AGL | U84011 | amylase-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) | glycogen debranching enzyme isoform 6 |
| 110 | 41136_s_at | APP | Y00264 | amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) | amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) |
| 111 | 40148_at | APBB2 | U62325 | amyloid beta (A4) precursor protein-binding, family B, member 2 (F65-like) | FE65-like protein |
| 112 | 38471_r_at | APPBP2 | D86981 | amyloid beta precursor protein (cytoplasmic tail) binding protein 2 | KIAA0228 protein |
| 113 | 38470_i_at | APPBP2 | D86981 | amyloid beta precursor protein (cytoplasmic tail) binding protein 2 | KIAA0228 protein |
| 114 | 35364_at | APPBP1 | U50939 | amyloid beta precursor protein binding protein 1, 59kD | amyloid precursor protein-binding protein 1 |
| 115 | 40064_at | ALS2CR3 | AB011121 | amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3 | KIAA0549 protein |
| 116 | 1577_at | AR | M23263 | androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease) | androgen receptor |
| 117 | 38842_at | AMOTL2 | AB023206 | angiomotin like 2 | angiomotin like 2 |
| 118 | 39315_at | ANGPT1 | D13628 | angiotensinogen 1 | angiotensinogen 1 |
| 119 | 1929_at | ANGPT1 | U83508 | angiotensinogen 1 | angiotensinogen 1 |

Fig 21

| | A | B | C | D | E |
|-----|------------|-----------------|----------|--|---|
| 120 | 36965_at | ANK3 | U13616 | ankyrin 3, node of Ranvier (ankyrin G) | ankyrin G |
| 121 | 37403_at | ANXA1 | X05908 | annexin A1 | annexin I |
| 122 | 36637_at | ANXA11 | L19605 | annexin A11 | 56K autoantigen |
| 123 | 769_s_at | ANXA2 | D00017 | annexin A2 | lipocortin II |
| 124 | 31684_at | ANXA2P1 | M62896 | annexin A2 pseudogene 1 | |
| 125 | 31444_s_at | ANXA2P3 | M62895 | annexin A2 pseudogene 3 | |
| 126 | 37374_at | ANXA4 | M82809 | annexin A4 | annexin IV (placental anticoagulant protein II) |
| 127 | 37670_at | ANXA7 | J04543 | annexin A7 | annexin VII isoform 1; annexin VII isoform 2 |
| 128 | 41138_at | MIC2 | M16279 | antigen identified by monoclonal antibodies 12E7, F21 and O13 | antigen |
| 129 | 40506_s_at | PABPC4; APP1; A | U75686 | APP-1; Homo sapiens polyadenylate binding protein mRNA, complete cds. | polyadenylate binding protein |
| 130 | 34370_at | ARGN1 | X81198 | archain 1 | archain |
| 131 | 32253_at | REER | AB007927 | arginine-glutamic acid dipeptide (RE) repeats | KIAA0458 protein |
| 132 | 549_at | RARS | S80343 | arginyl-tRNA synthetase | arginyl-tRNA synthetase |
| 133 | 39164_at | ARIH2 | AF099149 | ariadne homolog 2 (Drosophila) | TRIAD1 type I |
| 134 | 41729_at | ARIH1 | AJ009771 | ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila) | putative RING finger protein |
| 135 | 36057_at | ALEX2 | AB011084 | armadillo repeat protein ALEX2 | KIAA0512 protein |
| 136 | 40052_at | ACTR1A | X82206 | ARP1 actin-related protein 1 homolog A, centractin alpha (yeast) | alpha-centractin |
| 137 | 35734_at | ACTR2 | A1935551 | ARP2 actin-related protein 2 homolog (yeast) | |
| 138 | 35733_at | ACTR2 | AF006082 | ARP2 actin-related protein 2 homolog (yeast) | Arp2 |
| 139 | 35271_at | ACTR3 | AF006083 | ARP3 actin-related protein 3 homolog (yeast) | Arp3 |
| 140 | 40516_at | AHR | L19872 | aryl hydrocarbon receptor | AH-receptor |
| 141 | 36671_at | ASNS | M27396 | asparagine synthetase | asparagine synthetase |
| 142 | 41241_at | NARS | D84273 | asparaginyl-tRNA synthetase | Asparaginyl tRNA Synthetase |
| 143 | 38703_at | DNPEP | AF005050 | aspartyl aminopeptidase | aspartyl aminopeptidase |
| 144 | 34181_at | AGA | X55330 | aspartylglucosaminidase | aspartylglucosaminidase |

Fig 21

| | A | B | C | D | E |
|-----|------------|--------|----------|--|--|
| 145 | 37229_at | ATR | U49844 | ataxia telangiectasia and Rad3 related | FRAP-related protein |
| 146 | 34817_s_at | A2LP | U70671 | ataxin 2 related protein | ataxin-2 related protein |
| 147 | 379_at | APACD | AB006679 | ATP binding protein associated with cell differentiation | ATP binding protein |
| 148 | 40881_at | ACLY | X64330 | ATP citrate lyase | ATP-citrate (pro-S)-lyase |
| 149 | 41228_r_at | ATP5F1 | X60221 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1 | H+-ATP synthase subunit b |
| 150 | 34811_at | ATP5G3 | U09813 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 | mitochondrial ATP synthase subunit 9 precursor |
| 151 | 35760_at | ATP5H | AF087135 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d | F1FO-type ATPase subunit d |
| 152 | 38751_i_at | ATP5I | AA426364 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e | |
| 153 | 36107_at | ATP5J | AA845575 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6 | |
| 154 | 38693_at | ATP5L | AA917672 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g | |
| 155 | 40115_at | ATP5C1 | D16562 | ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1 | ATP synthase gamma-subunit |
| 156 | 39791_at | ATP2A2 | M23114 | ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 | ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 |
| 157 | 39790_at | ATP2A2 | M23115 | ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 | ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 |
| 158 | 38684_at | ATP2C1 | AJ010953 | ATPase, Ca++ transporting, type 2C, member 1 | putative Ca2+-transporting ATPase |
| 159 | 35831_at | ATP9A | AB014511 | ATPase, Class II, type 9A | KIAA0611 protein |
| 160 | 40853_at | ATP10D | AI478147 | ATPase, Class V, type 10D | |
| 161 | 36635_at | ATP11B | AB023173 | ATPase, Class VI, type 11B | KIAA0956 protein |
| 162 | 36523_at | ATP7A | L06133 | ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome) | Cu++-transporting P-type ATPase |
| 163 | 33854_at | ATP6M | AA877795 | ATPase, H+ transporting, lysosomal (vacuolar proton pump) | |

Fig 21

| | A | B | C | D | E |
|-----|------------|----------|----------|---|--|
| 164 | 37395_at | ATP6S14 | D49400 | ATPase, H+ transporting, lysosomal (vacuolar proton pump) 14kD | vacuolar ATPase |
| 165 | 36994_at | ATP6L | M62762 | ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD | vacuolar H+ ATPase proton channel subunit |
| 166 | 36167_at | ATP6F | D89052 | ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kD | proton-ATPase-like protein |
| 167 | 37367_at | ATP6E | X76228 | ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD | vacuolar H+ ATPase E subunit |
| 168 | 37948_at | ATP6C | J05682 | ATPase, H+ transporting, lysosomal (vacuolar proton pump) 42kD | H+ -ATPase C subunit |
| 169 | 33875_at | ATP6H | A1547262 | ATPase, H+ transporting, lysosomal (vacuolar proton pump) 9kD | |
| 170 | 40903_at | ATP6M8-9 | AL049929 | ATPase, H+ transporting, lysosomal (vacuolar proton pump) membrane sector associated protein M8-9 | hypothetical protein |
| 171 | 34889_at | ATP6A1 | AA056747 | ATPase, H+ transporting, lysosomal (vacuolar proton pump), alpha polypeptide, 70kD, isoform 1 | |
| 172 | 40568_at | ATP6B2 | L35249 | ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 2 | vacuolar H+ ATPase 56,000 subunit |
| 173 | 35770_at | ATP6S1 | D16469 | ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1 | ORF |
| 174 | 37669_s_at | ATP1B1 | U16799 | ATPase, Na+/K+ transporting, beta 1 polypeptide | Na, K-ATPase beta subunit |
| 175 | 32563_at | ATP1B3 | U51478 | ATPase, Na+/K+ transporting, beta 3 polypeptide | sodium/potassium-transporting ATPase beta-3 subunit |
| 176 | 35717_at | ABCA8 | AB020629 | ATP-binding cassette, sub-family A (ABC1), member 8 | KIAA0822 protein |
| 177 | 38261_at | ABCC3 | AF085692 | ATP-binding cassette, sub-family C (CFTR/MRP), member 3 | multidrug resistance-associated protein 3B |
| 178 | 35648_at | KIAA0442 | AB007902 | autism-related protein 1 | autism-related protein 1 |
| 179 | 38068_at | AMFR | M63175 | autocrine motility factor receptor | autocrine motility factor receptor |
| 180 | 38433_at | AXL | M76125 | AXL receptor tyrosine kinase | tyrosine kinase receptor |
| 181 | 35268_at | AXOT | AL050171 | axotrophin | hypothetical protein DKFZp586F1122 similar to axotrophin |

Fig 21

| | A | B | C | D | E |
|-----|----------|--------------|----------|--|--|
| 182 | 35350_at | GALNAC4S-6ST | AB011170 | B cell RAG associated protein | KIAA0598 protein |
| 183 | 41562_at | BMI1 | L13689 | B lymphoma Mo-MLV insertion region (mouse) | murine leukemia viral (bmi-1) oncogene homolog |
| 184 | 1728_at | BMI1 | L13689 | B lymphoma Mo-MLV insertion region (mouse) | murine leukemia viral (bmi-1) oncogene homolog |
| 185 | 36578_at | BIRC2 | U37547 | baculoviral IAP repeat-containing 2 | MIHB |
| 186 | 41278_at | BAF53A | AF041474 | BAF53 | BAF53a |
| 187 | 33175_at | BBS4 | AA156237 | Bardet-Biedl syndrome 4 | |
| 188 | 40790_at | BHLHB2 | AB004066 | basic helix-loop-helix domain containing, class B, 2 | |
| 189 | 40108_at | BZAP45 | D13630 | basic leucine-zipper protein BZAP45 | basic leucine-zipper protein BZAP45 |
| 190 | 40202_at | BTEB1 | D31716 | basic transcription element binding protein 1 | GC box binding protein |
| 191 | 35055_at | BTF3 | X53281 | basic transcription factor 3 | general transcription factor |
| 192 | 38364_at | BCE-1 | AF068197 | BCE-1 protein | BCE-1 |
| 193 | 40091_at | BCL6 | U00115 | B-cell CLL/lymphoma 6 (zinc finger protein 51) | zinc-finger protein |
| 194 | 37294_at | BTG1 | X61123 | B-cell translocation gene 1, anti-proliferative | B-cell translocation protein 1 |
| 195 | 32060_at | BNIP2 | U15173 | BCL2/adenovirus E1B 19kD interacting protein 2 | BCL2/adenovirus E1B 19kD-interacting protein 2 |
| 196 | 38010_at | BNIP3 | AF002697 | BCL2/adenovirus E1B 19kD interacting protein 3 | E1B 19K/Bcl-2-binding protein Nip3 |
| 197 | 39436_at | BNIP3L | AF079221 | BCL2/adenovirus E1B 19kD interacting protein 3-like | BCL2/adenovirus E1B 19kDa-interacting protein 3a |
| 198 | 34798_at | BAG1 | Z35491 | BCL2-associated athanogene | glucocorticoid receptor-associated protein RAP46 |
| 199 | 35291_at | BAG2 | AL050287 | BCL2-associated athanogene 2 | hypothetical protein |
| 200 | 36463_at | BAG5 | AB020680 | BCL2-associated athanogene 5 | KIAA0873 protein |
| 201 | 38050_at | BTF | D79986 | Bcl-2-associated transcription factor | KIAA0164 gene product |
| 202 | 38101_at | BDG-29 | AB011151 | BDG-29 protein | KIAA0579 protein |
| 203 | 39378_at | BECN1 | U17999 | beclin 1 (coiled-coil, myosin-like BCL2 interacting protein) | |
| 204 | 39160_at | PDHB | D90086 | beta subunit; Human pyruvate dehydrogenase (EC 1.2.4.1) beta subunit gene, exons 1-10. | pyruvate dehydrogenase (lipoamide) beta |

Fig 21

| | A | B | C | D | E |
|-----|------------|--------|----------|---|---|
| 205 | 34644_at | B2M | AB021288 | beta-2-microglobulin | beta 2-microglobulin |
| 206 | 40601_at | BBP | AI057115 | beta-amyloid binding protein precursor | |
| | | | | beta-hexosaminidase alpha chain; Human | |
| 207 | 39340_at | HEXA | M16424 | beta-hexosaminidase alpha chain (HEXA) | hexosaminidase A preproprotein |
| 208 | 38126_at | BGN | J04599 | gene, exon 14. | biglycan preproprotein |
| 209 | 33198_at | BART1 | AA206524 | biglycan | |
| | | | | binder of Arl Two | |
| 210 | 37274_at | Btd | AF018631 | biotin-amide amidohydrolase; Homo sapiens biotinidase (BTD) gene, exons 2, 3, and 4 and complete cds. | biotinidase |
| | | | | biphenyl hydrolase-like (serine hydrolase; breast epithelial mucin-associated antigen) | biphenyl hydrolase-related protein |
| 211 | 40912_s_at | BPHL | X81372 | bladder cancer associated protein | bladder cancer associated protein |
| 212 | 35267_g_at | BLCAP | AL049288 | bladder cancer associated protein | bladder cancer associated protein |
| 213 | 35266_at | BLCAP | AL049288 | bleomycin hydrolase | bleomycin hydrolase |
| 214 | 37700_at | BLMH | X92106 | bone morphogenetic protein receptor, type IA | ALK-3 |
| 215 | 39565_at | BMPR1A | Z22535 | BRAF35/HDAC2 complex (80 kDa) | |
| 216 | 39551_at | BHC80 | N98667 | brain abundant, membrane attached signal protein 1 | neuronal tissue-enriched acidic protein |
| 217 | 32607_at | BASP1 | AF039656 | brain-abundant, membrane attached signal protein 1 | |
| 218 | 32606_at | BASP1 | AA135683 | brain acyl-CoA hydrolase | acyl-CoA thioester hydrolase |
| 219 | 37945_at | BACH | U91316 | brain cell membrane protein 1 | brain cell membrane protein 1 |
| 220 | 37958_at | BCMP1 | AL049257 | brain-derived neurotrophic factor | brain-derived neurotrophic factor |
| 221 | 40023_at | BDNF | X60201 | branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) | branched chain alpha-ketoacid dehydrogenase E1 beta subunit |
| 222 | 41683_i_at | BCKDHB | U50708 | breast cancer anti-estrogen resistance 3 | breast cancer antiestrogen resistance 3 protein |
| 223 | 36812_at | BCAR3 | U92715 | breast cancer anti-estrogen resistance 3 | |
| | | | | breifeldin A-inhibited guanine nucleotide-exchange protein 1 | |
| 224 | 38306_at | BIG1 | AA477576 | bromodomain containing 3 | bromodomain containing protein 3 |
| 225 | 37947_at | BRD3 | D26362 | BTB and CNC homology 1, basic leucine zipper transcription factor 1 | BTB and CNC homology 1, basic leucine zipper transcription factor 1 |
| 226 | 31895_at | BACH1 | AB002803 | zipper transcription factor 1 | |

Fig 21

| | A | B | C | D | E |
|-----|------------|----------|----------|---|--|
| 227 | 36634_at | BTG2 | U72649 | BTG family, member 2 | BTG2 |
| 228 | 37218_at | BTG3 | D64110 | BTG family, member 3 | ANA |
| 229 | 41547_at | BUB3 | AF047472 | BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast) | spleen mitotic checkpoint BUB3 |
| 230 | 34783_s_at | BUB3 | AF047473 | BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast) | testis mitotic checkpoint BUB3 |
| 231 | 32781_f_at | BPAG1 | AA058762 | bullous pemphigoid antigen 1 (230/240kD) | |
| 232 | 32780_at | BPAG1 | AB018271 | bullous pemphigoid antigen 1 (230/240kD) | KIAA0728 protein |
| 233 | 32629_f_at | BTN3A1 | U90552 | butyrophilin, subfamily 3, member A1 | butyrophilin |
| 234 | 39357_at | C2F | U72514 | C2f protein | C2f |
| 235 | 40709_at | LOC58502 | W27601 | C2H2 (Kruppel-type) zinc finger protein | |
| 236 | 37031_at | C9orf10 | D80005 | C9orf10 protein | C9orf10 protein |
| 237 | 33856_at | CXX1 | Y13374 | CAAX box 1 | putative prenylated protein |
| 238 | 36976_at | CDH11 | D21255 | cadherin 11, type 2, OB-cadherin (osteoblast) | OB-cadherin-2 |
| 239 | 2087_s_at | CDH11 | D21254 | cadherin 11, type 2, OB-cadherin (osteoblast) | OB-cadherin-1 |
| 240 | 2053_at | CDH2 | M34064 | cadherin 2, type 1, N-cadherin (neuronal) | cadherin 2, type 1 preproprotein |
| 241 | 31670_s_at | CAMK2G | U81554 | calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma | CaM kinase II isoform |
| 242 | 38716_at | CAMKK2 | AB018330 | calcium/calmodulin-dependent protein kinase kinase 2, beta | KIAA0787 protein |
| 243 | 31854_at | CASK | AF035582 | calcium/calmodulin-dependent serine protein kinase (MAGUK family) | CASK |
| 244 | 41738_at | CALD1 | M64110 | caldesmon 1 | caldesmon |
| 245 | 41739_s_at | CALD1 | M83216 | caldesmon 1 | caldesmon |
| 246 | 41288_at | CALM1 | AL036744 | calmodulin 1 (phosphorylase kinase, delta) | |
| 247 | 911_s_at | CALM2 | M19311 | calmodulin 2 (phosphorylase kinase, delta) | calmodulin 2 (phosphorylase kinase, delta) |
| 248 | 40125_at | CANX | L10284 | calnexin | calnexin |
| 249 | 37001_at | CAPN2 | M23254 | calpain 2, (m/l) large subunit | neutral protease large subunit |
| 250 | 36138_at | CAPNS1 | X04106 | calpain, small subunit 1 | calpain, small subunit 1 |

Fig 21

| | A | B | C | D | E |
|-----|------------|---------|----------|---|--|
| 251 | 41257_at | CAST | D16217 | calpastatin | calpastatin |
| 252 | 33385_g_at | CAST | U31346 | calpastatin | calpastatin |
| 253 | 40953_at | CNN3 | S80562 | calponin 3, acidic | acidic calponin |
| 254 | 37345_at | CALU | AF013759 | calumenin | calumenin |
| 255 | 37535_at | CREB1 | M27691 | cAMP responsive element binding protein 1 | cAMP responsive element binding protein 1, isoform A; cAMP responsive element binding protein 1, isoform B |
| 256 | 40849_s_at | CREB3 | U88528 | cAMP responsive element binding protein 3 (human) | transcription factor LZIP |
| 257 | 39438_at | CREBL2 | AF039081 | cAMP responsive element binding protein-like 2 | Cre binding protein-like 2 |
| 258 | 32065_at | CREM | S68134 | cAMP responsive element modulator | cyclic AMP-responsive element modulator |
| 259 | 32067_at | CREM | S68271 | cAMP responsive element modulator | beta isoform |
| 260 | 32066_g_at | CREM | S68134 | cAMP responsive element modulator | cyclic AMP-responsive element modulator |
| 261 | 40910_at | CAPZA1 | U56637 | capping protein (actin filament) muscle Z-line, alpha 1 | cyclic AMP-responsive element modulator |
| 262 | 36841_at | CAPZA2 | U03851 | capping protein (actin filament) muscle Z-line, alpha 2 | beta isoform |
| 263 | 37012_at | CAPZB | U03271 | capping protein (actin filament) muscle Z-line, beta | capping protein alpha subunit isoform 1 |
| 264 | 32094_at | CHST3 | AB017915 | carbohydrate (chondroitin 6) | capping protein alpha |
| 265 | 41447_at | CHSY1 | AB023207 | sulfotransferase 3 | F-actin capping protein beta subunit |
| 266 | 41395_at | CHST1 | AB003791 | carbohydrate (chondroitin 6) | chondroitin 6-sulfotransferase |
| 267 | 37960_at | CHST2 | AB014679 | carbohydrate (chondroitin) synthase 1 | KIAA0990 protein |
| 268 | 36454_at | CA12 | AF037335 | carbohydrate (keratan sulfate Gal-6) | keratan sulfate Gal-6-sulfotransferase |
| 269 | 34876_at | CPD | U65090 | sulfotransferase 1 | N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST) |
| 270 | 36606_at | CPE | X51405 | carbohydrate (N-acetylglucosamine-6-O) | carboxic anhydride precursor |
| 271 | 35632_at | CBLB | U26710 | sulfotransferase 2 | carboxypeptidase D |
| 272 | 40184_at | CSNK1A1 | L37042 | carboxic anhydride XII | carboxypeptidase E precursor |
| 273 | 36949_at | CSNK1D | U29171 | carboxypeptidase D | cbl-b |
| | | | | carboxypeptidase E | casein kinase I-alpha |
| | | | | Cas-Br-M (murine) ectropic retroviral transforming sequence b | casein kinase I delta |

Fig 21

| | A | B | C | D | E |
|-----|------------|---------|----------|---|---|
| 274 | 38019_at | CSNK1E | L37043 | casein kinase 1, epsilon | casein kinase I-epsilon |
| 275 | 1211_s_at | CRADD | U84388 | CASP2 and RIPK1 domain containing adaptor with death domain | death domain containing protein CRADD |
| 276 | 1867_at | CFLAR | AF005775 | CASP8 and FADD-like apoptosis regulator | caspase-like apoptosis regulatory protein 2 |
| 277 | 195_s_at | CASP4 | U28014 | caspase 4, apoptosis-related cysteine protease | cysteine protease |
| 278 | 33774_at | CASP8 | X98172 | caspase 8, apoptosis-related cysteine protease | MACH-alpha-1 |
| 279 | 41156_g_at | CTNNA1 | U03100 | catenin (cadherin-associated protein), alpha 1 (102kD) | alpha2(E)-catenin |
| 280 | 41155_at | CTNNA1 | U03100 | catenin (cadherin-associated protein), alpha 1 (102kD) | alpha2(E)-catenin |
| 281 | 2085_s_at | CTNNA1 | D14705 | catenin (cadherin-associated protein), alpha 1 (102kD) | 'human alpha-catenin' |
| 282 | 2069_s_at | CTNNA1 | L23805 | catenin (cadherin-associated protein), alpha 1 (102kD) | alpha1(E)-catenin |
| 283 | 35331_at | CTNNAL1 | U97067 | catenin (cadherin-associated protein), alpha-like 1 | alpha-catenin-like protein |
| 284 | 40777_at | CTNNB1 | X87838 | catenin (cadherin-associated protein), beta 1 (88kD) | beta-catenin |
| 285 | 40444_s_at | CTNND1 | AB002382 | catenin (cadherin-associated protein), delta 1 | |
| 286 | 38466_at | CTSK | X82153 | cathepsin K (pseudosynthesis) | Cathepsin O |
| 287 | 37391_at | CTSL | X12451 | cathepsin L | pro-(cathepsin L) |
| 288 | 36915_at | CTSO | A1810485 | cathepsin O | |
| 289 | 36119_at | CAV1 | AF070648 | caveolin 1, caveolae protein, 22kD | |
| 290 | 339_at | CAV2 | AF035752 | caveolin 2 | caveolin-2 |
| 291 | 33113_at | CITED2 | U65093 | Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 | msg-related gene 1 |
| 292 | 1052_s_at | CEBPD | M83667 | CCAAT/enhancer binding protein (C/EBP), delta | NF-IL6-beta protein |
| 293 | 39219_at | CEBPG | U20240 | CCAAT/enhancer binding protein (C/EBP), gamma | C/EBP_gamma |

Fig 21

| | A | B | C | D | E |
|-----|------------|---------|----------|--|--|
| 294 | 33861_at | CNOT2 | AI123426 | CCR4-NOT transcription complex, subunit 2 | |
| 295 | 32820_at | CNOT4 | U71267 | CCR4-NOT transcription complex, subunit 4 | potential transcriptional repressor NOT4Hp |
| 296 | 34819_at | CD164 | D14043 | CD164 antigen, sialomucin | MGC-24 precursor |
| 297 | 34699_at | CD2AP | AL050105 | CD2-associated protein | hypothetical protein |
| 298 | 33823_at | CD36L2 | D12676 | CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal integral membrane protein II) | 85kDa human lysosomal sialoglycoprotein |
| 299 | 2036_s_at | CD44 | M59040 | CD44 antigen (homing function and Indian blood group system) | cell adhesion molecule |
| 300 | 35282_r_at | CD81 | M33680 | CD81 antigen (target of antiproliferative antibody 1) | CD81 antigen |
| 301 | 39389_at | CD9 | M38690 | CD9 antigen (p24) | CD9 antigen |
| 302 | 32175_at | CDC10 | S72008 | CDC10 cell division cycle 10 homolog (S. cerevisiae) | cell division cycle 10 |
| 303 | 40404_s_at | CDC16 | U18291 | CDC16 cell division cycle 16 homolog (S. cerevisiae) | CDC16Hs |
| 304 | 31877_at | CDC23 | AF053977 | CDC23 (cell division cycle 23, yeast, homolog) | cell division cycle protein 23 |
| 305 | 40690_at | CKS2 | X54942 | CDC28 protein kinase 2 | Cks1 protein homologue |
| 306 | 33362_at | CEP3 | AF094521 | Cdc42 effector protein 3 | MSE55-related protein |
| 307 | 32833_at | CLK1 | M59287 | CDC-like kinase 1 | |
| 308 | 41535_at | CDK2AP1 | AF006484 | CDK2-associated protein 1 | putative oral tumor suppressor protein |
| 309 | 41343_at | CDS2 | Y16521 | GDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 2 | CDS2 protein |
| 310 | 33397_at | CDIPT | AL050383 | GDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase) | |
| 311 | 40591_at | CDC27 | S78234 | cell division cycle 27 | H-NUC |
| 312 | 450_g_at | CGR19 | U66469 | cell growth regulatory with ring finger domain | cell growth regulator CGR19 |
| 313 | 36514_at | CGR19 | U66469 | cell growth regulatory with ring finger domain | cell growth regulator CGR19 |

Fig 21

| A | B | C | D | E |
|----------------|----------|----------|--|--|
| 314 35311_at | CREG | AF084523 | cellular repressor of E1A-stimulated genes | cellular repressor of E1A-stimulated genes |
| 315 41333_at | CENTB2 | D26069 | centaurin, beta 2 | centaurin, beta 2 |
| 316 34676_at | CENTG2 | AB029022 | centaurin, gamma 2 | KIAA1099 protein |
| 317 38410_at | CETN2 | X72964 | centrin, EF-hand protein, 2 | caltractin |
| 318 35232_f_at | CETN3 | AI056696 | centrin, EF-hand protein, 3 (CDC31 homolog, yeast) | |
| 319 31894_at | CENPC1 | M95724 | centromere protein C 1 | centromere autoantigen C |
| 320 33805_at | CAP350 | AB007949 | centrosome-associated protein 350 | KIAA0480 protein |
| 321 36190_at | CDR2 | M63256 | cerebellar degeneration-related protein (62kD) | major Yo paraneoplastic antigen |
| 322 32262_at | CGI-01 | AL049669 | CGI-01 protein | hypothetical protein |
| 323 40931_at | LOC50999 | AL080084 | CGI-100 protein | |
| 324 38500_at | LOC51014 | AB002450 | CGI-109 protein | |
| 325 34359_at | LOC51020 | AA524058 | CGI-130 protein | |
| 326 38667_at | LOC51031 | AA189161 | CGI-150 protein | |
| 327 41824_at | LOC51096 | AI140114 | CGI-48 protein | |
| 328 34862_at | LOC51097 | AA005018 | CGI-49 protein | |
| 329 37199_at | LOC51626 | AI760932 | CGI-60 protein | |
| 330 41411_at | LOC51103 | AI566877 | CGI-65 protein | |
| 331 39814_s_at | LOC51635 | AI052724 | CGI-86 protein | |
| 332 35759_at | CCT2 | AF026166 | chaperonin containing TCP1, subunit 2 (beta) | chaperonin-containing TCP-1 beta subunit homolog |
| 333 40774_at | CCT3 | X74801 | chaperonin containing TCP1, subunit 3 (gamma) | gamma subunit of CCT chaperonin |
| 334 32594_at | CCT4 | AF026291 | chaperonin containing TCP1, subunit 4 (delta) | chaperonin containing t-complex polypeptide 1, delta subunit |
| 335 38416_at | CCT6A | L27706 | chaperonin containing TCP1, subunit 6A (zeta 1) | chaperonin-like protein |
| 336 38720_at | CCT7 | AF026292 | chaperonin containing TCP1, subunit 7 (eta) | chaperonin containing t-complex polypeptide 1, eta subunit |
| 337 39767_at | CCT8 | D13627 | chaperonin containing TCP1, subunit 8 (theta) | chaperonin containing TCP1, subunit 8 (theta) |
| 338 41000_at | CHES1 | U68723 | checkpoint suppressor 1 | checkpoint suppressor 1 |
| 339 37855_at | CTBS | M95767 | chitinase, di-N-acetyl- | di-N-acetylchitinase |

Fig 21

| | A | B | C | D | E |
|-----|------------|----------|----------|---|---|
| 340 | 38732_at | CLNS1A | X91788 | chloride channel, nucleotide-sensitive, 1A | lcn protein |
| 341 | 33891_at | CLIC4 | AL080061 | chloride intracellular channel 4 | |
| 342 | 32363_at | CH25H | AF059214 | cholesterol 25-hydroxylase | cholesterol 25-hydroxylase |
| 343 | 38112_g_at | CSPG2 | X15998 | chondroitin sulfate proteoglycan 2 (versican) | chondroitin sulfate proteoglycan 2 (versican) |
| 344 | 38111_at | CSPG2 | X15998 | chondroitin sulfate proteoglycan 2 (versican) | chondroitin sulfate proteoglycan 2 (versican) |
| 345 | 34763_at | CSPG6 | AF020043 | chondroitin sulfate proteoglycan 6 (barnacan) | chromosome-associated polypeptide |
| 346 | 37304_at | CBX1 | U35451 | chromobox homolog 1 (HP1 beta homolog Drosophila) | heterochromatin protein p25 |
| 347 | 38085_at | CBX3 | AI740522 | chromobox homolog 3 (HP1 gamma homolog, Drosophila) | |
| 348 | 38084_at | CBX3 | AA648295 | chromobox homolog 3 (HP1 gamma homolog, Drosophila) | |
| 349 | 36137_at | CHD4 | X86691 | chromodomain helicase DNA binding protein 4 | Mi-2 protein |
| 350 | 32111_at | CDYL | AL050164 | chromodomain protein, Y chromosome-like | hypothetical protein |
| 351 | 39550_at | C1orf17 | AB011156 | chromosome 1 open reading frame 17 | KIAA0584 protein |
| 352 | 39033_at | C1orf8 | Z78368 | chromosome 1 open reading frame 8 | |
| 353 | 32217_at | C12orf22 | AF052105 | chromosome 12 open reading frame 22 | TGF-beta induced apoptosis protein 12 |
| 354 | 40979_at | C14orf3 | AJ243310 | chromosome 14 open reading frame 3 | C14orf3 protein |
| 355 | 40045_g_at | C18orf1 | AF009425 | chromosome 18 open reading frame 1 | clone 22 |
| 356 | 36860_at | C19orf7 | AB028987 | chromosome 19 open reading frame 7 | KIAA1064 protein |
| 357 | 34287_at | C21orf80 | AB023175 | chromosome 21 open reading frame 80 | KIAA0958 protein |
| 358 | 33406_at | C22orf2 | AL050345 | chromosome 22 open reading frame 2 | hypothetical protein |
| 359 | 33778_at | C22orf4 | AL096779 | chromosome 22 open reading frame 4 | hypothetical protein |
| 360 | 41758_at | C22orf5 | AL096879 | chromosome 22 open reading frame 5 | hypothetical protein |
| 361 | 38690_at | C3orf4 | AL080097 | chromosome 3 open reading frame 4 | hypothetical protein |
| 362 | 36013_at | C4orf1 | AF006621 | chromosome 4 open reading frame 1 | embryonic lung protein |
| 363 | 36955_at | C5orf8 | U10362 | chromosome 5 open reading frame 8 | GP36b glycoprotein |
| 364 | 41375_at | C6orf28 | AJ245416 | chromosome 6 open reading frame 28 | G7b protein |
| 365 | 41454_at | C6orf34 | W27949 | chromosome 6 open reading frame 34 | |
| 366 | 36139_at | C6orf5 | AL050289 | chromosome 6 open reading frame 5 | hypothetical protein |

Fig 21

| | A | B | C | D | E |
|-----|------------|-----------|----------|---|---|
| 367 | 35193_at | CHC1L | AF060219 | chromosome condensation 1-like | RCC1-like G exchanging factor RLG |
| 368 | 34292_at | CXorf12 | X92475 | chromosome X open reading frame 12 | chromosome X open reading frame 12 |
| 369 | 41314_at | CS | AF047042 | citrate synthase | citrate synthase |
| 370 | 41159_at | CLTC | D21260 | clathrin, heavy polypeptide (Hc) | clathrin heavy chain |
| 371 | 38657_s_at | CLTA | M20471 | clathrin, light polypeptide (Lca) | clathrin, light polypeptide A, isoform a; |
| 372 | 35743_at | CPSF4 | U79569 | cleavage and polyadenylation specific factor 4, 30kD subunit | clathrin, light polypeptide A, isoform b |
| 373 | 32723_at | CSTF1 | L02547 | cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kD | no arches |
| 374 | 41183_at | CSTF3 | U15782 | cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD | cleavage stimulation factor |
| 375 | 38711_at | CLASP2 | AB014527 | CLIP-associating protein 2 | cleavage stimulation factor 77kDa subunit |
| 376 | 36017_at | LOC57213 | AF055016 | CLLL6 protein | KIAA0627 protein |
| 377 | 36780_at | CLU | M25915 | clusterin (complement lysis inhibitor, SP-40, 40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J) | CLLL6 protein |
| 378 | 35180_at | LOC113251 | AL050205 | c-Mpl binding protein | clusterin (complement lysis inhibitor, SP-40, 40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J) |
| 379 | 40811_at | COASTER | AB011148 | coactivator for steroid receptors | apolipoprotein J |
| 380 | 38052_at | F13A1 | M14539 | coagulation factor XIII, A1 polypeptide | KIAA0576 protein |
| 381 | 36972_at | RNP24 | X92098 | coated vesicle membrane protein | coagulation factor XIII A1 subunit precursor |
| 382 | 34326_at | COPB | X82103 | coatamer protein complex, subunit beta (beta prime) | transmembrane protein |
| 383 | 36677_at | COPB2 | X70476 | coatamer protein complex, subunit beta 2 | beta-Coat protein |
| 384 | 35205_at | COBRA1 | AL050280 | cofactor of BRCA1 | subunit of coatamer complex |
| 385 | 36648_at | CRSP9 | AF031383 | cofactor required for Sp1 transcriptional activation, subunit 9 (33kD) | hypothetical protein |
| 386 | 33659_at | CFL1 | X95404 | cofilin 1 (non-muscle) | hMed7 |
| 387 | 40879_at | BICD2 | AB014599 | coiled-coil protein BICD2 | cofilin |
| 388 | 39864_at | CIRBP | D78134 | cold inducible RNA binding protein | KIAA0699 protein |
| 389 | 39839_at | CSDA | M24069 | cold shock domain protein A | CIRP |
| 390 | 32307_s_at | COL1A2 | V00503 | collagen, type I, alpha 2 | cold shock domain protein A |
| 391 | 32306_g_at | COL1A2 | J03464 | collagen, type I, alpha 2 | alpha 2 type I collagen preproprotein |
| 392 | 32305_at | COL1A2 | J03464 | collagen, type I, alpha 2 | alpha 2 type I collagen preproprotein |

Fig 21

| | A | B | C | D | E |
|-----|------------|------------|----------|--|---|
| 393 | 32488_at | | | collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) | prepro-alpha-1 type 3 collagen |
| 394 | 36659_at | COL3A1 | X14420 | collagen, type IV, alpha 2 | alpha (2) chain |
| 395 | 38420_at | COL4A2 | X05610 | collagen, type V, alpha 2 | procollagen alpha 2(V) |
| 396 | 38722_at | COL5A2 | Y14690 | collagen, type VI, alpha 1 | alpha-1 collagen VI (AA 574-1009) |
| 397 | 38077_at | COL6A1 | X15880 | collagen, type VI, alpha 3 | collagen type VI, alpha 3 chain |
| 398 | 37459_at | COL6A3 | X52022 | collagen, type VIII, alpha 1 | alpha 1(VIII) collagen |
| | | COL8A1 | X57527 | | alpha 1 type XI collagen, isoform A |
| | | | | | preproprotein; alpha 1 type XI collagen, isoform B preproprotein; alpha 1 type XI collagen, isoform C preproprotein |
| 399 | 37892_at | COL11A1 | J04177 | collagen, type XI, alpha 1 | collagen, isoform C preproprotein |
| 400 | 35168_f_at | COL16A1 | M92642 | collagen, type XVI, alpha 1 | alpha-1 type XVI collagen |
| 401 | 37668_at | C1QBP | M69039 | complement component 1, q | complement component 1, q subcomponent binding protein precursor |
| 402 | 39409_at | C1R | M14058 | subcomponent binding protein | complement component 1, r subcomponent |
| | | | | complement component 1, r | complement component 1, r subcomponent |
| 403 | 40496_at | C1S | J04080 | subcomponent | complement component 1, s subcomponent |
| 404 | 36638_at | CTGF | X78947 | connective tissue growth factor | connective tissue growth factor |
| 405 | 41202_s_at | OS4 | AF000152 | conserved gene amplified in osteosarcoma | OS-4 protein |
| 406 | 33770_at | CHUK | AF009225 | conserved helix-loop-helix ubiquitous kinase | IkB kinase alpha subunit |
| 407 | 1789_at | COPS5 | U65928 | COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis) | Jun activation domain binding protein |
| 408 | 32539_at | COP9 | U51205 | COP9 homolog | COP9 signalosome subunit 1 CSN1 |
| 409 | 40138_at | MOV34-34KD | U70735 | COP9 subunit 6 (MOV34 homolog, 34 kD) | 34 kDa Mov34 homolog |
| 410 | 40452_at | CPNE1 | U83246 | copine I | copine I |
| 411 | 39706_at | CPNE3 | AB014536 | copine III | KIAA0636 protein |
| 412 | 37999_at | CPO | D16611 | coproporphyrinogen oxidase (coproporphyrin, harderoporphyria) | coproporphyrinogen oxidase |
| 413 | 37026_at | COPEB | AF001461 | core promoter element binding protein | Kruppel-like zinc finger protein Zf9 |
| 414 | 41175_at | CBFB | L20298 | core-binding factor, beta subunit | transcription factor |
| 415 | 32803_at | CN1L | AF104398 | cornichon-like | cornichon |

Fig 21

| | A | B | C | D | E |
|-----|------------|--------------|----------|---|--|
| 416 | 34723_at | COX11 | U79270 | COX11 homolog, cytochrome c oxidase assembly protein (yeast) | COX11 homolog |
| 417 | 37907_at | F8A; DXS522E | M34677 | CpG island protein; Human nested gene protein gene, complete cds. | coagulation factor VIII-associated protein |
| 418 | 38664_at | CFDP1 | AB009285 | craniofacial development protein 1 | craniofacial development protein 1 |
| 419 | 33831_at | CREBBP | U47741 | CREB binding protein (Rubinstein-Taybi syndrome) | CREB-binding protein |
| 420 | 36948_at | CRI1 | AL109701 | CREBBP/EP300 inhibitory protein 1 | C15orf3 |
| 421 | 38148_at | CRY1 | D83702 | cytochrome 1 (photolyase-like) | photolyase |
| 422 | 37902_at | CRY2 | L13278 | crystallin, zeta (quinone reductase) | zeta-crystallin |
| 423 | 40167_s_at | LOC55884 | AF038187 | CS box-containing WD protein | |
| 424 | 38804_at | CSE1L | AF053641 | CSE1 chromosome segregation 1-like (yeast) | cellular apoptosis susceptibility protein |
| 425 | 1768_s_at | CSK | X59932 | c-src tyrosine kinase | c-src-kinase |
| 426 | 41309_g_at | CTBP1 | U37408 | C-terminal binding protein 1 | phosphoprotein CIBP |
| 427 | 40780_at | CTBP2 | AF016507 | C-terminal binding protein 2 | C-terminal binding protein 2 |
| 428 | 39723_at | CUL1 | AF062536 | cullin 1 | cullin 1 |
| 429 | 40141_at | CUL4B | AB014595 | cullin 4B | KIAA0695 protein |
| 430 | 31823_at | CUTL1 | M74099 | cut-like 1, CCAAT displacement protein (Drosophila) | cut-like 1, CCAAT displacement protein |
| 431 | 36872_at | ARPP-19 | AL120559 | cyclic AMP phosphoprotein, 19 kD | |
| 432 | 41808_at | DMTF1 | AF052102 | cyclin D binding myb-like transcription factor 1 | cyclin D binding myb-like transcription factor 1 |
| 433 | 38418_at | CCND1 | X59798 | cyclin D1 (PRAD1; parathyroid adenomatosis 1) | cyclin |
| 434 | 2020_at | CCND1 | M73554 | cyclin D1 (PRAD1; parathyroid adenomatosis 1) | bcl-1 |
| 435 | 36650_at | CCND2 | D13639 | cyclin D2 | cyclin D2 |
| 436 | 40225_at | GAK | D88435 | cyclin G associated kinase | HsGAK |
| 437 | 37723_at | CCNG2 | U47414 | cyclin G2 | cyclin G2 |
| 438 | 1913_at | CCNG2 | U47414 | cyclin G2 | cyclin G2 |
| 439 | 1924_at | CCNH | U11791 | cyclin H | cyclin H |
| 440 | 1836_at | CCNI | D50310 | cyclin I | cyclin I |
| 441 | 1792_g_at | CDK2 | M68520 | cyclin-dependent kinase 2 | cdc2-related protein kinase |

Fig 21

| | A | B | C | D | E |
|-----|------------|---------|----------|--|---|
| 442 | 33317_at | CDK7 | L20320 | cyclin-dependent kinase 7 (MO15 homolog, <i>Xenopus laevis</i> , cdk-activating kinase) | protein serine/threonine kinase |
| 443 | 1969_s_at | CDK7 | X77743 | cyclin-dependent kinase 7 (MO15 homolog, <i>Xenopus laevis</i> , cdk-activating kinase) | CDK activating kinase |
| 444 | 35140_at | CDK8 | R59697 | cyclin-dependent kinase 8 | |
| 445 | 2031_s_at | CDKN1A | U03106 | cyclin-dependent kinase inhibitor 1A (p21, Cip1) | cyclin-dependent kinase inhibitor 1A |
| 446 | 33847_s_at | CDKN1B | A1304854 | cyclin-dependent kinase inhibitor 1B (p27, Kip1) | |
| 447 | 36053_at | CDKN2C | AF041248 | cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4) | cyclin-dependent kinase inhibitor |
| 448 | 38700_at | CSRP1 | M33146 | cysteine and glycine-rich protein 1 | cysteine and glycine-rich protein 1 |
| 449 | 41401_at | CSRP2 | U57646 | cysteine and glycine-rich protein 2 | cysteine and glycine-rich protein 2 |
| 450 | 40936_at | CRIM1 | A1651806 | cysteine-rich motor neuron 1 | |
| 451 | 38772_at | CYR61 | Y11307 | cysteine-rich, angiogenic inducer, 61 | CYR61 protein |
| 452 | 40408_at | CARS | L06845 | cysteinyl-tRNA synthetase | cysteinyl-tRNA synthetase |
| 453 | 39317_at | CMAH | D86324 | cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminic acid hydroxylase) | CMP-N-acetylneuraminic acid hydroxylase |
| 454 | 34340_at | CYB5-M | AA173896 | cytochrome b5 outer mitochondrial membrane precursor | |
| 455 | 35818_at | HCS | D00265 | cytochrome c | cytochrome c |
| 456 | 39921_at | COX5B | A1526089 | cytochrome c oxidase subunit Vb | |
| 457 | 41206_r_at | COX6A1 | A1540925 | cytochrome c oxidase subunit VIa polypeptide 1 | |
| 458 | 36165_at | COX6C | W51774 | cytochrome c oxidase subunit VIc | |
| 459 | 39031_at | COX7A1 | AA152406 | cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) | |
| 460 | 41760_at | COX7A2 | AA978033 | cytochrome c oxidase subunit VIIa polypeptide 2 (liver) | |
| 461 | 34330_at | COX7A2L | AB007618 | cytochrome c oxidase subunit VIIa polypeptide 2 like | |
| 462 | 34381_at | COX7C | A1708889 | cytochrome c oxidase subunit VIIc | COX7RP |

Fig 21

| | A | B | C | D | E |
|-----|------------|----------|----------|---|--|
| 463 | 38080_at | COX8 | AI525665 | cytochrome c oxidase subunit VIII | |
| 464 | 35819_at | CYC1 | X06994 | cytochrome c-1 | cytochrome c-1 |
| 465 | 33389_at | CYP51 | U23942 | cytochrome P450, 51 (lanosterol 14-alpha-demethylase) | lanosterol 14-demethylase cytochrome P450 |
| 466 | 859_at | CYP1B1 | U03688 | cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) | cytochrome P450 |
| 467 | 40071_at | CYP1B1 | U03688 | cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) | cytochrome P450 |
| 468 | 37509_at | CRLF3 | AF046059 | cytokine receptor-like factor 3 | cytokine receptor related protein 4 |
| 469 | 37306_at | KIAA0068 | D38549 | cytoplasmic FMRP interacting protein 1 | |
| 470 | 1706_at | A-RAF-1 | U01337 | cytoplasmic; Human Ser/Thr protein kinase (A-RAF-1) gene, complete cds. | Ser/Thr protein kinase |
| 471 | 34338_at | CKAP1 | D49738 | cytoskeleton-associated protein 1 | cytoskeleton associated protein |
| 472 | 32529_at | CKAP4 | X69910 | cytoskeleton-associated protein 4 | P63 protein |
| 473 | 40282_s_at | DF | M84526 | D component of complement (adipsin) | adipsin/complement factor D |
| 474 | 40877_s_at | MN7 | AF041080 | D15F37 (pseudogene) | |
| 475 | 1243_at | DDB2 | U18300 | damage-specific DNA binding protein 2 (48kD) | DDBb p48 |
| 476 | 36616_at | DAZAP2 | D31767 | DAZ associated protein 2 | DAZ associated protein 2 |
| 477 | 37663_at | DDX1 | X70649 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 | member of DEAD box protein family |
| 478 | 35306_at | DDX15 | AB001636 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 15 | ATP-dependent RNA helicase #46 |
| 479 | 40490_at | DDX21 | U41387 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 21 | Gu protein |
| 480 | 39744_at | DDX3 | AF000982 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3 | dead box, X isoform |
| 481 | 34647_at | DDX5 | X52104 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kD) | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 |
| 482 | 36153_at | DDX9 | L13848 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase II; leukophysin) | RNA helicase A |
| 483 | 41872_at | DFNA5 | AF073308 | deafness, autosomal dominant 5 | nonsyndromic hearing impairment protein |

Fig 21

| A | B | C | D | E |
|----------------|-----------|----------|--|---|
| 484 1356_at | DAP3 | U18321 | death associated protein 3 | ionizing radiation resistance conferring protein |
| 485 39114_at | DEPP | AB022718 | decidual protein induced by progesterone | DEPP |
| 486 37638_at | DOCK1 | D50857 | dedicator of cyto-kinesis 1 | DOCK180 protein |
| 487 38413_at | DAD1 | D15057 | defender against cell death 1 | DAD-1 |
| 488 32824_at | CLN2 | AF039704 | deficient in late-infantile neuronal ceroid lipofuscinosis; Homo sapiens lysosomal pepstatin insensitive protease (CLN2) gene, complete cds. | lysosomal pepstatin insensitive protease |
| 489 33337_at | DEGS | AF002668 | degenerative spermatocyte homolog, lipid desaturase (Drosophila) | MLD |
| 490 38992_at | DEK | X64229 | DEK oncogene (DNA binding) | putative oncogene |
| 491 37951_at | DLC1 | AF035119 | deleted in liver cancer 1 | deleted in liver cancer-1 |
| 492 33791_at | DLEU1 | Y15227 | deleted in lymphocytic leukemia, 1 | deleted in lymphocytic leukemia, 1 |
| 493 38744_at | DSS1 | N95406 | Deleted in split-hand/split-foot 1 region | |
| 494 36629_at | DSIP1 | A1635895 | delta sleep inducing peptide, immunoreactor | |
| 495 35814_at | GA17 | AF064603 | dendritic cell protein | GA17 protein |
| 496 38385_at | DSTN | S65738 | destrin (actin depolymerizing factor) | actin depolymerizing factor |
| 497 39410_at | DDEF2 | AB007860 | development and differentiation enhancing factor 2 | development- and differentiation-enhancing factor 2 |
| 498 39044_s_at | DGKD | D73409 | diacylglycerol kinase, delta (130kD) | diacylglycerol kinase delta |
| 499 38003_s_at | DGKZ | U94905 | diacylglycerol kinase, zeta (104kD) | diacylglycerol kinase zeta |
| 500 33920_at | DIAPH1 | AF051782 | diaphanous homolog 1 (Drosophila) | diaphanous 1 |
| 501 37692_at | DBI | A1557240 | diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein) | |
| 502 39041_at | DLAT | Y00978 | dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) | PDC-E2 precursor (AA -54 to 561) |
| 503 40607_at | DPYSL2 | U97105 | dihydropyrimidinase-like 2 | N2A3 |
| 504 36149_at | DPYSL3 | D78014 | dihydropyrimidinase-like 3 | dihydropyrimidinase related protein-3 |
| 505 39503_s_at | DPYSL4 | AB006713 | dihydropyrimidinase-like 4 | dihydropyrimidinase related protein 4 |
| 506 38220_at | DPYD | U20938 | dihydropyrimidine dehydrogenase | dihydropyrimidine dehydrogenase |
| 507 40485_at | HSA249128 | AA176780 | DIPB protein | |

Fig 21

| | A | B | C | D | E |
|-----|------------|------------|----------|---|---|
| 508 | 479_at | DAB2 | U53446 | disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) | DOC-2 |
| 509 | 36643_at | DDR1 | L20817 | discoidin domain receptor family, member 1 | tyrosine protein kinase |
| 510 | 40575_at | DLG5 | AB011155 | discs, large (Drosophila) homolog 5 | KIAA0583 protein |
| 511 | 33753_at | DAAM1 | AB014566 | dishevelled associated activator of morphogenesis 1 | KIAA0666 protein |
| 512 | 33150_at | SAS10 | AI126004 | disruptor of silencing 10 | |
| 513 | 40916_at | dJ635G19.1 | AL035494 | dJ635G19.1 (LAMR1 (Laminin Receptor 1 (67kD) (RPSA, 40S Ribosomal Protein SA, P40)) pseudogene); match: cDNAs: Em:X15005 Em:J03799 Em:X61156 Em:M64923 Em:X06406 Em:AF140348 Em:J02870 Em:L16589 Em:Z22749 Em:D25224 Em:M14199 Em:M27798; match: ESTs: Em:AA642 | dJ635G19.2.1 (novel protein (isoform 1)) |
| 514 | 38456_s_at | dJ734P14.1 | AL049650 | dJ734P14.1 (KRAB box and C2H2 Zinc finger domain protein pseudogene) match: cDNAs: Em:M27878 Em:M29580 Em:U27186 Em:D31763 Em:AB007872 Em:U09386 Em:U09413 Em:X17617 Em:AF011573 Em:AF020591 Em:X78925 match: proteins: Sw:P52736 Sw:Q06730 Sw:P51523 Tr:Q14585 Sw:P15620 Sw:Q02386 Sw:P51786 Sw:Q99676 Tr:O60792 Sw:Q03923 Sw:O75820 Tr:Q61116 Tr:Q64247 | dJ734P14.2.1 (snRNP (small nuclear ribonucleoprotein particle) protein B) |

Fig 21

| | A | B | C | D | E |
|-----|------------|------------|----------|---|--|
| 515 | 38455_at | dJ734P14.1 | AL049650 | dJ734P14.1 (KRAB box and C2H2 Zinc finger domain protein pseudogene) match: cDNAs: Em:M27878 Em:M29580 Em:U27186 Em:D31763 Em:AB007872 Em:U09366 Em:U09413 Em:X17617 Em:AF011573 Em:AF020591 Em:X78925 match: proteins: Sw:P52736 Sw:Q06730 Sw:P51523 Tr:Q14585 Sw:P15620 Sw:Q02386 Sw:P51786 Sw:Q99676 Tr:O60792 Sw:Q03923 Sw:O75820 Tr:Q61116 Tr:Q64247 | dJ734P14.2.1 (snRNP (small nuclear ribonucleoprotein particle) protein B) |
| 516 | 35809_g_at | dJ862K6.4 | AL031681 | dJ862K6.4 (pseudogene similar to part of NBP (Nucleotide Binding Protein)) match: proteins: Sw:P53384 Sw:P52920 Sw:P21590 Sw:Q57731 Sw:P40558 | dJ862K6.2.2 (splicing factor, arginine/serine-rich 6 (SRP55-2)(isoform 2)) |
| 517 | 35808_at | dJ862K6.4 | AL031681 | dJ862K6.4 (pseudogene similar to part of NBP (Nucleotide Binding Protein)) match: proteins: Sw:P53384 Sw:P52920 Sw:P21590 Sw:Q57731 Sw:P40558 | dJ862K6.2.2 (splicing factor, arginine/serine-rich 6 (SRP55-2)(isoform 2)) |
| 518 | 32433_at | dJ90L6.1 | Z97353 | dJ90L6.1 (RPL15 (60S Ribosomal Protein L15) pseudogene); match: proteins: Sw:O74895 Sw:P51417 Sw:P39030 Sw:O17445 Sw:P54780 Sw:O23515 Sw:O65050 Wp:CE12148 Sw:P30736 Sw:P41051 Sw:P54060 Sw:O65082 Sw:P52818 Sw:P79324 Sw:O82712 Sw:O13418 Sw:O82528 Sw:P05748; Human DNA sequence from clone RP1-90L6 on chromosome 22q11.21-11.23 Contains an RPL15 (60S Ribosomal Protein L15) pseudogene, ESTs, STSs and GSSs, complete sequence. | |

Fig 21

| | A | B | C | D | E |
|-----|------------|---------------|----------|---|---|
| 519 | 34183_at | DKFZP434C171 | AL080169 | DKFZP434C171 protein | hypothetical protein |
| 520 | 40801_at | DKFZP434C212 | AA643063 | DKFZP434C212 protein | |
| 521 | 38400_at | DKFZP434D1335 | AI920820 | DKFZP434D1335 protein | |
| 522 | 33392_at | DKFZP434J154 | AL080155 | DKFZP434J154 protein | hypothetical protein |
| 523 | 39411_at | DKFZP434J214 | AL080156 | DKFZP434J214 protein | hypothetical protein |
| 524 | 40564_at | DKFZP564A043 | N42007 | DKFZP564A043 protein | |
| 525 | 37000_at | DKFZP564B167 | AL035304 | DKFZP564B167 protein | hypothetical protein |
| 526 | 33433_at | DKFZP564F0522 | AL049943 | DKFZP564F0522 protein | hypothetical protein |
| 527 | 41437_at | DKFZP564F1123 | AL080118 | DKFZP564F1123 protein | hypothetical protein |
| 528 | 39442_at | DKFZP564G0222 | AL080115 | DKFZP564G0222 protein | hypothetical protein |
| 529 | 40437_at | DKFZP564G2022 | AL049944 | DKFZP564G2022 protein | hypothetical protein |
| 530 | 36456_at | DKFZP564I052 | AL080063 | DKFZP564I052 protein | hypothetical protein |
| 531 | 38033_at | DKFZP564M1416 | AL049934 | DKFZP564M1416 protein | hypothetical protein |
| 532 | 36078_at | DKFZP564O0423 | AL080120 | DKFZP564O0423 protein | hypothetical protein |
| 533 | 38256_s_at | DKFZP564O092 | W21827 | DKFZP564O092 protein | |
| 534 | 39034_at | DKFZP564O123 | AL080122 | DKFZP564O123 protein | hypothetical protein |
| 535 | 41662_at | DKFZP566B183 | AL050272 | DKFZP566B183 protein | hypothetical protein |
| 536 | 32807_at | DKFZP566C134 | AF04292 | DKFZP566C134 protein | |
| 537 | 38687_at | DKFZP566D193 | AL050051 | DKFZP566D193 protein | hypothetical protein |
| 538 | 33776_at | DKFZP566K023 | AL050062 | DKFZP566K023 protein | hypothetical protein |
| 539 | 41335_at | DC8 | AL050084 | DKFZP566O1646 protein | hypothetical protein |
| 540 | 36961_at | DKFZP586A011 | AL050286 | DKFZP586A011 protein | hypothetical protein |
| 541 | 38717_at | DKFZP586A0522 | AL050159 | DKFZP586A0522 protein | hypothetical protein |
| 542 | 40831_at | DKFZP586B0923 | AL050190 | DKFZP586B0923 protein | hypothetical protein |
| 543 | 34821_at | DKFZP586D0623 | AL050197 | DKFZP586D0623 protein | hypothetical protein |
| 544 | 39986_at | DKFZP586D0919 | AL050100 | DKFZP586D0919 protein | hypothetical protein |
| 545 | 34269_at | DKFZP586F1019 | AL050102 | DKFZP586F1019 protein | hypothetical protein |
| 546 | 35736_at | DKFZP586F1918 | AL050091 | DKFZP586F1918 protein | hypothetical protein |
| 547 | 40832_s_at | DKFZP586G011 | AL050126 | DKFZP586G011 protein | hypothetical protein |
| 548 | 36007_at | DKFZP586L151 | AL050137 | DKFZP586L151 protein | hypothetical protein |
| 549 | 34833_at | DKFZP586O0120 | AL050157 | DKFZP586O0120 protein | hypothetical protein |
| 550 | 37333_at | DNMT1 | X63692 | DNA (cytosine-5)-methyltransferase 1 | DNA (cytosine-5)-methyltransferase |
| | | | | DNA segment on chromosome X (unique) | |
| 551 | 40891_f_at | DXS9879E | X92896 | 9879 expressed sequence | ITBA2 protein |
| 552 | 34215_at | DXYS155E | L03426 | DNA segment on chromosome X and Y (unique) 155 expressed sequence | DNA segment on chromosome X and Y (unique) 155 expressed sequence |

Fig 21

| | A | B | C | D | E |
|-----|------------|---------|----------|---|---|
| 553 | 1252_at | D5S346 | M73547 | DNA segment, single copy probe LNS-CAV/LNS-CAII (deleted in polyposis) | polyposis locus-encoded protein |
| 554 | 37162_at | D10S170 | S72869 | DNA segment, single copy, probe pH4 (transforming sequence, thyroid-1, DnaJ (Hsp40) homolog, subfamily A, member 1) | DNA segment, single copy, probe pH4 (transforming sequence, thyroid-1, DnaJ (Hsp40) homolog, subfamily A, member 1) |
| 555 | 39118_at | DNAJA1 | L08069 | DnaJ (Hsp40) homolog, subfamily A, member 1 | DNAJ (Hsp40) homolog, subfamily A, member 1 |
| 556 | 276_at | DNAJA1 | L08069 | DnaJ (Hsp40) homolog, subfamily A, member 1 | DNAJ (Hsp40) homolog, subfamily A, member 1 |
| 557 | 41233_at | DNAJB6 | AB014888 | DnaJ (Hsp40) homolog, subfamily B, member 6 | MRJ |
| 558 | 35799_at | DNAJB9 | AL080081 | DnaJ (Hsp40) homolog, subfamily B, member 9 | hypothetical protein |
| 559 | 36166_at | DNAJC8 | AF083190 | DnaJ (Hsp40) homolog, subfamily C, member 8 | SPF31 |
| 560 | 816_g_at | DOK1 | U70987 | docking protein 1, 62kD (downstream of tyrosine kinase 1) | GAP binding protein p62dok |
| 561 | 34433_at | DOK1 | AF035299 | docking protein 1, 62kD (downstream of tyrosine kinase 1) | docking protein 1 |
| 562 | 34879_at | DPM1 | AF007875 | dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit | dolichol monophosphate mannosyltransferase |
| 563 | 38957_at | DCAMKL1 | AB002367 | doublecortin and CaM kinase-like 1 | doublecortin and CaM kinase-like 1 |
| 564 | 32168_s_at | DSCR1 | U85267 | Down syndrome critical region gene 1 | Down syndrome critical region protein 1 |
| 565 | 36088_at | DSCR2 | AJ006291 | Down syndrome critical region gene 2 | leucine rich protein |
| 566 | 35166_at | DSCR3 | D87343 | Down syndrome critical region gene 3 | DCRA |
| 567 | 32621_at | DR1 | M97388 | down-regulator of transcription 1, TBP-binding (negative cofactor 2) | TATA binding protein-associated phosphoprotein |
| 568 | 37981_at | DBN1 | D17530 | drebrin 1 | drebrin E |
| 569 | 40920_at | cdc14B | AF023158 | dual specific protein; Homo sapiens tyrosine phosphatase (cdc14B) mRNA, complete cds. | tyrosine phosphatase |
| 570 | 39727_at | DUSP11 | AF023917 | dual specificity phosphatase 11 (RNA/RNP complex 1-interacting) | PIR1 |
| 571 | 38272_at | DUSP14 | AF038844 | dual specificity phosphatase 14 | MKP-1 like protein tyrosine phosphatase |
| 572 | 41225_at | DUSP3 | AL049417 | dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related) | |

Fig 21

| | A | B | C | D | E |
|-----|------------|----------|----------|---|--|
| 573 | 41193_at | DUSP6 | AB013382 | dual specificity phosphatase 6 | DUSP6 |
| 574 | 36946_at | DYRK1A | D86550 | dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A | serine/threonine protein kinase |
| 575 | 1512_at | DYRK1A | D86550 | dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A | serine/threonine protein kinase |
| 576 | 760_at | DYRK2 | Y09216 | dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 | dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 isoform 1 |
| 577 | 39931_at | DYRK3 | Y12735 | dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 | Dyrk3 protein |
| 578 | 38368_at | DUT | U31930 | dUTP pyrophosphatase | deoxyuridine nucleotidohydrolase |
| 579 | 38475_at | DCTN2 | U50733 | dynactin 2 (p50) | dynamitin |
| 580 | 34891_at | PIN | AI540958 | dynein, cytoplasmic, light polypeptide | |
| 581 | 34829_at | DKC1 | U59151 | dyskeratosis congenita 1, dyskerin | Cbl5p homolog |
| 582 | 32234_at | DYT1 | AF007871 | dystonia 1, torsion (autosomal dominant; torsin A) | torsinA |
| 583 | 36989_at | DAG1 | L19711 | dystroglycan 1 (dystrophin-associated glycoprotein 1) | dystroglycan |
| 584 | 40488_at | DMD | M18533 | dystrophin (muscular dystrophy, Duchenne and Becker types) | dystrophin |
| 585 | 40106_at | E1B-AP5 | AJ007509 | E1B-55kDa-associated protein 5 | E1B-55kDa-associated protein |
| 586 | 33354_at | SMURF2 | AA630312 | E3 ubiquitin ligase SMURF2 | |
| 587 | 40375_at | EGR3 | X63741 | early growth response 3 | transcription factor |
| 588 | 36135_at | EBNA1BP2 | U86602 | EBNA1 binding protein 2 | nuclear protein p40 |
| 589 | 37730_at | p100 | U22055 | EBNA-2 co-activator (100kD) | 100 kDa coactivator |
| 590 | 33254_at | EVI5 | AF008915 | ecotropic viral integration site 5 | EVI-5 homolog |
| 591 | 39542_at | ENC1 | AF059611 | ectodermal-neural cortex (with BTB-like domain) | nuclear matrix protein NRP/B |
| 592 | 41124_r_at | ENPP2 | L35594 | ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin) | autotaxin |
| 593 | 41123_s_at | ENPP2 | L35594 | ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin) | autotaxin |
| 594 | 32551_at | EFEMP1 | U03877 | EGF-containing fibulin-like extracellular matrix protein 1 | extracellular protein |

Fig 21

| | A | B | C | D | E |
|-----|-----------|------------|----------|---|---|
| 595 | 36488_at | EGFL5 | AB011542 | EGF-like-domain, multiple 5 | MEGF9 |
| 596 | 40509_at | ETFA | J04058 | electron-transfer-flavoprotein, alpha polypeptide (glutamic aciduria II) | electron transfer flavoprotein, alpha polypeptide |
| 597 | 36881_at | ETFB | X71129 | electron-transfer-flavoprotein, beta polypeptide | electron transfer flavoprotein beta subunit |
| 598 | 1288_s_at | EEF1A | J04617 | elongation factor EF-1-alpha; Human elongation factor EF-1-alpha gene, complete cds. | eukaryotic translation elongation factor 1 alpha 1 |
| 599 | 31853_at | EED | AF080227 | embryonic ectoderm development | embryonic ectoderm development protein |
| 600 | 39861_at | EMS1 | M98343 | ems1 sequence (mammary tumor and squamous cell carcinoma-associated (p80/85 src substrate) | amplixin |
| 601 | 41478_at | dJ477H23.1 | AL033538 | end of last exon based on GENSCAN prediction presumably this gene and dJ477H23.2 are part of the same gene match: ESTs: Em:AA354847 | dJ477H23.1 (novel protein) |
| 602 | 37408_at | ENDO180 | AB014609 | endocytic receptor (macrophage mannose receptor family) | KIAA0709 protein |
| 603 | 37914_at | ENDOFIN | AB002303 | endosome-associated FYVE-domain protein | endosome-associated FYVE-domain protein |
| 604 | 39010_at | ENSA | A1658639 | endosulfine alpha | |
| 605 | 40387_at | EDG2 | U80811 | endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2 | lysophosphatidic acid receptor homolog |
| 606 | 40874_at | EDF1 | AJ005259 | endothelial differentiation-related factor 1 | endothelial differentiation-related factor 1 |
| 607 | 39079_at | ERH | D85758 | enhancer of rudimentary homolog (Drosophila) | human protein homologous to DROER protein |
| 608 | 2035_s_at | ENO1 | M55914 | enolase 1, (alpha) | c-myc binding protein |
| 609 | 34335_at | EFNB2 | A1765533 | ephrin-B2 | |
| 610 | 37731_at | EPS15 | Z29064 | epidermal growth factor receptor pathway substrate 15 | epidermal growth factor receptor pathway substrate 15 |
| 611 | 1467_at | EPS8 | U12535 | epidermal growth factor receptor pathway substrate 8 | epidermal growth factor receptor kinase substrate |
| 612 | 37762_at | EMP1 | Y07909 | epithelial membrane protein 1 | progression associated protein |
| 613 | 39631_at | EMP2 | U52100 | epithelial membrane protein 2 | XMP |

Fig 21

| | A | B | C | D | E |
|-----|------------|------------|----------|--|---------------|
| 614 | 35816_at | cystatin B | U46892 | EPM1 disease gene; cysteine protease inhibitor; Human cystatin B gene, complete cds. | cystatin B |
| 615 | 32585_at | EPB41L2 | AF027299 | erythrocyte membrane protein band 4.1-like 2 | protein 4.1-G |
| 616 | 38375_at | ESD | AF112219 | esterase D/formylglutathione hydrolase | esterase D |
| 617 | 38283_at | EBAG9 | AB007619 | estrogen receptor binding site associated, antigen, 9 | EBAG9 |
| 618 | 37161_at | | W28948 | ESTs | |
| 619 | 40885_s_at | | N30151 | ESTs | |
| 620 | 33328_at | C15 | W28612 | ESTs | |
| 621 | 33453_at | ATP6S1 | AI400326 | ESTs | |
| 622 | 31801_at | | AI808712 | ESTs | |
| 623 | 41598_at | | AA890010 | ESTs | |
| 624 | 32744_at | RPS21 | AI526078 | ESTs, Highly similar to RS21_HUMAN 40S RIBOSOMAL PROTEIN S21 [H.sapiens] | |
| 625 | 39750_at | | W61005 | ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens] | |
| 626 | 34906_g_at | | AA977136 | ESTs, Moderately similar to GLK5_HUMAN GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 5 PRECURSOR [H.sapiens] | |
| 627 | 35787_at | | AI986201 | ESTs, Moderately similar to T46365 hypothetical protein DKFZp434A1518.1 [H.sapiens] | |
| 628 | 41463_at | | AL042729 | ESTs, Weakly similar to 0903209A peptide PD basic Pro rich [H.sapiens] | |
| 629 | 41273_at | | AL046940 | ESTs, Weakly similar to N-WASP [H.sapiens] | |
| 630 | 38097_at | PIG8 | AF010313 | etoposide-induced mRNA | Pig8 |
| 631 | 40888_f_at | EEF1A1 | W28170 | eukaryotic translation elongation factor 1 alpha 1 | |

fig 21

| | A | B | C | D | E |
|-----|------------|--------|----------|--|---|
| 632 | 35175_f_at | EEF1A2 | X70940 | eukaryotic translation elongation factor 1 alpha 2 | elongation factor 1 alpha-2 |
| 633 | 35748_at | EEF1B2 | X60489 | eukaryotic translation elongation factor 1 beta 2 | elongation factor-1-beta |
| 634 | 41256_at | EEF1D | Z21507 | eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) | human elongation factor-1-delta |
| 635 | 1676_s_at | EEF1G | M55409 | eukaryotic translation elongation factor 1 gamma | pancreatic tumor-related protein |
| 636 | 36587_at | EEF2 | Z11692 | eukaryotic translation elongation factor 2 | human elongation factor 2 |
| 637 | 663_at | EIF1A | L18960 | eukaryotic translation initiation factor 1A | protein synthesis factor |
| 638 | 34278_at | EIF1A | L18960 | eukaryotic translation initiation factor 1A | protein synthesis factor |
| 639 | 1154_at | EIF2S1 | J02645 | eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kD) | eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kD) |
| 640 | 40515_at | EIF2B2 | AF035280 | eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) | eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) |
| 641 | 1644_at | EIF3S2 | U36764 | eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD) | TGF-beta receptor interacting protein 1 |
| 642 | 35327_at | EIF3S3 | U54559 | eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD) | translation initiation factor eIF3 p40 subunit |
| 643 | 32576_at | EIF3S5 | U94855 | eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD) | translation initiation factor 3 47 kDa subunit |
| 644 | 38681_at | EIF3S6 | U62962 | eukaryotic translation initiation factor 3, subunit 6 (48kD) | murine mammary tumor integration site 6 (oncogene homolog) |
| 645 | 35298_at | EIF3S7 | U54558 | eukaryotic translation initiation factor 3, subunit 7 (zeta, 66/67kD) | translation initiation factor eIF3 p66 subunit |
| 646 | 35323_at | EIF3S9 | U78525 | eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD) | eukaryotic translation initiation factor |
| 647 | 41785_at | EIF4G2 | U73824 | eukaryotic translation initiation factor 4 gamma, 2 | p97 |
| 648 | 33907_at | EIF4G3 | AF012072 | eukaryotic translation initiation factor 4 gamma, 3 | eIF4GII |

Fig 21

| | A | B | C | D | E |
|-----|------------|----------|----------|--|---|
| 649 | 1420_s_at | EIF4A2 | D30655 | eukaryotic translation initiation factor 4A, isoform 2 | eukaryotic initiation factor 4AII |
| 650 | 37752_at | EIF4E | M15353 | eukaryotic translation initiation factor 4E | cap-binding protein |
| 651 | 35263_at | EIF4EBP2 | N73769 | eukaryotic translation initiation factor 4E binding protein 2 | |
| 652 | 167_at | EIF5 | U49436 | eukaryotic translation initiation factor 5 | translation initiation factor 5 |
| 653 | 37318_at | ETF1 | X81625 | eukaryotic translation termination factor 1 | C11 protein |
| 654 | 1885_at | ERCC3 | M31899 | excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing) | excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing) |
| 655 | 2063_at | ERCC5 | L20046 | excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome)) | excision repair protein |
| 656 | 33734_at | HSD11B1 | AL022398 | exons 1-4 beyond this clone; match: proteins P28845 P50172 P51975 Q29608 | dJ434O14.1 (Hydroxysteroid (11-beta) Dehydrogenase 1 (EC 1.1.1.146)) |
| 657 | 222_at | EXT1 | S79639 | exostoses (multiple) 1 | exostoses (multiple) 1 |
| 658 | 36526_at | EXTL2 | AF000416 | exostoses (multiple)-like 2 | EXT-like protein 2 |
| 659 | 38809_s_at | EXTL3 | AB011091 | exostoses (multiple)-like 3 | KIAA0519 protein |
| 660 | 37729_at | XPO1 | Y08614 | exportin 1 (CRM1 homolog, yeast) | exportin 1 |
| 661 | 38753_at | XPOT | AF039022 | exportin, tRNA (nuclear export receptor for tRNAs) | exportin t |
| 662 | 39673_i_at | ECM2 | AB011792 | extracellular matrix protein 2, female organ and adipocyte specific | extracellular matrix protein |
| 663 | 39674_r_at | ECM2 | AB011792 | extracellular matrix protein 2, female organ and adipocyte specific | extracellular matrix protein |
| 664 | 35226_at | EYA2 | U71207 | eyes absent homolog 2 (Drosophila) | Eab1 |
| 665 | 38318_at | FAM8A1 | AL050128 | family with sequence similarity 8, member A1 | |
| 666 | 31879_at | FUBP3 | U69127 | far upstream element (FUSE) binding protein 3 | FUSE binding protein 3 |

Fig 21

| A | B | C | D | E |
|---------------|---------|---------------|---|---|
| 667 37325_at | FDPS | D14697 | farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) | farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) |
| 668 34848_at | FDFT1 | X69141 | farnesyl-diphosphate farnesyltransferase 1 | farnesyl-diphosphate farnesyltransferase |
| 669 1499_at | FNTA | L10413 | farnesyltransferase, CAAX box, alpha | farnesyl-protein transferase alpha-subunit |
| 670 38755_at | FADD | X84709 | Fas (TNFRSF6)-associated via death domain | mediator of receptor induced toxicity |
| 671 37743_at | FEZ1 | U60060 | fasciculation and elongation protein zeta 1 (zyglin I) | FEZ1 |
| 672 38651_at | FEZ2 | U60061 | fasciculation and elongation protein zeta 2 (zyglin II) | FEZ2 |
| 673 40454_at | FAT | X87241 | FAT tumor suppressor homolog 1 (Drosophila) | homologue of Drosophila Fat protein |
| 674 40082_at | FACL2 | D10040 | fatty-acid-Coenzyme A ligase, long-chain 2 | long-chain acyl-CoA synthetase |
| 675 33880_at | FACL3 | D89053 | fatty-acid-Coenzyme A ligase, long-chain 3 | Acyl-CoA synthetase 3 |
| 676 33881_at | FACL3 | AA977580 | fatty-acid-Coenzyme A ligase, long-chain 3 | |
| 677 33360_at | FBXL11 | AB023221 | F-box and leucine-rich repeat protein 11 | KIAA1004 protein |
| 678 37205_at | FBXL7 | AB020647 | F-box and leucine-rich repeat protein 7 | KIAA0840 protein |
| 679 32854_at | FBXW1B | AB014596 | F-box and WD-40 domain protein 1B | KIAA0696 protein |
| 680 32169_at | FBXO21 | AB020682 | F-box only protein 21 | KIAA0875 protein |
| 681 35337_at | FBXO7 | AL050254 | F-box only protein 7 | hypothetical protein |
| 682 33817_at | D10S102 | S63912 | FBRNP; heterogeneous ribonucleoprotein homolog; This sequence comes from Fig. 3; D10S102=FBRNP [human, fetal brain, mRNA, 3043 nt]. | FBRNP |
| 683 1877_g_at | nitH | HG1103-HT1103 | Fe protein | dinitrogenase reductase |
| 684 34678_at | FER1L3 | AL096713 | fer-1-like 3, myoferlin (C. elegans) | hypothetical protein |
| 685 32148_at | FARP1 | A1701049 | FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) | |

Fig 21

| | A | B | C | D | E |
|-----|------------|-------|----------|---|--|
| 686 | 33943_at | FTH1 | L20941 | ferritin, heavy polypeptide 1 | ferritin heavy chain |
| 687 | 41091_at | FALZ | U05237 | fetal Alzheimer antigen | fetal Alzheimer antigen |
| 688 | 32535_at | FBN1 | X63556 | fibrillin 1 (Marfan syndrome) | fibrillin |
| 689 | 39945_at | FAP | U09278 | fibroblast activation protein, alpha | fibroblast activation protein |
| 690 | 1380_at | FGF7 | M60828 | fibroblast growth factor 7 (keratinocyte growth factor) | keratinocyte growth factor |
| 691 | 2057_g_at | FGFR1 | M34641 | | fibroblast growth factor receptor 1, isoform 1 precursor; fibroblast growth factor receptor 1, isoform 2 precursor; fibroblast growth factor receptor 1, isoform 3 precursor; fibroblast growth factor receptor 1, isoform 4 precursor; fibroblast growth factor receptor 1, isoform 5 precursor; fibroblast growth factor receptor 1, isoform 6 precursor; fibroblast growth factor receptor 1, isoform 7 precursor; fibroblast growth factor receptor 1, isoform 8 precursor; fibroblast growth factor receptor 1, isoform 9 precursor |
| 692 | 31720_s_at | FN1 | M10905 | | fibronectin 1, isoform 1 preproprotein; fibronectin 1, isoform 2 preproprotein |
| 693 | 31719_at | FN1 | X02761 | | fibronectin precursor |
| 694 | 34853_at | FLRT2 | AB007865 | | fibronectin leucine rich transmembrane protein 2 |
| 695 | 38026_at | FBLN1 | U01244 | | fibulin-1D |
| 696 | 39038_at | FBLN5 | AF093118 | | UP50 |
| 697 | 38078_at | FLNB | AF042166 | | beta-filamin |
| 698 | 38761_s_at | FKBP9 | AA487755 | | |
| 699 | 40665_at | FMO3 | M83772 | | flavoprotein |
| 700 | 35254_at | FLN29 | AB007447 | | FLN29 |
| 701 | 38356_at | FST | M19481 | | folliculin isoform FST317 precursor; folliculin isoform FST344 precursor |

Fig 21

| A | B | C | D | E |
|----------------|-----------|----------|---|--|
| | | | forkhead (Drosophila)-like 7; FREAC3; Homo sapiens forkhead/winged helix-like transcription factor 7 (FKHL7) gene, complete cds. | forkhead/winged helix-like transcription factor 7 |
| 702 41027_at | FKHL7 | AF078096 | | |
| 703 36319_at | FOXF2 | U13220 | forkhead box F2 | forkhead protein FREAC-2 |
| 704 40570_at | FOXO1A | AF032885 | forkhead box O1A (rhabdomyosarcoma) | forkhead protein |
| 705 34740_at | FOXO3A | AF032886 | forkhead box O3A | forkhead protein |
| 706 32542_at | FHL1 | AF063002 | four and a half LIM domains 1 | LIM protein SLIMMER |
| 707 38422_s_at | FHL2 | U29332 | four and a half LIM domains 2 | heart protein |
| 708 41649_at | FHX | AF038177 | FOXJ2 forkhead factor | |
| 709 34997_r_at | FZD5 | U43318 | frizzled homolog 5 (Drosophila) | transmembrane receptor |
| 710 34472_at | FZD6 | AB012911 | frizzled homolog 6 (Drosophila) | Frizzled-6 |
| 711 33222_at | FZD7 | AB017365 | frizzled homolog 7 (Drosophila) | frizzled-7 |
| 712 38923_at | FRG1 | L76159 | FSHD region gene 1 | FSHD region gene 1 |
| 713 38139_at | FPGT | AF017445 | fructose-1-phosphate guanylyltransferase | GDP-L-fucose pyrophosphorylase |
| 714 41814_at | FUCA1 | M29877 | fucosidase, alpha-L-1, tissue | fucosidase, alpha-L-1, tissue |
| 715 40022_at | FCMD | AB008226 | Fukuyama type congenital muscular dystrophy (fukutin) | fukutin |
| 716 32546_at | FH | U59309 | fumarate hydratase | fumarate precursor |
| 717 36145_at | SIAHBP1 | U51586 | fuse-binding protein-interacting repressor | siah binding protein 1 |
| 718 40480_s_at | FYN | M14333 | FYN oncogene related to SRC, FGR, YES | FYN oncogene related to SRC, FGR, YES |
| 719 2039_s_at | FYN | M14333 | FYN oncogene related to SRC, FGR, YES | FYN oncogene related to SRC, FGR, YES |
| 720 34288_at | RDC1 | U67784 | G protein-coupled receptor | orphan G protein-coupled receptor |
| 721 37308_at | GPR107 | AI888084 | G protein-coupled receptor 107 | |
| 722 37298_at | GABARAP | AF044671 | GABA(A) receptor-associated protein | MM46 |
| 723 35785_at | GABARAPL1 | W28281 | GABA(A) receptor-associated protein like 1 | |
| 724 35767_at | GABARAPL2 | AI565760 | GABA(A) receptor-associated protein-like 2 | |
| 725 37825_at | GALK2 | M84443 | galactokinase 2 | galactokinase |
| 726 37742_at | GLB1 | M34423 | galactosidase, beta 1 | galactosidase, beta 1 |

Fig 21

| | A | B | C | D | E |
|-----|------------|----------|----------|---|--|
| 727 | 37263_at | GGH | U55206 | gamma-glutamyl hydrolase (conjugase, foypolygammaglutamyl hydrolase) | human gamma-glutamyl hydrolase |
| 728 | 32531_at | GJA1 | X52947 | gap junction protein, alpha 1, 43kD (connexin 43) | connexin 43 |
| 729 | 36603_at | GCN1L1 | D86973 | GCN1 general control of amino-acid synthesis 1-like 1 (yeast) | |
| 730 | 35307_at | GDI2 | Y13286 | GDP dissociation inhibitor 2 | GDP dissociation inhibitor beta |
| 731 | 39386_at | KIAA0110 | D14811 | gene predicted from cDNA with a complete coding sequence | gene predicted from cDNA with a complete coding sequence |
| 732 | 32180_s_at | RES4-22 | AB000461 | gene with multiple splice variants near HD locus on 4p16.3 | gene with multiple splice variants near HD locus on 4p16.3 |
| 733 | 466_at | GTF2I | U77948 | general transcription factor II, i | Bruton's tyrosine kinase-associated protein-135 |
| 734 | 35450_s_at | GTF2I | AF015553 | general transcription factor II, i | TFII-I protein |
| 735 | 37010_at | GTF2A2 | AI203737 | general transcription factor IIA, 2 (12kD subunit) | |
| 736 | 869_at | GTF2A2 | U14193 | general transcription factor IIA, 2 (12kD subunit) | transcription factor IIA small 12 kDa subunit |
| 737 | 37882_at | GTF2E1 | X63468 | general transcription factor IIE, polypeptide 1 (alpha subunit, 56kD) | TFIIE-alpha |
| 738 | 37295_at | GTF2E2 | X63469 | general transcription factor IIE, polypeptide 2 (beta subunit, 34kD) | TFIIE-beta |
| 739 | 38782_at | GTF2H1 | M95809 | general transcription factor IIH, polypeptide 1 (62kD subunit) | basic transcription factor 62kD subunit |
| 740 | 40754_at | GTF2H3 | Z30093 | general transcription factor IIH, polypeptide 3 (34kD subunit) | basic transcription factor 2, 35 kD subunit |
| 741 | 36188_at | GTF3A | D32257 | general transcription factor IIIA | Xenopus transcription factor IIIA homologue |
| 742 | 35296_at | GGPS1 | AB019036 | geranylgeranyl diphosphate synthase 1 | geranylgeranyl pyrophosphate synthase |
| 743 | 763_at | GMFB | AB001106 | glia maturation factor, beta | glia maturation factor |
| 744 | 39793_at | GBAS | AF029786 | glioblastoma amplified sequence | GBAS |
| | | | | glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) | |
| 745 | 32643_at | GBE1 | L07956 | | 1,4-alpha-glucan branching enzyme |
| 746 | 34332_at | GNPI | D31766 | glucosamine-6-phosphate isomerase | glucosamine-6-phosphate isomerase |

Fig 21

| | A | B | C | D | E |
|-----|--------------|----------|----------|--|---|
| 747 | 38218_at | GCNT1 | M97347 | glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylglucosaminyltransferase) | beta-1,6-N-acetylglucosaminyltransferase |
| 748 | 39122_at | GPI | K03515 | glucose phosphate isomerase | neuroleukin |
| 749 | 39986_at | GRP58 | Z49835 | glucose regulated protein, 58kD | protein disulfide isomerase |
| 750 | 38042_at | G6PD | X03674 | glucose-6-phosphate dehydrogenase | glucose-6-phosphate dehydrogenase |
| 751 | 33308_at | GUSB | M15182 | glucuronidase, beta | glucuronidase, beta |
| 752 | 37341_at | GLUD1 | M20867 | glutamate dehydrogenase 1 | glutamate dehydrogenase 1 |
| 753 | 35485_at | GRM4 | X80818 | glutamate receptor, metabotropic 4 | metabotropic glutamate receptor type 4 |
| 754 | 40522_at | GLUL | X59834 | glutamate-ammonia ligase (glutamine synthase) | glutamate--ammonia ligase |
| 755 | 31850_at | GCLC | M90656 | glutamate-cysteine ligase, catalytic subunit | gamma-glutamylcysteine synthetase |
| 756 | 33163_r_at | GCLM | L35546 | glutamate-cysteine ligase, modifier subunit | gamma-glutamylcysteine synthetase light subunit |
| 757 | 35343_at | GOT1 | M37400 | glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1) | aspartate aminotransferase 1 |
| 758 | 40764_at | GOT2 | M22632 | glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) | aspartate aminotransferase 2 precursor |
| 759 | 34719_at | GLS | AB020645 | glutaminase | KIAA0838 protein |
| 760 | 32626_at | GFPT1 | M90516 | glutamine-fructose-6-phosphate transaminase 1 | glutamine:fructose-6-phosphate amidotransferase |
| 761 | 39640_at | GFPT2 | AB016789 | glutamine-fructose-6-phosphate transaminase 2 | Glutamine:fructose-6-phosphate amidotransferase |
| 762 | 35300_at | EPRS | X54326 | glutamyl-prolyl-tRNA synthetase | glutamyl-tRNA synthetase |
| 763 | 34311_at | GLRX | X76648 | glutaredoxin (thioltransferase) | glutaredoxin |
| 764 | 37033_s_at | GPX1 | X13710 | glutathione peroxidase 1 | |
| 765 | 40508_at | GSTA4 | AF025887 | glutathione S-transferase A4 | glutathione S-transferase A4-4 |
| 766 | 38386_r_at | GSS | U34683 | glutathione synthetase | glutathione synthetase |
| 767 | 824_at | GSTT1p28 | U90313 | glutathione S-transferase like; glutathione transferase omega | glutathione-S-transferase homolog |
| 768 | AFFX-HUMGAP1 | GAPD | M33197 | glyceraldehyde-3-phosphate dehydrogenase | glyceraldehyde-3-phosphate dehydrogenase |
| 769 | 35905_s_at | GAPD | U34995 | glyceraldehyde-3-phosphate dehydrogenase | |

CS 21

| | A | B | C | D | E |
|-----|--------------|--------|----------|---|---|
| 770 | AFFX-HUMGAP1 | GAPD | M33197 | glyceraldehyde-3-phosphate dehydrogenase | glyceraldehyde-3-phosphate dehydrogenase |
| 771 | 39392_at | GNPAT | AJ002190 | glyceronephosphate O-acyltransferase | dihydroxyacetone phosphate acyltransferase |
| 772 | 37357_at | GCSH | D00723 | glycine cleavage system protein H (aminomethyl carrier) | glycine cleavage system protein H (aminomethyl carrier) |
| 773 | 39665_at | GLRB | U33267 | glycine receptor, beta | glycine receptor beta subunit |
| 774 | 40645_at | GSK3B | L33801 | glycogen synthase kinase 3 beta | protein kinase |
| 775 | 40876_at | GYG | U31525 | glycogenin | glycogenin |
| 776 | 35334_at | GYG2 | U94362 | glycogenin 2 | glycogenin-2 alpha |
| 777 | 38379_at | GPNMB | X76534 | glycoprotein (transmembrane) nmb | glycoprotein (transmembrane) nmb |
| 778 | 37251_s_at | GPM6B | AF016004 | glycoprotein M6B | |
| 779 | 33126_at | AD-017 | L13435 | glycosyltransferase AD-017 | |
| 780 | 36582_g_at | GARS | U09510 | glycyl-tRNA synthetase | glycyl-tRNA synthetase |
| 781 | 36581_at | GARS | U09510 | glycyl-tRNA synthetase | glycyl-tRNA synthetase |
| 782 | 36201_at | GLO1 | D13315 | glyoxalase I | lactoyl glutathione lyase |
| 783 | 40133_s_at | GRHPR | W28944 | glyoxylate reductase/hydroxypyruvate reductase | |
| 784 | 37449_i_at | GNAS | X04409 | | guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform alpha-s-2; neuroendocrine secretory protein 55; guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform XL-alpha-s; guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform alpha-s-1 |
| 785 | 37448_s_at | GNAS | X56009 | GNAS complex locus GNAS complex locus | alpha subunit of GsGTP binding protein |

Fig 21

| | A | B | C | D | E |
|-----|------------|-----------|----------|---|---|
| 786 | 37450_r_at | GNAS | X04409 | GNAS complex locus | guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform alpha-s-2; neuroendocrine secretory protein 55; guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform XL-alpha-s; guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform alpha-s-1 |
| 787 | 37959_at | GGA3 | D63876 | golgi associated, gamma adaptin ear containing, ARF binding protein 3 | ADP-ribosylation factor binding protein 3, isoform short; ADP-ribosylation factor binding protein 3, isoform long |
| 788 | 32713_at | GOLGA1 | U51587 | golgi autoantigen, golgin subfamily a, 1 | Golgi complex autoantigen golgin-97 |
| 789 | 32150_at | GOLGA4 | X82834 | golgi autoantigen, golgin subfamily a, 4 | 256 kD golgin |
| 790 | 36827_at | GOLPH1 | AF020762 | golgi phosphoprotein 1 | unknown protein |
| 791 | 38620_at | GOSR2 | AA905543 | golgi SNAP receptor complex member 2 | |
| 792 | 34737_at | GOLTC1 | AF058718 | golgi transport complex 1 (90 kD subunit) | putative 13 S Golgi transport complex 90kD subunit brain-specific isoform |
| 793 | 41767_r_at | KIAA0855 | AB020662 | golgin-67 | KIAA0855 protein |
| 794 | 36950_at | HSGP25L2G | X90872 | gp25L2 protein | |
| 795 | 36035_at | GPAA1 | AB02135 | GPAA1P anchor attachment protein 1 homolog (yeast) | glycosylphosphatidylinositol anchor attachment 1 (GPAA1) |
| 796 | 32595_at | GRSF1 | U07231 | G-rich RNA sequence binding factor 1 | G-rich sequence factor-1 |
| 797 | 39822_s_at | GADD45B | AF078077 | growth arrest and DNA-damage-inducible, beta | growth arrest and DNA-damage-inducible protein GADD45beta |
| 798 | 39821_s_at | GADD45B | N95168 | growth arrest and DNA-damage-inducible, beta | |
| 799 | 661_at | GAS1 | L13698 | growth arrest-specific 1 | growth arrest-specific 1 |
| 800 | 41839_at | GAS1 | L13698 | growth arrest-specific 1 | growth arrest-specific 1 |
| 801 | 37658_at | GAS6 | L13720 | growth arrest-specific 6 | growth-arrest-specific protein |
| 802 | 1598_g_at | GAS6 | L13720 | growth arrest-specific 6 | growth-arrest-specific protein |
| 803 | 37615_at | GRB10 | D86962 | growth factor receptor-bound protein 10 | growth factor receptor-bound protein 10 |
| 804 | 41752_at | GHITM | W28190 | growth hormone inducible transmembrane protein | |

Fig 21

| | A | B | C | D | E |
|-----|------------|--------------------|----------|---|---|
| 805 | 160030_at | GHR | X06562 | growth hormone receptor | growth hormone receptor |
| 806 | 40113_at | GS3955 | D87119 | GS3955 protein | GS3955 |
| 807 | 37279_at | GEM | U10550 | GTP binding protein overexpressed in skeletal muscle | Gem |
| 808 | 33809_at | GNAI1 | AL049933 | guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1 | hypothetical protein |
| 809 | 37307_at | GNAI2 | X04828 | guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2 | guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2 |
| 810 | 34608_at | GNB2L1 | M24194 | guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 | MHC B complex protein 12.3 |
| 811 | 35272_at | GNNG5 | AI541042 | guanine nucleotide binding protein (G protein), gamma 5 | |
| 812 | 37735_at | GNNG10 | U31383 | guanine nucleotide binding protein 10 | G protein gamma-10 subunit |
| 813 | 35735_at | GBP1 | M55542 | guanylate binding protein 1, interferon-inducible, 67kD | guanylate binding protein isoform I |
| 814 | 905_at | GUK1 | L76200 | guanylate kinase 1 | guanylate kinase |
| 815 | 32249_at | HFL1 | M65292 | H factor (complement)-like 1 | factor H homologue |
| 816 | 32250_at | HF1 | X07523 | H factor 1 (complement) | complement factor H |
| 817 | 420_at | ACTH-R | X65633 | H.sapiens ACTH-R gene for adrenocorticotrophic hormone receptor. | candidate adrenocorticotrophic hormone receptor |
| 818 | 31673_s_at | cell adhesion regu | X65784 | H.sapiens CAR gene. | cell matrix adhesion regulator |
| 819 | 37003_at | CD63; MLA1; ME4 | X62654 | H.sapiens gene for Me491/CD63 antigen. | ME491 /CD63 antigen |
| 820 | 38076_at | P1 gene for c subu | X69907 | H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form). | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1 |
| 821 | 35125_at | hrp S6 | X67309 | H.sapiens gene for ribosomal protein S6. | ribosomal protein S6 |
| 822 | 34646_at | rpS7 | Z25749 | H.sapiens gene for ribosomal protein S7. | ribosomal protein S7 |
| 823 | 31510_s_at | hH3.3B | Z48950 | H.sapiens HH3.3B gene for histone H3.3. | histone H3.3 |

Fig 21

| | A | B | C | D | E |
|-----|------------|------------|----------|---|---|
| 824 | 33820_g_at | ldhB | X13794 | H.sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (and joined CDS). | lactate dehydrogenase B |
| 825 | 33819_at | ldhB | X13794 | H.sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (and joined CDS). | lactate dehydrogenase B |
| 826 | 34787_at | ORF1 | X93209 | H.sapiens mRNA for NRD1 convertase. | NRD1 convertase |
| 827 | 36012_at | PIBF1 | Y09631 | H.sapiens mRNA for PIBF1 protein, complete. | PIBF1 protein |
| 828 | 31526_f_at | tre | X63547 | H.sapiens mRNA for tre oncogene (clone 213). | oncogene |
| 829 | 40471_at | PxP | Y09048 | H.sapiens PxP gene. | PxP protein |
| 830 | 37038_at | PXMP1 | X83467 | H.sapiens PXMP1 gene, exon 1 (and joined CDS). | 70kD peroxisomal integral membrane protein |
| 831 | 31583_at | rpS8 | X67247 | H.sapiens rpS8 gene for ribosomal protein S8. | ribosomal protein S8 |
| 832 | 1685_at | SPHAR | X82554 | H.sapiens SPHAR gene for cyclin-related protein. | S-phase response (cyclin-related) |
| 833 | 38127_at | syndecan-1 | Z48199 | H.sapiens syndecan-1 gene (exons 2-5). | syndecan 1 |
| 834 | 37310_at | uPA | X02419 | H.sapiens uPA gene. | urokinase-plasminogen activator |
| 835 | 34308_at | H2AFL | U90551 | H2A histone family, member L | histone 2A-like protein |
| 836 | 39337_at | H2AFZ | M37583 | H2A histone family, member Z | H2A histone family, member Z |
| 837 | 33458_r_at | H2BFL | AI688098 | H2B histone family, member L | |
| 838 | 40818_at | LOC51580 | D14041 | H-2K binding factor-2 | H-2K binding factor-2 |
| 839 | 254_at | H3F3A | M11353 | H3 histone, family 3A | H3 histone, family 3A |
| 840 | 39969_at | H4FG | AA255502 | H4 histone family, member G | |
| 841 | 32591_at | HCDI | AI494623 | HCDI protein | |
| 842 | 35215_at | HDCMA18P | AL049996 | HDCMA18P protein | hypothetical protein |
| 843 | 39353_at | HSPE1 | AI912041 | heat shock 10kD protein 1 (chaperonin 10) | |
| 844 | 37720_at | HSPD1 | M22382 | heat shock 60kD protein 1 (chaperonin) | mitochondrial matrix protein |
| 845 | 36614_at | HSPA5 | X87949 | heat shock 70kD protein 5 (glucose-regulated protein, 78kD) | heat shock 70kD protein 5 (glucose-regulated protein, 78kD) |
| 846 | 41510_s_at | HSPA9B | L15189 | heat shock 70kD protein 9B (mortalin-2) | MTHSP75 |

Fig 21

| | A | B | C | D | E |
|-----|------------|----------|----------|---|--|
| 847 | 32316_s_at | HSPCA | X15183 | heat shock 90kD protein 1, alpha | heat shock 90kD protein 1, alpha |
| 848 | 33984_at | HSPCB | M16660 | heat shock 90kD protein 1, beta | heat shock 90kD protein 1, beta |
| 849 | 31906_at | HSBP1 | AF068754 | heat shock factor binding protein 1 | heat shock factor binding protein 1 HSBP1 |
| 850 | 1468_at | TRAP1 | U12595 | heat shock protein 75 | tumor necrosis factor type 1 receptor associated protein |
| 851 | 38054_at | HBXIP | AF029890 | hepatitis B virus x interacting protein | hepatitis B virus X interacting protein |
| 852 | 38779_r_at | HDGF | D16431 | hepatoma-derived growth factor (high-mobility group protein 1-like) | hepatoma-derived GF |
| 853 | 35644_at | HEPH | AB014598 | hephaestin | KIAA0698 protein |
| 854 | 38094_at | HNRPA1 | M65028 | heterogeneous nuclear ribonucleoprotein A/B | hnRNP type A/B protein |
| 855 | 37334_at | HNRPA0 | U23803 | heterogeneous nuclear ribonucleoprotein A0 | heterogeneous ribonucleoprotein A0 |
| 856 | 34987_s_at | HNRPA1 | X79536 | heterogeneous nuclear ribonucleoprotein A1 | hnRNPcore protein A1 |
| 857 | 36654_s_at | HNRPA2B1 | M29065 | heterogeneous nuclear ribonucleoprotein A2/B1 | heterogeneous nuclear ribonucleoprotein A2/B1, isoform A2; heterogeneous nuclear ribonucleoprotein A2/B1, isoform B1 |
| 858 | 33666_at | HNRPC | M16342 | heterogeneous nuclear ribonucleoprotein C (C1/C2) | heterogeneous nuclear ribonucleoprotein C, isoform b; heterogeneous nuclear ribonucleoprotein C, isoform a |
| 859 | 38016_at | HNRPD | M94630 | heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kD) | DNA-binding protein |
| 860 | 33845_at | HNRPH1 | W28483 | heterogeneous nuclear ribonucleoprotein H1 (H) | |
| 861 | 41132_r_at | HNRPH2 | U01923 | heterogeneous nuclear ribonucleoprotein H2 (H') | heterogeneous nuclear ribonucleoprotein H2 |
| 862 | 41283_at | HNRPH3 | AF052131 | heterogeneous nuclear ribonucleoprotein H3 (2H9) | heterogeneous nuclear ribonucleoprotein H3, isoform a; heterogeneous nuclear ribonucleoprotein H3, isoform b |
| 863 | 40836_s_at | HNRPH3 | W26677 | heterogeneous nuclear ribonucleoprotein H3 (2H9) | |

Fig 21

| A | B | C | D | E |
|--------------|---------|----------|--|---|
| 864 39415_at | HNRPK | X72727 | heterogeneous nuclear ribonucleoprotein K | transformation upregulated nuclear protein |
| 865 35201_at | HNRPL | X16135 | heterogeneous nuclear ribonucleoprotein L | heterogeneous nuclear ribonucleoprotein L |
| 866 37717_at | HNRPM | L03532 | heterogeneous nuclear ribonucleoprotein M | M4 protein |
| 867 39792_at | HNRPR | AF000364 | heterogeneous nuclear ribonucleoprotein R | heterogeneous nuclear ribonucleoprotein R |
| 868 38654_at | HNRPU | X65488 | heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) | hnRNP U protein |
| 869 32818_at | HXB | X78565 | hexabrachion (tenascin C, cytactin) | human tenascin-C |
| 870 39827_at | RTP801 | AA522530 | HIF-1 responsive RTP801 | |
| 871 31504_at | HDLBP | M64098 | high density lipoprotein binding protein (vigilin) | high density lipoprotein binding protein |
| 872 32220_at | HMG1 | D63874 | high-mobility group (nonhistone chromosomal) protein 1 | HMG-1 |
| 873 306_s_at | HMG14 | J02621 | high-mobility group (nonhistone chromosomal) protein 14 | high-mobility group (nonhistone chromosomal) protein 14 |
| 874 35738_at | HMG17L3 | A1347088 | high-mobility group (nonhistone chromosomal) protein 17-like 3 | |
| 875 38065_at | HMG2 | X62534 | high-mobility group (nonhistone chromosomal) protein 2 | high-mobility group (nonhistone chromosomal) protein 2 |
| 876 38843_at | HMG2L1 | AL079310 | high-mobility group protein 2-like 1 | hypothetical protein |
| 877 35693_at | HPCAL1 | AF070616 | hippocalcin-like 1 | BDP-1 protein |
| 878 1009_at | HINT1 | U51004 | histidine triad nucleotide binding protein 1 | protein kinase C inhibitor |
| 879 34231_at | HBOA | AF074606 | histone acetyltransferase | histone acetyltransferase |
| 880 41855_at | HAT1 | AF030424 | histone acetyltransferase 1 | histone acetyltransferase 1 |
| 881 38771_at | HDAC1 | D50405 | histone deacetylase 1 | RPD3 protein |
| 882 34368_at | HDAC2 | U31814 | histone deacetylase 2 | transcriptional regulator homolog RPD3 |
| 883 38271_at | HDAC4 | AB006626 | histone deacetylase 4 | KIAA0288 protein |
| 884 39046_at | H2AV | AL049324 | histone H2A.F/Z variant | |
| 885 39092_at | H2AV | AW007731 | histone H2A.F/Z variant | |
| 886 38824_at | HTATIP2 | AF039103 | HIV-1 Tat interactive protein 2, 30 kD | Tat-interacting protein TIP30 |
| 887 40220_at | HIS1 | AB021179 | HMBA-inducible | HEXIM1 protein |

Fig 21

| A | | | B | C | D | E |
|-----|------------|--|------------|----------|--|---|
| 888 | 39809_at | | HBP1 | AF019214 | HMG-box containing protein 1 | HMG box containing protein 1 |
| | | | | | HMG-domain containing protein which is the 57 kd subunit within SWI/SNF-related BAF complexes; contains a proline-rich N-terminus, a kinesin-like coiled-coil region, and a highly acidic c-terminus; Homo sapiens BAF57 (BAF57) gene, complete cds. | |
| 889 | 33828_at | | BAF57 | AF035262 | | BAF57 |
| 890 | 39348_at | | HRMT1L1 | X99209 | HMT1 hnRNP methyltransferase-like 1 (S. cerevisiae) | arginine methyltransferase |
| 891 | 32825_at | | HRMT1L2 | Y10805 | HMT1 hnRNP methyltransferase-like 2 (S. cerevisiae) | arginine methyltransferase |
| | | | | | HNRNP Core Protein A1 LIKE | |
| 892 | 31463_s_at | | dJ256G22.1 | AL022097 | pseudogene; match: proteins P04256 Q28521 P49312 P09651 P51991 P51992 P51968 P17130 P22626 | |
| 893 | 38943_at | | HCCS | U36787 | holocytochrome c synthase (cytochrome c heme-lyase) | holocytochrome c-type synthetase |
| 894 | 39610_at | | HOXB2 | X16665 | homeo box B2 | homeo box B2 |
| 895 | 40674_s_at | | HOXC6 | S82986 | homeo box C6 | homeo box C6 |
| 896 | 38233_at | | HOMER-3 | AF093265 | Homer, neuronal immediate early gene, 3 | homer-3 |
| 897 | 34401_at | | UQCRFS1 | L32977 | Homo sapiens (clone 117252) ubiquinol cytochrome c reductase Rieske iron-sulphur protein (UQCRFS1) gene, exon 2. | Rieske Fe-S protein |
| | | | | | Homo sapiens (clone FFE-7) type II inosine monophosphate dehydrogenase (IMPDH2) gene, exons 1-13, complete cds. | inosine monophosphate dehydrogenase type II |
| 898 | 36624_at | | IMPDH2 | L33842 | | |
| 899 | 37599_at | | AOX1 | AF017060 | Homo sapiens aldehyde oxidase (AOX1) gene, exon 35 and complete cds. | aldehyde oxidase |
| 900 | 39740_g_at | | NACA | AF054187 | Homo sapiens alpha NAC mRNA, complete cds. | alpha NAC |

Fig 21

| A | | B | C | D | E |
|-----|------------|--------|----------|---|----------------|
| 901 | 39739_at | NACA | AF054187 | Homo sapiens alpha NAC mRNA, complete cds. | alpha NAC |
| 902 | 41154_r_at | CTNNA1 | AF102803 | Homo sapiens alphaE-catenin (CTNNA1) gene, exon 18 and complete cds. | alphaE-catenin |
| 903 | 41153_f_at | CTNNA1 | AF102803 | Homo sapiens alphaE-catenin (CTNNA1) gene, exon 18 and complete cds. | alphaE-catenin |
| 904 | 39324_at | | AL050078 | Homo sapiens cDNA FLJ10784 f1s, clone NT2RP4000448, highly similar to Homo sapiens mRNA; cDNA DKFZp566G0746 | |
| 905 | 35310_at | | D45288 | Homo sapiens cDNA FLJ13267 f1s, clone OVARC1000964 | |
| 906 | 35754_at | | L40391 | Homo sapiens cDNA FLJ13553 f1s, clone PLACE1007454 | |
| 907 | 33325_at | | W26667 | Homo sapiens cDNA FLJ14821 f1s, clone OVARC1000556, highly similar to RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.-) | |
| 908 | 38102_at | | W28575 | Homo sapiens cDNA FLJ25016 f1s, clone CBL01574 | |
| 909 | 41253_s_at | | A1983043 | Homo sapiens cDNA FLJ30436 f1s, clone BRACE2009037 | |
| 910 | 39162_at | | AA156987 | Homo sapiens cDNA FLJ30544 f1s, clone BRAWH2001412 | |
| 911 | 41807_at | | AL040137 | Homo sapiens cDNA FLJ31959 f1s, clone NT2RP7007422 | |
| 912 | 38643_at | | W87466 | Homo sapiens cDNA FLJ33151 f1s, clone UTERU2000263 | |
| 913 | 34246_at | | AA418437 | Homo sapiens cDNA: FLJ21175 f1s, clone CAS11071 | |
| 914 | 40813_at | | A1768188 | Homo sapiens cDNA: FLJ21243 f1s, clone COL01164 | |

Fig 21

| | A | B | C | D | E |
|-----|------------|-----------------|----------|---|--|
| 915 | 40923_at | | | Homo sapiens cDNA: FLJ21449 f1s, clone COL04483, highly similar to AF010235 Homo sapiens mRNA from chromosome 5q31-33 region | |
| 916 | 38993_r_at | | AA290994 | Homo sapiens cDNA: FLJ21904 f1s, clone HEP03585 | |
| 917 | 38093_at | | W27522 | Homo sapiens cDNA: FLJ21927 f1s, clone HEP04178, highly similar to HSU90909 Human clone 23722 mRNA sequence | |
| 918 | 34840_at | | U90909 | Homo sapiens cDNA: FLJ22642 f1s, clone HS106970 | |
| 919 | 32838_at | smooth muscle m | AI700633 | Homo sapiens cDNA: FLJ23324 f1s, clone HEP12482, highly similar to HUMMYOHC B Human nonmuscle myosin heavy chain-B (MYH10) mRNA | smooth muscle myosin heavy chain isoform SMemb |
| 920 | 33737_f_at | | S67247 | Homo sapiens cervical cancer suppressor-1 mRNA, complete cds | |
| 921 | 41663_at | | AI871359 | Homo sapiens clone 23570 mRNA sequence | |
| 922 | 36815_at | | AF038202 | Homo sapiens clone 23700 mRNA sequence | |
| 923 | 41841_at | | AF038185 | Homo sapiens clone 23718 mRNA sequence | |
| 924 | 37794_at | | AF052138 | Homo sapiens clone 23903 mRNA sequence | |
| 925 | 38764_at | | AF035281 | Homo sapiens clone 23938 mRNA sequence | |
| 926 | 35342_at | | AF007142 | Homo sapiens clone 24416 mRNA sequence | |
| 927 | 31867_at | | AF052159 | Homo sapiens clone 24630 mRNA sequence | |
| 928 | 36758_at | | AF052174 | Homo sapiens clone 24674 mRNA sequence | |
| 929 | 41864_at | | AF070578 | Homo sapiens clone 24790 mRNA sequence | |

Fig 21

| | A | B | C | D | E |
|-----|------------|------------------|----------|--|---|
| 930 | 38070_at | | AL080234 | Homo sapiens clone FBD3 Cri-du-chat critical region mRNA | |
| 931 | 34773_at | TBCA | AF038952 | Homo sapiens cofactor A protein mRNA, complete cds. | cofactor A protein |
| 932 | 39027_at | COX4 | AF017115 | Homo sapiens cytochrome c oxidase subunit IV precursor (COX4) gene, nuclear gene encoding mitochondrial protein, complete cds. | cytochrome c oxidase subunit IV precursor |
| 933 | 40878_f_at | D15F37 | AF041081 | Homo sapiens D15F37 pseudogene, S4 allele, mRNA sequence. | |
| 934 | 631_g_at | DCTD | L39874 | Homo sapiens deoxycytidylate deaminase gene, complete cds. | deoxycytidylate deaminase |
| 935 | 630_at | DCTD | L39874 | Homo sapiens deoxycytidylate deaminase gene, complete cds. | deoxycytidylate deaminase |
| 936 | 33936_at | GALC | D86181 | Homo sapiens DNA for galactocerebrosidase, exon 17 and complete cds. | galactocerebrosidase |
| 937 | 40134_at | ATP5J2; ATP5JL | AF047436 | Homo sapiens F1Fo-ATPase synthase f subunit mRNA, complete cds. | F1Fo-ATPase synthase f subunit |
| 938 | 36103_at | SCYA3; LD78ALP | D90144 | Homo sapiens gene for LD78 alpha precursor, complete cds. | LD78 alpha precursor |
| 939 | 40725_at | GOSR1; P28; GS2 | AF047438 | Homo sapiens GOS28/P28 protein mRNA, complete cds. | GOS28/P28 protein |
| 940 | 38708_at | RAN; TC4; ARA24 | AF054183 | Homo sapiens GTP binding protein mRNA, complete cds. | GTP binding protein |
| 941 | 35790_at | VPS26; HB58; HB | AF054179 | Homo sapiens H beta 58 homolog mRNA, complete cds. | H beta 58 homolog |
| 942 | 36576_at | H2AFY; H2A.y; H2 | AF054174 | Homo sapiens histone macroH2A1.2 mRNA, complete cds. | histone macroH2A1.2 |
| 943 | 35303_at | INSIG1 | U96876 | Homo sapiens insulin induced protein 1 (INSIG1) gene, complete cds. | insulin induced protein 1 |
| 944 | 1038_s_at | interferon-gamma | U19247 | Homo sapiens interferon-gamma receptor alpha chain gene, exon 7 and complete cds. | interferon-gamma receptor alpha chain |

Fig 21

| | A | B | C | D | E |
|-----|------------|----------------------------|----------|--|--|
| 945 | 895_at | MIF | L19686 | Homo sapiens macrophage migration inhibitory factor (MIF) gene, complete cds. | macrophage migration inhibitory factor |
| 946 | 38967_at | C14orf12; MP68; P1AF054175 | | Homo sapiens mitochondrial proteolipid 68MP homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds. | mitochondrial proteolipid 68MP homolog |
| 947 | 31881_at | | Y14155 | Homo sapiens mRNA for Hmob33 protein, 3' untranslated region | |
| 948 | 34677_f_at | tl132 | AJ012755 | Homo sapiens mRNA for TL132 | TL132 protein |
| 949 | 38786_at | | AL079279 | Homo sapiens mRNA full length insert cDNA clone EUOIMAGE 248114 | |
| 950 | 33418_at | | AL096752 | Homo sapiens mRNA; cDNA DKFZp434A012 (from clone DKFZp434A012) | |
| 951 | 38630_at | | AL080192 | Homo sapiens mRNA; cDNA DKFZp434B102 (from clone DKFZp434B102) | |
| 952 | 41529_g_at | | W72239 | Homo sapiens mRNA; cDNA DKFZp434M162 (from clone DKFZp434M162) | |
| 953 | 36451_at | | AI743299 | Homo sapiens mRNA; cDNA DKFZp434M245 (from clone DKFZp434M245) | |
| 954 | 36821_at | DKFZp564A026 | AL050367 | Homo sapiens mRNA; cDNA DKFZp564A026 (from clone DKFZp564A026) | hypothetical protein |
| 955 | 37366_at | | AL049969 | Homo sapiens mRNA; cDNA DKFZp564A072 (from clone DKFZp564A072) | |
| 956 | 39506_at | | AA933984 | Homo sapiens mRNA; cDNA DKFZp564B222 (from clone DKFZp564B222) | |
| 957 | 39748_at | | AL050021 | Homo sapiens mRNA; cDNA DKFZp564D016 (from clone DKFZp564D016) | |

Fig 21

| A | B | C | D | E |
|----------------|---|----------|--|---|
| 958 38357_at | | AL049321 | Homo sapiens mRNA; cDNA DKFZp564D156 (from clone DKFZp564D156) | |
| 959 33716_at | | N95443 | Homo sapiens mRNA; cDNA DKFZp564E122 (from clone DKFZp564E122) | |
| 960 35301_at | | AL049941 | Homo sapiens mRNA; cDNA DKFZp564E2222 (from clone DKFZp564E2222) | |
| 961 35842_at | | AL049265 | Homo sapiens mRNA; cDNA DKFZp564F053 (from clone DKFZp564F053) | |
| 962 40552_s_at | | AL049987 | Homo sapiens mRNA; cDNA DKFZp564F112 (from clone DKFZp564F112) | |
| 963 39170_at | | AL049957 | Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323) | |
| 964 34303_at | | AL049949 | Homo sapiens mRNA; cDNA DKFZp564L0822 (from clone DKFZp564L0822) | |
| 965 36509_at | | AL049998 | Homo sapiens mRNA; cDNA DKFZp564L222 (from clone DKFZp564L222) | |
| 966 40353_at | | AL049962 | Homo sapiens mRNA; cDNA DKFZp564P0823 (from clone DKFZp564P0823) | |
| 967 35290_at | | AL050081 | Homo sapiens mRNA; cDNA DKFZp566J2146 (from clone DKFZp566J2146) | |
| 968 38079_at | | AL049367 | Homo sapiens mRNA; cDNA DKFZp586B0918 (from clone DKFZp586B0918) | |
| 969 32195_at | | AL049450 | Homo sapiens mRNA; cDNA DKFZp586B1922 (from clone DKFZp586B1922) | |

Fig 21

| | A | B | C | D | E |
|-----|------------|-------|----------|--|---|
| 970 | 39379_at | | AL049397 | Homo sapiens mRNA; cDNA DKFZp586C1019 (from clone DKFZp586C1019) | |
| 971 | 37575_at | | AL050192 | Homo sapiens mRNA; cDNA DKFZp586C1723 (from clone DKFZp586C1723) | |
| 972 | 34283_at | | AL050125 | Homo sapiens mRNA; cDNA DKFZp586F071 (from clone DKFZp586F071) | |
| 973 | 39600_at | | AL080110 | Homo sapiens mRNA; cDNA DKFZp586G1922 (from clone DKFZp586G1922) | |
| 974 | 34752_at | | AL080111 | Homo sapiens mRNA; cDNA DKFZp586G2222 (from clone DKFZp586G2222) | |
| 975 | 39103_s_at | | H98552 | Homo sapiens mRNA; cDNA DKFZp586I0523 (from clone DKFZp586I0523) | |
| 976 | 36092_at | | AL080213 | Homo sapiens mRNA; cDNA DKFZp586I1823 (from clone DKFZp586I1823) | |
| 977 | 35187_at | | AL080216 | Homo sapiens mRNA; cDNA DKFZp586K1123 (from clone DKFZp586K1123) | |
| 978 | 35363_at | DDX17 | AL080113 | Homo sapiens mRNA; cDNA DKFZp586K2322 (from clone DKFZp586K2322) | |
| 979 | 41013_at | | AL080114 | Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp586M2022) | |
| 980 | 41690_at | | AL049471 | Homo sapiens mRNA; cDNA DKFZp586N012 (from clone DKFZp586N012) | |
| 981 | 40349_at | | AL049442 | Homo sapiens mRNA; cDNA DKFZp586N1720 (from clone DKFZp586N1720) | |

Fig 21

| | A | B | C | D | E |
|-----|------------|-----------------|----------|---|--|
| 982 | 32672_at | | | Homo sapiens mRNA; cDNA DKFZp586N1918 (from clone DKFZp586N1918) | |
| 983 | 36668_at | DIA1 | AL049387 | Homo sapiens NADH-cytochrome b5 reductase (b5R) gene, exon 9. | NADH-cytochrome b5 reductase |
| 984 | 38542_at | | M28713 | Homo sapiens nucleophosmin phosphoprotein (NPM) gene, 3' flanking sequence. | |
| 985 | 40587_s_at | | U89322 | Homo sapiens p18 protein mRNA, complete cds. | p18 protein |
| 986 | 41448_at | EEF1E1; P18 | AF054186 | Homo sapiens PAC clone RP1-170O19 from 7p15-p21, complete sequence. | even-skipped homeo box 1 (homolog of Drosophila) |
| 987 | 36159_s_at | HOXA4 | AC004080 | Homo sapiens prion protein (PrP) gene, complete cds. | prion protein |
| 988 | 32756_at | PrP | U29185 | Homo sapiens putative dienyol-CoA isomerase (ECH1) gene, exons 7-10, and complete cds. | putative dienyol-CoA isomerase |
| 989 | 35824_at | ECH1 | AF030249 | Homo sapiens RP58 gene, complete CDS. | RP58 protein |
| 990 | 39169_at | RP58 | AJ223321 | Homo sapiens Sec61 gamma mRNA, complete cds. | Sec61 gamma |
| 991 | 41222_at | SEC61G | AF054184 | Homo sapiens signal transducer and activator of transcription 6 (STAT6) gene, exons 15 through 23 and complete cds. | signal transducer and activator of transcription 6 |
| 992 | 38817_at | STAT6 | AF067575 | Homo sapiens sperm acrosomal protein mRNA, complete cds. | sperm acrosomal protein |
| 993 | 36033_at | SPAG7; ACRP; F3 | AF047437 | Homo sapiens splicing factor, arginine/serine-rich 12 (SFRS12) mRNA, complete cds | |
| 994 | 31481_s_at | TMSB10 | AL049309 | Homo sapiens thymosin beta-10 gene, 3'end. | thymosin beta-10 |
| 995 | 1693_s_at | M92383 | D11139 | Homo sapiens TIMP gene for tissue inhibitor of metalloproteinases, partial cds. | tissue inhibitor of metalloproteinases |

Fig 21

| A | B | C | D | E |
|-----------------|------------------|----------|---|------------------------------------|
| 996 37311_at | TALDO1; TAL-H; | AF010400 | Homo sapiens transaldolase-related protein gene, exons 3-8 and complete cds. | transaldolase-related protein |
| 997 32229_at | EIF4EL3; 4EHP; 4 | AF038957 | Homo sapiens translation initiation factor 4e mRNA, complete cds. | translation initiation factor 4e |
| 998 1323_at | UBB | X04803 | Homo sapiens ubiquitin gene. | ubiquitin |
| 999 32153_s_at | UBB | U49869 | Homo sapiens ubiquitin gene. | ubiquitin |
| 1000 38372_at | | U66042 | Homo sapiens unknown mRNA | |
| 1001 38814_at | ATP6V1G1; ATP6 | AF038954 | Homo sapiens vacuolar H(+)-ATPase subunit mRNA, complete cds. | vacuolar H(+)-ATPase subunit |
| 1002 41597_s_at | SEC22L1; SEC22 | AF047442 | Homo sapiens vesicle trafficking protein sec22b mRNA, complete cds. | vesicle trafficking protein sec22b |
| 1003 34957_at | X5L | Y18504 | Homo sapiens X5L gene. | XAP-5-like protein |
| 1004 38662_at | | AL047596 | Homo sapiens, clone IMAGE:3028427, mRNA, partial cds | |
| 1005 38312_at | | AL050002 | Homo sapiens, clone IMAGE:3140802, mRNA | |
| 1006 33388_at | | AL080223 | Homo sapiens, clone IMAGE:3855224, mRNA, partial cds | |
| 1007 38676_at | | AA059408 | Homo sapiens, clone IMAGE:4132509, mRNA | |
| 1008 40238_at | | AI674208 | Homo sapiens, clone IMAGE:4150198, mRNA, partial cds | |
| 1009 32119_at | | AL049423 | Homo sapiens, clone IMAGE:4182947, mRNA | |
| 1010 38650_at | IGFBP5 | L27560 | Homo sapiens, clone IMAGE:4183312, mRNA, partial cds | |
| 1011 1396_at | IGFBP5 | L27560 | Homo sapiens, clone IMAGE:4183312, mRNA, partial cds | |
| 1012 40432_at | | AA522891 | Homo sapiens, clone IMAGE:4391536, mRNA | |
| 1013 36130_f_at | MT1E | R92331 | Homo sapiens, Similar to RNA helicase-related protein, clone MGC:9246 IMAGE:3892441, mRNA, complete cds | |

Fig 21

| | A | B | C | D | E |
|------|------------|--------------|----------|--|--|
| 1014 | 41246_at | | AI743134 | Homo sapiens, Similar to serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2, clone MGC:23129 IMAGE:4578406, mRNA, complete cds | |
| 1015 | 41533_at | | U79298 | Homo sapiens, similar to unknown, clone MGC:39325 IMAGE:540447, mRNA, complete cds | |
| 1016 | 39733_at | HERPUD1 | AF055001 | homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1 | homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1 |
| 1017 | 525_g_at | hPMS1 | U13695 | homolog of yeast mutL gene; Human homolog of yeast mutL (hPMS1) gene, complete cds. | postmeiotic segregation 1 |
| 1018 | 32545_r_at | RSU-1 | L12535 | homologous to mouse Rsu-1; putative; Human RSU-1/RSP-1 mRNA, complete cds. | ras suppressor protein 1 |
| 1019 | 32544_s_at | RSU-1 | L12535 | homologous to mouse Rsu-1; putative; Human RSU-1/RSP-1 mRNA, complete cds. | ras suppressor protein 1 |
| 1020 | 39800_s_at | HAX1 | U68566 | HS1 binding protein | HAX-1 |
| 1021 | 38104_at | DECR1; NADPH | U78302 | Human 2,4-dienoyl-CoA reductase gene, exon 10 and complete cds. | 2,4-dienoyl-CoA reductase |
| 1022 | 37708_r_at | ADH5 | M81118 | Human alcohol dehydrogenase chi polypeptide (ADH5) gene exons 8-9, complete cds. | alcohol dehydrogenase |
| 1023 | 37707_i_at | ADH5 | M81118 | Human alcohol dehydrogenase chi polypeptide (ADH5) gene exons 8-9, complete cds. | alcohol dehydrogenase |
| 1024 | 39333_at | COL4A1 | M26576 | Human alpha-1 collagen type IV gene, exon 52. | alpha-1 type IV collagen |
| 1025 | 38417_at | AMPD2 | M91029 | Human AMP deaminase (AMPD2) mRNA. | AMP deaminase isoform L splicing variant |
| 1026 | 37747_at | ANX5 | U05770 | Human annexin V (ANX5) gene, exon 13. | annexin V |

Fig 21

| A | B | C | D | E |
|-----------------|------------------|----------|--|--|
| 1027 41143_at | CALM1 | U12022 | Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds. | calmodulin |
| 1028 239_at | CTSD | M63138 | Human cathepsin D (catD) gene, exons 7, 8, and 9. | cathepsin D |
| 1029 1916_s_at | c-fos | V01512 | Human cellular oncogene c-fos (complete sequence). | v-fos FBJ murine osteosarcoma viral oncogene homolog |
| 1030 1915_s_at | c-fos | V01512 | Human cellular oncogene c-fos (complete sequence). | v-fos FBJ murine osteosarcoma viral oncogene homolog |
| 1031 32583_at | JUN | J04111 | Human c-jun proto oncogene (JUN), complete cds, clone hCJ-1. | v-jun avian sarcoma virus 17 oncogene homolog |
| 1032 1895_at | JUN | J04111 | Human c-jun proto oncogene (JUN), complete cds, clone hCJ-1. | v-jun avian sarcoma virus 17 oncogene homolog |
| 1033 41604_at | | U79297 | Human clone 23589 mRNA sequence | |
| 1034 32185_at | | U00946 | Human clone A9A2BRB5 (CAC)n/(GTG)n repeat-containing mRNA | |
| 1035 33667_at | PPIA | X52851 | Human cyclophilin gene for cyclophilin (EC 5.2.1.8). | peptidylprolyl isomerase |
| 1036 38459_g_at | CYB5 | L39945 | Human cytochrome b5 (CYB5) gene, exon 6 and complete cds. | cytochrome b5 |
| 1037 38458_at | CYB5 | L39945 | Human cytochrome b5 (CYB5) gene, exon 6 and complete cds. | cytochrome b5 |
| 1038 36163_at | DLD; E3; LAD; DL | L13761 | Human dihydrolipoamide dehydrogenase gene, exon 14. | dihydrolipoamide dehydrogenase |
| 1039 1424_s_at | YWHAH; YWHA1 | D78577 | Human DNA for 14-3-3 protein eta chain, exon2 and complete cds. | 14-3-3 protein eta chain |
| 1040 31797_at | dJ73H22.1 | AL035699 | Human DNA sequence from clone 73H22 on chromosome 6q23, complete sequence. | dJ73H22.1 (TBP-like protein) |
| 1041 40193_at | ENO2 | X51956 | Human ENO2 gene for neuron specific (gamma) enolase. | human gamma enolase |
| 1042 38326_at | GOS2 | M69199 | Human GOS2 protein gene, complete cds. | GOS2 protein |
| 1043 40567_at | TUBA3; FLJ25113 | X01703 | Human gene for alpha-tubulin (b alpha 1). | alpha-tubulin |

Fig 21

| | A | B | C | D | E |
|------|------------|------------------|--------|--|---|
| 1044 | 39775_at | SERP1G1; C1IN | X54486 | Human gene for C1-inhibitor. | C1 inhibitor |
| 1045 | 40862_i_at | CKB; CKBB | X15334 | Human gene for creatine kinase B (EC 2.7.3.2). | creatine kinase B |
| 1046 | 37641_at | IFI44; p44; MTAP | D28915 | Human gene for hepatitis C-associated microtubular aggregate protein p44, exon 9 and complete cds. | hepatitis C-associated microtubular aggregate protein p44 |
| 1047 | 40211_at | HNRPA1; HNRNP | X12671 | Human gene for heterogeneous nuclear ribonucleoprotein (hnRNP) core protein A1. | hnRNP A1 protein |
| 1048 | 408_at | MGSA | X54489 | Human gene for melanoma growth stimulatory activity (MGSA). | melanoma growth stimulatory activity preprotein |
| 1049 | 36203_at | ODC1 | X16277 | Human gene for ornithine decarboxylase ODC (EC 4.1.1.17). | ornithine decarboxylase (ODC) |
| 1050 | 36873_at | VLDLR | D16532 | Human gene for very low density lipoprotein receptor, exon 19. | very low density lipoprotein receptor |
| 1051 | 34759_at | | U68494 | Human hbc647 mRNA sequence | |
| 1052 | 32805_at | AKR1C1; DD1; D | U05861 | Human hepatic dihydrodiol dehydrogenase gene, exon 9. | hepatic dihydrodiol dehydrogenase |
| 1053 | 41231_f_at | HMG17; MGC562 | X13546 | Human HMG-17 gene for non-histone chromosomal protein HMG-17. | put. HMG-17 protein |
| 1054 | 38294_at | HOXD4; HOX4; H | X17360 | Human HOX 5.1 gene for HOX 5.1 protein. | hox 5.1 protein |
| 1055 | 40637_at | HSP73 HSC70 HS | Y00371 | Human hsc70 gene for 71 kd heat shock cognate protein. | 71 Kd heat shock cognate protein |
| 1056 | 232_at | LAMB2 | M55210 | Human laminin B2 chain gene, exon 28. | laminin B2 chain |
| 1057 | 40767_at | TFPI | M59499 | Human lipoprotein-associated coagulation inhibitor (LACI) gene, exon 9 and complete cds. | lipoprotein-associated coagulation inhibitor |
| 1058 | 38637_at | LOX | L16895 | Human lysyl oxidase (LOX) gene, exon 7. | lysyl oxidase |
| 1059 | 37532_at | MCAD | M91432 | Human medium-chain acyl-CoA dehydrogenase (MCAD) gene, exon 12. | medium-chain acyl-CoA dehydrogenase |
| 1060 | 870_f_at | MT3; GIF; GIFB | M93311 | Human metallothionein-III gene, complete cds. | metallothionein-III |

Fig 21

| A | B | C | D | E |
|-----------------|-----------------|--------|---|--|
| 1061 40890_at | MTX | U46920 | Human melaxin (MTX) gene, complete cds. | metaxin |
| 1062 32145_at | ADD1 | X58141 | Human mRNA for erythrocyte adducin alpha subunit. | erythrocyte alpha adducin |
| 1063 37381_g_at | TF2B | X59268 | Human mRNA for general transcription factor IIB. | IIB protein |
| 1064 33683_at | TI-227H | D50525 | Human mRNA for TI-227H. | |
| 1065 41747_s_at | MEF2A | U49020 | Human myocyte-specific enhancer factor 2A (MEF2A) gene, last coding exon, and complete cds. | myocyte-specific enhancer factor 2A, C9 form; myocyte-specific enhancer factor 2A, C4 form |
| 1066 38066_at | NQO1 | M81600 | Human NAD(P)H:quinone oxidoreductase gene, exon 6. | NAD(P)H:quinone oxidoreductase |
| 1067 39729_at | NKEFB | L19185 | Human natural killer cell enhancing factor (NKEFB) mRNA, complete cds. | enhancer protein |
| 1068 33994_g_at | MLC | M22919 | Human nonmuscle/smooth muscle alkali myosin light chain gene, complete cds. | non-muscle myosin light chain; smooth muscle myosin light chain |
| 1069 32841_at | ZNFX; DM2; CNB1 | U19765 | Human nucleic acid binding protein gene, complete cds. | nucleic acid binding protein |
| 1070 32590_at | NCL | M60858 | Human nucleolin gene, complete cds. | nucleolin |
| 1071 1782_s_at | Op18 | M31303 | Human oncoprotein 18 (Op18) gene, complete cds. | oncoprotein 18 |
| 1072 216_at | PTGDS | M98539 | Human prostaglandin D2 synthase gene, exon 7. | prostaglandin D2 synthase (21kD, brain) |
| 1073 237_s_at | PPP2CA | M60483 | Human protein phosphatase 2A catalytic subunit-alpha gene, complete cds. | protein phosphatase-2A catalytic subunit-alpha |
| 1074 812_at | PPP1R2 | U68111 | Human protein phosphatase inhibitor 2 (PPP1R2) gene, exon 6 and complete cds. | protein phosphatase inhibitor 2 |
| 1075 33180_at | PPP1R2 | U68111 | Human protein phosphatase inhibitor 2 (PPP1R2) gene, exon 6 and complete cds. | protein phosphatase inhibitor 2 |
| 1076 35356_at | | W21884 | Human putative ribosomal protein S1 mRNA | |

Fig 21

| A | B | C | D | E |
|-----------------|-----------------------|----------|---|--|
| 1077 491_at | PTPRG | U46116 | Human receptor tyrosine phosphatase gamma (PTPRG) gene, exon 30 and complete cds. | receptor tyrosine phosphatase gamma |
| 1078 492_g_at | PTPRG | U46116 | Human receptor tyrosine phosphatase gamma (PTPRG) gene, exon 30 and complete cds. | receptor tyrosine phosphatase gamma |
| 1079 36611_at | ACP1 | U25849 | Human red cell-type low molecular weight acid phosphatase (ACP1) gene, exon 6 and 7, complete cds. | red cell-type low molecular weight acid phosphatase |
| 1080 174_s_at | SH3P18 | U61167 | Human SH3 domain-containing protein SH3P18 mRNA, complete cds | SH3 domain-containing protein SH3P18 |
| 1081 241_g_at | SRM | M64231 | Human spermidine synthase gene, complete cds. | spermidine synthase |
| 1082 36688_at | SCP-X/SCP-2 | U11313 | Human sterol carrier protein-X/sterol carrier protein-2 (SCP-X/SCP-2) gene, exon 16, and complete cds. | sterol carrier protein-X/sterol carrier protein-2 |
| 1083 32587_at | ZFP36L2; BRF2; TOP1P2 | U07802 | Human Tis11d gene, complete cds. | Tis11d |
| 1084 31680_at | | M55630 | Human topoisomerase I pseudogene 2. | |
| 1085 36446_s_at | HMG1L2 | L24521 | Human transformation-related protein mRNA, 3' end | transformation-related protein |
| 1086 39351_at | CD59 | M84349 | Human transmembrane protein (CD59) gene, exon 4. | CD59 protein |
| 1087 38727_at | THE1 | M23161 | Human transposon-like element mRNA | |
| 1088 41433_at | VCAM1 | M73255 | Human vascular cell adhesion molecule-1 (VCAM1) gene, complete CDS. | vascular cell adhesion molecule-1 |
| 1089 40121_at | HIP2 | U58522 | huntingtin interacting protein 2 | huntingtin interacting protein |
| 1090 35973_at | HYPH | AB023163 | Huntingtin interacting protein H | KIAA0946 protein |
| 1091 40196_at | HYA22 | D88153 | HYA22 protein | HYA22 |
| 1092 36952_at | HADHA | D16480 | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit | enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase alpha-subunit of trifunctional protein |

Fig 21

| A | B | C | D | E |
|---------------|---------|----------|---|---|
| | | | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit | 3-ketoacyl-CoA thiolase beta-subunit of trifunctional protein |
| 1093 39741_at | HADHB | D16481 | | |
| 1094 36626_at | HSD17B4 | X87176 | hydroxysteroid (17-beta) dehydrogenase 4 | 17beta-hydroxysteroid dehydrogenase |
| | | | Hypothetical protein of unknown function; Hypothetical 52 kDa protein; Hypothetical protein exhibits similarity to motifs found in (U79010) delta 6 desaturase, a hypothetical cytochrome b5 containing fusion protein, and hypothetical proteins encoded by (Z81122) T13F2.1 [Caenorhabditis elegans] and (Z70271) W08D2.4 [Caenorhabditis elegans]; DNA structure-specific endonuclease FEN1; FLAP ENDONUCLEASE-1; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN; Hypothetical human Best's macular dystrophy related protein; Simulated translation extends ORF of previously reported partial coding sequence for Best's macular dystrophy related protein (AF038536); Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence. | BC269730_1; BC269730_2; FEN1_HUMAN; BC269730_4 |
| 1095 41583_at | FEN1 | AC004770 | | |

Fig 21

| A | B | C | D | E |
|---------------|----------|----------|--|--|
| | | | <p>Hypothetical protein of unknown function; Hypothetical 52 kDa protein; Hypothetical protein exhibits similarity to motifs found in (U79010) delta 6 desaturase, a hypothetical cytochrome b5 containing fusion protein, and hypothetical proteins encoded by (Z81122) T13F2.1 [Caenorhabditis elegans] and (Z70271) W08D2.4 [Caenorhabditis elegans]; DNA structure-specific endonuclease FEN1; FLAP ENDONUCLEASE-1; MATURATION FACTOR 1 (MF1); DNase IV; RAD2 HUMAN; Hypothetical human Best's macular dystrophy related protein; Simulated translation extends ORF of previously reported partial coding sequence for Best's macular dystrophy related protein (AF038536); Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.</p> | <p>BC269730_1; BC269730_2; FEN1_HUMAN; BC269730_4 hypothetical protein CG018</p> |
| 109634224_at | FEN1 | AC004770 | | |
| 10971527_s_at | CG018 | U50527 | hypothetical gene CG018 | hypothetical protein CG018 |
| 109833466_at | LOC90355 | AF038182 | hypothetical gene supported by AF038182; BC009203 | hypothetical protein AF038182 |

Fig 21

| A | B | C | D | E |
|-----------------|----------|----------|---|---|
| | | | Hypothetical human protein (partial CDS); CDS constructed from combination of BLASTX, EST matches and Xgrail predictions. N-terminus of protein likely encoded in flanking cosmid R29942. Predicted protein exhibits weak similarity to hypothetical protein PID161226191 (AL021106) from <i>Drosophila melanogaster</i> ; Hypothetical human protein most similar to Rat ionotropic glutamate receptor (L34938); CDS constructed primarily from XGRail predictions and BLASTX similarity to (L34938) ionotropic glutamate receptor [<i>Rattus norvegicus</i>] and gil2160125 (U29873) NMDAR-L [<i>Rattus norvegicus</i>]. Also exhibits similarity to PID16258718 (Z78413) T01C3.10 [<i>Caenorhabditis elegans</i>]. C-terminus of hypothetical protein is ill-defined at this point; definition will require identification and characterization of appropriate cDNAs; Hypothetical 59.8 kDa human protein; CDS constructed from EST matches and Xgrail predictions. C-terminus of predicted protein not fully confirmed by EST or cDNA coverage. Hypothetical protein exhibits no significant database similarities when queried against | R32184_1; R32184_2; R32184_3 |
| 1099 35983_at | MGC2436 | AC004528 | hypothetical protein | |
| 1100 38440_s_at | FLJ20811 | AA015605 | | hypothetical protein, similar to (AC007017) putative RNA helicase A [<i>Arabidopsis thaliana</i>] |
| 1101 39140_at | LOC54505 | AL079292 | hypothetical protein | |
| 1102 37819_at | LOC54104 | AF007130 | hypothetical protein | |
| 1103 39517_at | LOC56007 | AF035313 | hypothetical protein 23851 | |
| 1104 41561_s_at | LOC55977 | AI651368 | hypothetical protein 24636 | |

Fig 21

| | A | B | C | D | E |
|------|------------|---------------|----------|---|-------------------------------|
| 1105 | 41128_at | LOC92703 | AF070537 | hypothetical protein BC013073 | |
| 1106 | 38972_at | LOC115207 | AF052169 | hypothetical protein BC013764 | |
| 1107 | 34864_at | CGI-57 | AF070638 | hypothetical protein CGI-57 | hypothetical protein CGI-57 |
| 1108 | 39960_at | CL640 | AF091086 | hypothetical protein CL640 | hypothetical protein CL640 |
| 1109 | 38837_at | DJ971N18.2 | W26226 | hypothetical protein DJ971N18.2 | |
| 1110 | 35142_at | DKFZP564D172 | AF070617 | hypothetical protein DKFZP564D172 | |
| 1111 | 34830_at | DKFZP564K0822 | W25986 | hypothetical protein DKFZP564K0822 | |
| 1112 | 31852_at | DKFZP564O043 | AL050390 | hypothetical protein DKFZP564O043 | |
| 1113 | 33895_at | DKFZP586F1318 | AL050373 | hypothetical protein DKFZP586F1318 | hypothetical protein |
| 1114 | 39692_at | DKFZP586F2423 | AL080209 | hypothetical protein DKFZP586F2423 | |
| 1115 | 35682_at | FLB6421 | AI133727 | hypothetical protein FLB6421 | |
| 1116 | 36647_at | FLJ10326 | AA526812 | hypothetical protein FLJ10326 | |
| 1117 | 34804_at | FLJ10618 | AL049246 | hypothetical protein FLJ10618 | |
| 1118 | 36840_at | FLJ10737 | AF052158 | hypothetical protein FLJ10737 | |
| 1119 | 35283_at | FLJ10738 | H05692 | hypothetical protein FLJ10738 | |
| 1120 | 37610_at | FLJ10803 | AI765280 | hypothetical protein FLJ10803 | |
| 1121 | 33173_g_at | FLJ10849 | T75292 | hypothetical protein FLJ10849 | |
| 1122 | 39923_at | FLJ10971 | AI935420 | hypothetical protein FLJ10971 | |
| 1123 | 38105_at | FLJ11021 | W26521 | hypothetical protein FLJ11021 similar to splicing factor, arginine/serine-rich 4 | |
| 1124 | 33394_at | FLJ11126 | AA034074 | hypothetical protein FLJ11126 | |
| 1125 | 35709_at | FLJ11149 | AF038172 | hypothetical protein FLJ11149 | |
| 1126 | 38141_at | FLJ11193 | AF038176 | hypothetical protein FLJ11193 | |
| 1127 | 40859_at | FLJ11806 | AI561196 | hypothetical protein FLJ11806 | |
| 1128 | 41177_at | FLJ12443 | AW024285 | hypothetical protein FLJ12443 | |
| 1129 | 41434_at | FLJ12552 | AF070557 | hypothetical protein FLJ12552 | hypothetical protein FLJ12552 |
| 1130 | 36580_at | FLJ13910 | AL050139 | hypothetical protein FLJ13910 | hypothetical protein FLJ13910 |
| 1131 | 32222_at | FLJ14639 | AA152202 | hypothetical protein FLJ14639 | |
| 1132 | 38710_at | FLJ20113 | AL096714 | hypothetical protein FLJ20113 | |
| 1133 | 38652_at | FLJ20154 | AF070644 | hypothetical protein FLJ20154 | |
| 1134 | 40868_at | FLJ20274 | AA442799 | hypothetical protein FLJ20274 | |
| 1135 | 34739_at | FLJ20275 | W26023 | hypothetical protein FLJ20275 | |
| 1136 | 34857_at | FLJ20986 | Z24724 | hypothetical protein FLJ20986 | |
| 1137 | 32251_at | FLJ21174 | AA149307 | hypothetical protein FLJ21174 | |
| 1138 | 40615_at | FLJ21439 | AA780049 | hypothetical protein FLJ21439 | |
| 1139 | 33915_at | FLJ23027 | W22655 | hypothetical protein FLJ23027 | |

Fig 21

| | A | B | C | D | E |
|------|-----------|-----------|----------|---|--|
| 1140 | 35198_at | LOC57146 | AF070596 | hypothetical protein from clone 24796 | hypothetical protein from clone 24796 |
| 1141 | 38483_at | HSA011916 | AJ011916 | hypothetical protein HSA011916 | hypothetical protein |
| 1142 | 41236_at | HSU79252 | U79252 | hypothetical protein HSU79252 | hypothetical protein HSU79252 |
| 1143 | 38443_at | MGC14433 | U79291 | hypothetical protein MGC14433 | |
| 1144 | 39811_at | MGC2749 | AA402538 | hypothetical protein MGC2749 | |
| 1145 | 32051_at | MGC2840 | AJ224875 | hypothetical protein MGC2840 similar to a putative glucosyltransferase | glucosyltransferase |
| 1146 | 35219_at | MGC3047 | AL050202 | hypothetical protein MGC3047 | |
| 1147 | 41696_at | MGC3077 | AL620381 | hypothetical protein MGC3077 | |
| 1148 | 41147_at | MGC4276 | AF038186 | hypothetical protein MGC4276 similar to CG8198 | hypothetical protein MGC4276 similar to CG8198 |
| 1149 | 37242_at | MGC5149 | U79260 | hypothetical protein MGC5149 | |
| 1150 | 36975_at | MGC8721 | W26659 | hypothetical protein MGC8721 | |
| 1151 | 35677_at | MGC9084 | AL035369 | hypothetical protein MGC9084 | hypothetical protein |
| 1152 | 32504_at | MY014 | AW024812 | hypothetical protein Myo14 | |
| 1153 | 38106_at | YR-29 | AJ012409 | hypothetical protein YR-29 | hypothetical protein |
| 1154 | 37640_at | HPRT1 | M31642 | hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome) | hypoxanthine phosphoribosyltransferase 1 |
| 1155 | 1039_s_at | HIF1A | U22431 | hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor) | hypoxia-inducible factor 1 alpha |
| 1156 | 39781_at | IGFBP4 | U20982 | IGF binding protein-4; Human insulin-like growth factor binding protein-4 (IGFBP4) | |
| 1157 | 38046_at | IK | AJ005579 | gene, promoter and complete cds. | insulin-like growth factor binding protein-4 |
| 1158 | 218_at | IK | S74221 | IK cytokine, down-regulator of HLA II | Prer protein |
| 1159 | 37690_at | ILVBL | U61263 | IK cytokine, down-regulator of HLA II | IK factor |
| 1160 | 36097_at | ETR101 | M62831 | ivB (bacterial acetolactate synthase)-like immediate early protein | acetolactate synthase homolog immediate early protein |
| 1161 | 1237_at | IER3 | S81914 | immediate early response 3 | immediate early response 3, isoform short; immediate early response 3, isoform long |
| 1162 | 34391_at | IGBP1 | Y08915 | immunoglobulin (CD79A) binding protein 1 | alpha 4 protein |

Fig 21

| A | B | C | D | E |
|------------------|----------|----------|--|--|
| 1163 38636_at | ISLR | AB003184 | immunoglobulin superfamily containing leucine-rich repeat | ISLR |
| 1164 40695_at | IMPDH1 | J05272 | IMP (inosine monophosphate) dehydrogenase 1 | IMP (inosine monophosphate) dehydrogenase 1 |
| 1165 36875_at | IBTK | AL050018 | inhibitor of Bruton's tyrosine kinase | hypothetical protein |
| 1166 36617_at | ID1 | X77956 | inhibitor of DNA binding 1, dominant negative helix-loop-helix protein | inhibitor of DNA binding 1, dominant negative helix-loop-helix protein |
| 1167 41215_s_at | ID2 | D13891 | inhibitor of DNA binding 2, dominant negative helix-loop-helix protein | Id-2H |
| 1168 34344_at | IKBKAP | AF044195 | inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein | IkappaB kinase complex associated protein |
| 1169 37659_at | IMMT | L42572 | inner membrane protein, mitochondrial (mitofilin) | transmembrane protein |
| 1170 755_at | ITPR1 | D26070 | inositol 1,4,5-trisphosphate receptor, type 1 | human type 1 inositol 1,4,5-trisphosphate receptor |
| 1171 32778_at | ITPR1 | D26070 | inositol 1,4,5-trisphosphate receptor, type 1 | human type 1 inositol 1,4,5-trisphosphate receptor |
| 1172 36154_at | IHPK1 | D87452 | inositol hexaphosphate kinase 1 | KIAA0263 protein |
| 1173 32697_at | IMPA1 | AF042729 | inositol(myo)-1(or 4)-monophosphatase 1 | lithium-sensitive myo-inositol monophosphatase A1 |
| 1174 36496_at | IMPA2 | AF014398 | inositol(myo)-1(or 4)-monophosphatase 2 | myo-inositol monophosphatase 2 |
| 1175 35833_at | LOC51141 | AL080184 | insulin induced protein 2 | |
| 1176 41049_at | IRS1 | S62539 | insulin receptor substrate 1 | insulin receptor substrate-1 |
| 1177 851_s_at | IRS1 | S62539 | insulin receptor substrate 1 | insulin receptor substrate-1 |
| 1178 38737_at | IGF1 | X57025 | insulin-like growth factor 1 (somatomedin C) | insulin-like growth factor I |
| 1179 1501_at | IGF1 | X57025 | insulin-like growth factor 1 (somatomedin C) | insulin-like growth factor I |
| 1180 160027_s_at | IGF2R | Y00285 | insulin-like growth factor 2 receptor | insulin-like growth factor 2 receptor |
| 1181 40422_at | IGFBP2 | X16302 | insulin-like growth factor binding protein 2 (36kD) | insulin-like growth factor binding protein 2 (36kD) |
| 1182 1737_s_at | IGFBP4 | M62403 | insulin-like growth factor binding protein 4 | insulin-like growth factor binding protein 4 |

Fig 21

| A | B | C | D | E |
|-----------------|------------------|----------|---|--|
| 1183 2062_at | IGFBP7 | L19182 | insulin-like growth factor binding protein 7 | |
| 1184 37991_at | ITM1 | L38961 | integral membrane protein 1 | integral membrane protein 1 |
| 1185 37326_at | A4 | U93305 | integral membrane protein; swiss-prot accession: O04901; may play role in cell differentiation in intestinal epithelium | LIM domain only 6 |
| 1186 41163_at | P24B | AL109672 | integral type I protein | p24B protein |
| 1187 32808_at | ITGB1; CD29; FN1 | X07979 | integrin beta 1 subunit precursor; Human mRNA for integrin beta 1 subunit. | integrin beta 1 isoform 1A precursor; integrin beta 1 isoform 1B precursor; integrin beta 1 isoform 1C-1 precursor; integrin beta 1 isoform 1C-2 precursor |
| 1188 1195_s_at | ICAP-1A | AF012024 | integrin cytoplasmic domain-associated protein 1 | integrin cytoplasmic domain associated protein |
| 1189 120_at | ITGA1 | X68742 | integrin, alpha 1 | |
| 1190 37484_at | ITGA1 | X68742 | integrin, alpha 1 | |
| 1191 36892_at | ITGA7 | AF032108 | integrin, alpha 7 | integrin alpha-7 |
| 1192 39071_at | ITGAV | M14648 | integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) | integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) |
| 1193 39754_at | ITGB5 | X53002 | integrin, beta 5 | |
| 1194 2058_s_at | ITGB5 | M35011 | integrin, beta 5 | integrin, beta 5 |
| 1195 40681_at | ITGBL1 | AB008375 | integrin, beta-like 1 (with EGF-like repeat domains) | osteoblast specific cysteine-rich protein |
| 1196 35365_at | ILK | U40282 | integrin-linked kinase | integrin-linked kinase |
| 1197 41743_i_at | OPTN; NRP; FIP2 | AF061034 | interacts with adenovirus E3-14.7KDa, a TNF-alpha cytolysis antagonist; leucine zipper protein; alternatively translated; long form; interacts with adenovirus E3-14.7KDa, a TNF-alpha cytolysis antagonist; leucine zipper protein; alternatively translated; short form; Homo sapiens FIP2 alternatively translated mRNA, complete cds. | FIP2 |

Fig 21

| A | B | C | D | E |
|-----------------|--------------------------|----------|--|--|
| | | | interacts with adenovirus E3-14.7KDa, a TNF-alpha cytolysis antagonist; leucine zipper protein; alternatively translated; long form; interacts with adenovirus E3-14.7KDa, a TNF-alpha cytolysis antagonist; leucine zipper protein; alternatively translated; sapiens FIP2 alternatively translated mRNA, complete cds. | FIP2 |
| 1198 41742_s_at | OPTN; NRP; FIP2 AF061034 | | interferon induced transmembrane protein 1 (9-27) | interferon induced transmembrane protein 1 (9-27) |
| 1199 676_g_at | IFITM1 | J04164 | interferon induced transmembrane protein 1 (9-27) | interferon induced transmembrane protein 1 (9-27) |
| 1200 675_at | IFITM1 | J04164 | interferon induced transmembrane protein 3 (1-8U) | interferon induced transmembrane protein 3 (1-8U) |
| 1201 41745_at | IFITM3 | X57352 | interferon, gamma-inducible protein 16 | interferon-gamma induced protein |
| 1202 1456_s_at | IFI16 | M63838 | interferon, gamma-inducible protein 30 | interferon, gamma-inducible protein 30 |
| 1203 925_at | IFI30 | J03909 | interferon, gamma-inducible protein 30 | interferon, gamma-inducible protein 30 |
| 1204 39728_at | IFI30 | J03909 | interferon-induced protein with tetra-tricopeptide repeats 1 | interferon-induced protein with tetra-tricopeptide repeats 1 |
| 1205 32814_at | IFIT1 | M24594 | interferon-related developmental regulator 1 | PC4 protein |
| 1206 37679_at | IFRD1 | Y10313 | interleukin 1 receptor, type I | interleukin 1 receptor, type I |
| 1207 1368_at | IL1R1 | M27492 | interleukin 10 receptor, beta | |
| 1208 33228_g_at | IL10RB | AI984234 | interleukin 10 receptor, beta | |
| 1209 33227_at | IL10RB | AI984234 | interleukin 27 | |
| 1210 38969_at | IL27 | AI828168 | interleukin 6 (interferon, beta 2) | interleukin 6 (interferon, beta 2) |
| 1211 38299_at | IL6 | X04430 | interleukin 8 | interleukin 8 |
| 1212 35372_r_at | IL8 | M17017 | interleukin enhancer binding factor 2, 45kD | NF45 protein |
| 1213 36189_at | ILF2 | U10323 | intermediate filament-like MGC:2625 | hypothetical protein |
| 1214 36030_at | DKFZP586I2223 | AL080214 | intersectin 1 (SH3 domain protein) | intersectin short form |
| 1215 35776_at | ITSN1 | AF064243 | intestinal cell kinase | KIAA0936 protein |
| 1216 41431_at | ICK | AB023153 | IQ motif containing GTPase activating protein 1 | ras GTPase-activating-like protein |
| 1217 1825_at | IQGAP1 | L33075 | | |

Fig 21

| A | B | C | D | E |
|-----------------|------------|----------|---|---|
| 1218 39023_at | IDH1 | AF020038 | isocitrate dehydrogenase 1 (NADP+), soluble | NADP-dependent isocitrate dehydrogenase |
| 1219 40112_at | IDH3B | AA522698 | isocitrate dehydrogenase 3 (NAD+) beta | |
| 1220 40111_g_at | IDH3B | U49283 | isocitrate dehydrogenase 3 (NAD+) beta | NAD+-specific isocitrate dehydrogenase beta precursor |
| 1221 40478_at | KIAA1162 | AL021396 | isoform 1 match: proteins: Tr:Q9UJA1 | hypothetical protein |
| 1222 32695_at | dJ196E23.1 | Z97632 | isoform 2 match: protein Q99991 | bombesin-like receptor 3 |
| 1223 40827_at | IARS | U04953 | isoleucine-tRNA synthetase | isoleucyl-tRNA synthetase |
| 1224 36985_at | IDI1 | X17025 | isopentenyl-diphosphate delta isomerase | isopentenyl-diphosphate delta isomerase |
| 1225 41775_at | ICMT | AF064084 | isoprenylcysteine carboxyl methyltransferase | prenylcysteine carboxyl methyltransferase |
| 1226 34877_at | JAK1 | AL039831 | Janus kinase 1 (a protein tyrosine kinase) | |
| 1227 34318_at | JM4 | AJ005896 | JM4 protein | JM4 protein |
| 1228 40957_at | JJAZ1 | D63881 | joined to JAZF1 | joined to JAZF1 |
| 1229 41250_at | JTV1 | U24169 | JTV1 gene | JTV-1 |
| 1230 41483_s_at | JUND | X56681 | jun D proto-oncogene | junD protein |
| 1231 1612_s_at | JUND | X56681 | jun D proto-oncogene | junD protein |
| 1232 40464_g_at | KPNB2 | U70322 | karyopherin (importin) beta 2 | transportin |
| 1233 39028_at | KPNB3 | Y08890 | karyopherin (importin) beta 3 | Ran_GTP binding protein 5 |
| 1234 35725_at | KPNA3 | D89618 | karyopherin alpha 3 (importin alpha 4) | karyopherin alph 3 |
| 1235 32487_s_at | KPNA4 | AB002533 | karyopherin alpha 4 (importin alpha 3) | Cip1 |
| 1236 32708_g_at | KATNA1 | A1191768 | katanin p60 (ATPase-containing) subunit A 1 | |
| 1237 37386_i_at | KDEL1 | X55885 | KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1 | KDEL receptor |
| 1238 39080_at | KDEL2 | M88458 | KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2 | KDEL receptor 2 |
| 1239 33402_at | KDEL3 | AL035081 | KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 | hypothetical protein |
| 1240 37150_at | AB026190 | AB026190 | kelch motif containing protein | kelch motif containing protein |
| 1241 32329_at | KRTHB6 | X99142 | keratin, hair, basic, 6 (monilethrix) | type II intermediate filament of hair keratin |
| 1242 39346_at | KHDRBS1 | M88108 | KH domain containing, RNA binding, signal transduction associated 1 | p62 |

Fig 21

| | A | B | C | D | E |
|------|------------|----------|--------|---|-----------------------|
| 1243 | 32679_at | KIAA0009 | D13634 | KIAA0009 gene product | KIAA0009 gene product |
| 1244 | 34760_at | KIAA0022 | D14664 | KIAA0022 gene product | KIAA0022 gene product |
| 1245 | 41129_at | KIAA0033 | D26067 | KIAA0033 protein | |
| 1246 | 38797_at | KIAA0062 | D31887 | KIAA0062 protein | |
| 1247 | 36978_at | KIAA0077 | D38521 | KIAA0077 protein | |
| 1248 | 37718_at | KIAA0096 | D43636 | KIAA0096 protein | |
| 1249 | 37293_at | KIAA0097 | D43948 | KIAA0097 gene product | KIAA0097 protein |
| | | | | KIAA0098 is a human counterpart of mouse chaperonin containing TCP-1 gene. Start codon is not identified. ha01413 cDNA clone for KIAA0098 has a 2-bp insertion between 736-737 of the sequence of KIAA0098.; Homo sapiens mRNA for KIAA0098 protein, partial cds. | |
| 1250 | 40417_at | KIAA0098 | D43950 | | KIAA0098 protein |
| 1251 | 39783_at | KIAA0100 | D43947 | KIAA0100 gene product | KIAA0100 protein |
| 1252 | 37359_at | KIAA0102 | D14658 | KIAA0102 gene product | KIAA0102 gene product |
| 1253 | 38031_at | KIAA0111 | D21853 | KIAA0111 gene product | KIAA0111 gene product |
| 1254 | 40279_at | KIAA0121 | D50911 | KIAA0121 gene product | KIAA0121 protein |
| 1255 | 36845_at | KIAA0136 | D50926 | KIAA0136 protein | |
| 1256 | 32099_at | KIAA0138 | D50928 | KIAA0138 gene product | KIAA0138 gene product |
| 1257 | 38472_at | KIAA0143 | D63477 | KIAA0143 protein | |
| 1258 | 41728_at | KIAA0152 | D63486 | KIAA0152 gene product | KIAA0152 gene product |
| 1259 | 37642_at | KIAA0157 | D63877 | KIAA0157 protein | KIAA0157 protein |
| 1260 | 32661_s_at | KIAA0170 | D79992 | KIAA0170 gene product | KIAA0170 gene product |
| 1261 | 37225_at | KIAA0172 | D79994 | KIAA0172 protein | |
| 1262 | 36942_at | KIAA0174 | D79996 | KIAA0174 gene product | KIAA0174 gene product |
| 1263 | 31863_at | KIAA0179 | D80001 | KIAA0179 protein | |
| 1264 | 37734_at | KIAA0184 | D80006 | KIAA0184 protein | |
| 1265 | 41669_at | KIAA0191 | D83776 | KIAA0191 protein | |
| 1266 | 36192_at | KIAA0193 | D83777 | KIAA0193 gene product | KIAA0193 gene product |
| 1267 | 38056_at | KIAA0195 | D83779 | KIAA0195 gene product | KIAA0195 gene product |
| 1268 | 38419_at | KIAA0196 | D83780 | KIAA0196 gene product | KIAA0196 gene product |
| 1269 | 38067_at | KIAA0202 | D86957 | KIAA0202 protein | |
| 1270 | 32586_at | KIAA0217 | D86971 | KIAA0217 protein | |
| 1271 | 38728_at | KIAA0225 | D86978 | KIAA0225 protein | |

Fig 21

| A | B | C | D | E |
|-----------------|----------|----------|-----------------------|-----------------------|
| 1272 40971_at | KIAA0229 | D86982 | KIAA0229 protein | |
| 1273 37748_at | KIAA0232 | D86985 | KIAA0232 gene product | KIAA0232 protein |
| 1274 38892_at | KIAA0240 | D87077 | KIAA0240 protein | |
| 1275 40765_at | KIAA0251 | D87438 | KIAA0251 protein | |
| 1276 41634_at | KIAA0256 | D87445 | KIAA0256 gene product | KIAA0256 protein |
| 1277 36971_at | KIAA0257 | D87446 | KIAA0257 protein | |
| 1278 32237_at | KIAA0265 | D87454 | KIAA0265 protein | |
| 1279 39405_at | KIAA0266 | D87455 | KIAA0266 gene product | KIAA0266 gene product |
| 1280 35039_at | KIAA0276 | D87466 | KIAA0276 protein | |
| 1281 38592_s_at | KIAA0284 | A1828210 | KIAA0284 protein | |
| 1282 41381_at | KIAA0308 | AB002306 | KIAA0308 protein | |
| 1283 37943_at | KIAA0321 | AB002319 | KIAA0321 protein | |
| 1284 32592_at | KIAA0323 | AB002321 | KIAA0323 protein | |
| 1285 39797_at | KIAA0349 | AB002347 | KIAA0349 protein | |
| 1286 34661_at | KIAA0350 | AB002348 | KIAA0350 protein | KIAA0350 protein |
| 1287 32208_at | KIAA0355 | AB002353 | KIAA0355 gene product | KIAA0355 gene product |
| 1288 32223_at | KIAA0365 | AB002363 | KIAA0365 gene product | |
| 1289 33442_at | KIAA0367 | AB002365 | KIAA0367 protein | |
| 1290 35830_at | KIAA0370 | AB002368 | KIAA0370 protein | |
| 1291 40517_at | KIAA0372 | AB002370 | KIAA0372 gene product | KIAA0372 gene product |
| 1292 34837_at | KIAA0376 | AB002374 | KIAA0376 protein | |
| 1293 41457_at | KIAA0423 | AB007883 | KIAA0423 protein | |
| 1294 35167_at | KIAA0433 | AB007893 | KIAA0433 protein | KIAA0433 protein |
| 1295 33340_at | KIAA0438 | AB007898 | KIAA0438 gene product | KIAA0438 gene product |
| 1296 40805_at | KIAA0440 | AB007900 | KIAA0440 protein | KIAA0440 protein |
| 1297 32091_at | KIAA0446 | AB007915 | KIAA0446 gene product | KIAA0446 protein |
| 1298 41243_at | KIAA0447 | AB007916 | KIAA0447 gene product | KIAA0447 protein |
| 1299 32206_at | KIAA0451 | AB007920 | KIAA0451 gene product | KIAA0451 protein |
| 1300 36069_at | SRGAP2 | AB007925 | KIAA0456 protein | KIAA0456 protein |
| 1301 37230_at | KIAA0469 | AB007938 | KIAA0469 gene product | KIAA0469 protein |
| 1302 33893_r_at | KIAA0470 | AB007939 | KIAA0470 gene product | KIAA0470 protein |
| 1303 34445_at | KIAA0471 | AB007940 | KIAA0471 gene product | KIAA0471 protein |
| 1304 35318_at | KIAA0475 | AB007944 | KIAA0475 gene product | KIAA0475 protein |
| 1305 35786_at | KIAA0476 | AB007945 | KIAA0476 gene product | KIAA0476 protein |
| 1306 35762_at | KIAA0483 | AB007952 | KIAA0483 protein | KIAA0483 protein |
| 1307 41830_at | KIAA0494 | AB007963 | KIAA0494 gene product | KIAA0494 protein |

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| | A | B | C | D | E |
|------|------------|----------|----------|-----------------------|----------------------|
| 1308 | 35534_at | KIAA0514 | AB011086 | KIAA0514 gene product | KIAA0514 protein |
| 1309 | 38724_at | KIAA0515 | AB011087 | KIAA0515 protein | KIAA0515 protein |
| 1310 | 34192_at | KIAA0532 | AB011104 | KIAA0532 protein | KIAA0532 protein |
| 1311 | 33787_at | KIAA0537 | AB011109 | KIAA0537 gene product | KIAA0537 protein |
| 1312 | 35184_at | KIAA0546 | AB011118 | KIAA0546 protein | KIAA0546 protein |
| 1313 | 31849_at | KIAA0564 | AB011136 | KIAA0564 protein | KIAA0564 protein |
| 1314 | 39434_at | KIAA0592 | AB011164 | KIAA0592 protein | KIAA0592 protein |
| 1315 | 41379_at | KIAA0594 | AB011166 | KIAA0594 protein | KIAA0594 protein |
| 1316 | 32866_at | KIAA0605 | AB011177 | KIAA0605 gene product | KIAA0605 protein |
| 1317 | 39852_at | KIAA0610 | AB011182 | KIAA0610 protein | KIAA0610 protein |
| 1318 | 40160_at | KIAA0618 | AL080109 | KIAA0618 gene product | hypothetical protein |
| 1319 | 40083_at | KIAA0625 | AB014525 | KIAA0625 protein | KIAA0625 protein |
| 1320 | 33241_at | KIAA0626 | AB014526 | KIAA0626 gene product | KIAA0626 protein |
| 1321 | 39376_at | KIAA0630 | AB014530 | KIAA0630 protein | KIAA0630 protein |
| 1322 | 34353_at | KIAA0648 | AB014548 | KIAA0648 protein | KIAA0648 protein |
| 1323 | 38082_at | KIAA0650 | AB014550 | KIAA0650 protein | KIAA0650 protein |
| 1324 | 39117_at | KIAA0662 | AB014562 | KIAA0662 gene product | KIAA0662 protein |
| 1325 | 41170_at | KIAA0663 | AB014563 | KIAA0663 gene product | KIAA0663 protein |
| 1326 | 31826_at | KIAA0674 | AB014574 | KIAA0674 protein | KIAA0674 protein |
| 1327 | 39403_at | KIAA0678 | AB014578 | KIAA0678 protein | KIAA0678 protein |
| 1328 | 39519_at | KIAA0692 | AB014592 | KIAA0692 protein | KIAA0692 protein |
| 1329 | 39380_at | KIAA0697 | AB014597 | KIAA0697 protein | KIAA0697 protein |
| 1330 | 39705_at | KIAA0700 | AB014600 | KIAA0700 protein | KIAA0700 protein |
| 1331 | 41620_at | KIAA0716 | AB018259 | KIAA0716 gene product | KIAA0716 protein |
| 1332 | 33835_at | KIAA0721 | AB018264 | KIAA0721 protein | KIAA0721 protein |
| 1333 | 35177_at | KIAA0725 | AB018268 | KIAA0725 protein | KIAA0725 protein |
| 1334 | 41218_at | KIAA0729 | AB018272 | KIAA0729 protein | KIAA0729 protein |
| 1335 | 38694_at | KIAA0738 | AB018281 | KIAA0738 gene product | KIAA0738 protein |
| 1336 | 39771_at | KIAA0740 | AB018283 | KIAA0740 gene product | KIAA0740 protein |
| 1337 | 41585_at | KIAA0746 | AB018289 | KIAA0746 protein | KIAA0746 protein |
| 1338 | 38424_at | KIAA0747 | AB018290 | KIAA0747 protein | KIAA0747 protein |
| 1339 | 40848_g_at | KIAA0750 | AB018293 | KIAA0750 gene product | KIAA0750 protein |
| 1340 | 32224_at | KIAA0769 | AB018312 | KIAA0769 gene product | KIAA0769 protein |
| 1341 | 36474_at | KIAA0776 | AB018319 | KIAA0776 protein | KIAA0776 protein |
| 1342 | 33251_at | KIAA0779 | AB018322 | KIAA0779 protein | KIAA0779 protein |
| 1343 | 35999_i_at | KIAA0781 | AB018324 | KIAA0781 protein | KIAA0781 protein |

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| | A | B | C | D | E |
|------|------------|------------|----------|------------------|-----------------------------|
| 1344 | 41224_at | KIAA0788 | AB018331 | KIAA0788 protein | KIAA0788 protein |
| 1345 | 34285_at | KIAA0795 | AB018338 | KIAA0795 protein | KIAA0795 protein |
| 1346 | 39614_at | KIAA0802 | AB018345 | KIAA0802 protein | KIAA0802 protein |
| 1347 | 36588_at | KIAA0810 | AB018353 | KIAA0810 protein | KIAA0810 protein |
| 1348 | 40492_at | KIAA0826 | AB020633 | KIAA0826 protein | KIAA0826 protein |
| 1349 | 40455_at | KIAA0830 | AB020637 | KIAA0830 protein | KIAA0830 protein |
| 1350 | 41372_at | KIAA0831 | AB020638 | KIAA0831 protein | KIAA0831 protein |
| 1351 | 36888_at | KIAA0841 | AB020648 | KIAA0841 protein | KIAA0841 protein |
| 1352 | 39597_at | KIAA0843 | AB020650 | KIAA0843 protein | KIAA0843 protein |
| 1353 | 41503_at | KIAA0854 | AB020661 | KIAA0854 protein | KIAA0854 protein |
| 1354 | 38730_at | KIAA0864 | AB020671 | KIAA0864 protein | KIAA0864 protein |
| 1355 | 39021_at | KIAA0877 | AB020684 | KIAA0877 protein | KIAA0877 protein |
| 1356 | 32215_i_at | KIAA0878 | AB020685 | KIAA0878 protein | KIAA0878 protein |
| 1357 | 38254_at | KIAA0882 | AB020689 | KIAA0882 protein | KIAA0882 protein |
| 1358 | 35720_at | KIAA0893 | AB020700 | KIAA0893 protein | KIAA0893 protein |
| 1359 | 40423_at | KIAA0903 | AB020710 | KIAA0903 protein | KIAA0903 protein |
| 1360 | 41421_at | KIAA0909 | AB020716 | KIAA0909 protein | KIAA0909 protein |
| 1361 | 41498_at | KIAA0911 | AB020718 | KIAA0911 protein | KIAA0911 protein |
| 1362 | 39777_at | KIAA0916 | AF075587 | KIAA0916 protein | protein associated with Myc |
| 1363 | 32735_at | KIAA0931 | AB023148 | KIAA0931 protein | KIAA0931 protein |
| 1364 | 33408_at | KIAA0934 | AB023151 | KIAA0934 protein | KIAA0934 protein |
| 1365 | 35369_at | KIAA0937 | AB023154 | KIAA0937 protein | KIAA0937 protein |
| 1366 | 33235_at | KIAA0938 | AB023155 | KIAA0938 protein | KIAA0938 protein |
| 1367 | 32740_at | Rab11-FIP2 | AB023158 | KIAA0941 protein | KIAA0941 protein |
| 1368 | 35794_at | KIAA0942 | AB023159 | KIAA0942 protein | KIAA0942 protein |
| 1369 | 41595_at | KIAA0947 | AB023164 | KIAA0947 protein | KIAA0947 protein |
| 1370 | 38649_at | KIAA0970 | AB023187 | KIAA0970 protein | KIAA0970 protein |
| 1371 | 34396_at | KIAA0978 | AB023195 | KIAA0978 protein | KIAA0978 protein |
| 1372 | 32085_at | KIAA0981 | AB023198 | KIAA0981 protein | KIAA0981 protein |
| 1373 | 35199_at | KIAA0982 | AB023199 | KIAA0982 protein | KIAA0982 protein |
| 1374 | 32769_at | KIAA0993 | AB023210 | KIAA0993 protein | KIAA0993 protein |
| 1375 | 34751_at | KIAA0997 | A1970189 | KIAA0997 protein | |
| 1376 | 34808_at | KIAA0999 | AB023216 | KIAA0999 protein | KIAA0999 protein |
| 1377 | 33193_at | KIAA1001 | AW052084 | KIAA1001 protein | |
| 1378 | 36002_at | KIAA1012 | AB023229 | KIAA1012 protein | KIAA1012 protein |
| 1379 | 35802_at | KIAA1014 | AB023231 | KIAA1014 protein | KIAA1014 protein |

Fig 21

| A | B | C | D | E |
|-----------------|----------|----------|---|---------------------------------|
| 1380 39615_at | KIAA1026 | AB028949 | KIAA1026 protein | KIAA1026 protein |
| 1381 34089_at | KIAA1030 | AB028953 | KIAA1030 protein | KIAA1030 protein |
| 1382 41651_at | KIAA1033 | AB028956 | KIAA1033 protein | KIAA1033 protein |
| 1383 41708_at | KIAA1034 | AB028957 | KIAA1034 protein | KIAA1034 protein |
| 1384 35163_at | KIAA1041 | AB028964 | KIAA1041 protein | KIAA1041 protein |
| 1385 38778_at | KIAA1046 | AB028969 | KIAA1046 protein | KIAA1046 protein |
| 1386 41268_g_at | KIAA1049 | AB028972 | KIAA1049 protein | KIAA1049 protein |
| 1387 40855_at | KIAA1053 | AB028976 | KIAA1053 protein | KIAA1053 protein |
| 1388 39400_at | KIAA1055 | AB028978 | KIAA1055 protein | KIAA1055 protein |
| 1389 33877_s_at | KIAA1067 | AB028990 | KIAA1067 protein | KIAA1067 protein |
| 1390 34688_at | KIAA1078 | AB029001 | KIAA1078 protein | KIAA1078 protein |
| 1391 33924_at | KIAA1091 | AB029014 | KIAA1091 protein | KIAA1091 protein |
| 1392 32508_at | KIAA1096 | AL096857 | KIAA1096 protein | hypothetical protein |
| 1393 41179_at | KIAA1100 | AB029023 | KIAA1100 protein | KIAA1100 protein |
| 1394 34839_at | KIAA1104 | AB029027 | KIAA1104 protein | KIAA1104 protein |
| 1395 33457_at | RAP140 | AB029028 | KIAA1105 protein | KIAA1105 protein |
| 1396 36814_at | KIAA1109 | AB029032 | KIAA1109 protein | KIAA1109 protein |
| 1397 34274_at | KIAA1116 | AB029039 | KIAA1116 protein | KIAA1116 protein |
| 1398 37617_at | KIAA1128 | U90912 | KIAA1128 protein | |
| 1399 33358_at | KIAA1157 | W29087 | KIAA1157 protein | |
| 1400 40308_at | KIAA1240 | AI830496 | KIAA1240 protein | |
| 1401 33811_at | KIAA1254 | AI761567 | KIAA1254 protein | |
| 1402 38674_at | KIAA1354 | AA115140 | KIAA1354 protein | |
| 1403 32730_at | KIAA1750 | AL080059 | KIAA1750 protein | |
| 1404 32171_at | KIAA1856 | AL080102 | KIAA1856 protein | hypothetical protein |
| 1405 39897_at | KIAA1966 | N36997 | KIAA1966 protein | |
| 1406 32846_s_at | KTN1 | D13629 | kinectin 1 (kinesin receptor) | kinectin 1 |
| 1407 39057_at | KNS2 | L04733 | kinesin 2 (60-70kD) | kinesin light chain |
| 1408 32079_at | KIF13B | AB014539 | kinesin family member 13B | KIAA0639 protein |
| 1409 33345_at | KIF3C | AF035621 | kinesin family member 3C | kinesin-related protein |
| 1410 34294_at | KIFC3 | AL041493 | kinesin family member C3 | |
| 1411 41474_at | KIF2 | Y08319 | kinesin heavy chain member 2 | kinesin-2 |
| 1412 40779_at | KIFAP3 | U59919 | kinesin-associated protein 3 | SMAP |
| 1413 34216_at | KLF7 | AA478904 | Kruppel-like factor 7 (ubiquitous) | |
| 1414 38768_at | HADHSC | X96752 | L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain | 3-hydroxyacyl-CoA dehydrogenase |

Gis 21

| A | B | C | D | E |
|-----------------|----------|----------|---|--|
| 1415 41485_at | LDHA | X02152 | lactate dehydrogenase A | lactate dehydrogenase A |
| 1416 288_s_at | LBR | L25931 | lamin B receptor | lamin B receptor |
| 1417 256_s_at | LAMR1 | M14199 | laminin receptor 1 (67kD, ribosomal protein SA) | laminin receptor 1 |
| 1418 37671_at | LAMA4 | S78569 | laminin, alpha 4 | laminin alpha 4 chain |
| 1419 581_at | LAMB1 | M61916 | laminin, beta 1 | laminin B1 |
| 1420 39441_at | LANCL1 | Y11395 | LanC lantibiotic synthetase component C-like 1 (bacterial) | lanthionine synthetase C-like protein 1 |
| 1421 1495_at | LTBP1 | M34057 | latent transforming growth factor beta binding protein 1 | latent transforming growth factor beta binding protein 1 precursor |
| 1422 37906_at | LTBP2 | Z37976 | latent transforming growth factor beta binding protein 2 | LTBP-2 precursor |
| 1423 33412_at | LGALS1 | A1535946 | lectin, galactoside-binding, soluble, 1 (galectin 1) | |
| 1424 35367_at | LGALS3 | AB006780 | lectin, galactoside-binding, soluble, 3 (galectin 3) | galectin-3 |
| 1425 37754_at | LGALS3BP | L13210 | lectin, galactoside-binding, soluble, 3 binding protein | Mac-2 binding protein |
| 1426 1846_at | LGALS8 | L78132 | lectin, galactoside-binding, soluble, 8 (galectin 8) | |
| 1427 34267_r_at | LEPR | U50748 | leptin receptor | prostate carcinoma tumor antigen |
| 1428 33830_at | HSOBRGRP | AW026535 | leptin receptor gene-related protein | leptin receptor |
| 1429 33829_at | HSOBRGRP | Y12670 | leptin receptor gene-related protein | leptin receptor gene-related protein |
| 1430 38985_at | LEPROTL1 | AF063805 | leptin receptor overlapping transcript-like 1 | brain myoD47 protein |
| 1431 41320_s_at | LRRFIP1 | U69609 | leucine rich repeat (in FLII) interacting protein 1 | transcription repressor |
| 1432 39967_at | LDOC1 | AB019527 | leucine zipper, down-regulated in cancer 1 | LDOC1 protein |
| 1433 41754_at | LRPPRC | M92439 | leucine-rich PPR-motif containing | leucine-rich PPR-motif containing protein |
| 1434 37470_at | LAIR1 | AF013249 | leukocyte-associated Ig-like receptor 1 | leukocyte-associated Ig-like receptor-1 |
| 1435 38081_at | LTA4H | J03459 | leukocyte-associated A4 hydrolase | leukotriene A4 hydrolase |
| 1436 36062_at | LPXN | AF062075 | leupaxin | leupaxin |
| 1437 35278_at | RPS29 | AI541542 | libtest16.A02.r bvrnorm Homo sapiens cDNA 5' mRNA sequence. | |
| 1438 39687_at | E46L | AI524873 | like mouse brain protein E46 | |

G321

| A | B | C | D | E |
|-----------------|-----------|----------|--|----------------------------------|
| 1439 39686_g_at | E46L | AL050282 | like mouse brain protein E46 | hypothetical protein |
| 1440 39685_at | E46L | AL050282 | like mouse brain protein E46 | hypothetical protein |
| 1441 39163_at | KIDINS220 | W27233 | likely homolog of rat kinase D-interacting substance of 220 kDa | |
| 1442 32669_at | SOC5 | AB014571 | likely ortholog of mouse suppressors of cytokine signalling 5 | KIAA0671 protein |
| 1443 40555_at | TC10 | AL043108 | likely ortholog of mouse TC10-alpha | |
| 1444 40844_at | TSBP | D63875 | likely ortholog of mouse TPR-containing, SH2-binding phosphoprotein | KIAA0155 gene product |
| 1445 41248_at | CSTF2T | AB014589 | likely ortholog of mouse variant polyadenylation protein CSTF-64 | KIAA0689 protein |
| 1446 35805_at | GRASP55 | AA447263 | likely ortholog of rat golgi stacking protein homolog GRASP55 | |
| 1447 39232_at | LIMS1 | U09284 | LIM and senescent cell antigen-like domains 1 | PINCH protein |
| 1448 36181_at | LASP1 | X82456 | LIM and SH3 protein 1 | LIM and SH3 domain protein |
| 1449 38617_at | LIMK2 | D45906 | LIM domain kinase 2 | LIMK-2 |
| 1450 1452_at | LMO4 | U24576 | LIM domain only 4 | breast tumor autoantigen |
| 1451 31936_s_at | LKAP | AB007890 | limkain b1 | KIAA0430 protein |
| 1452 38745_at | LIPA | X76488 | lipase A, lysosomal acid, cholesterol esterase (Wolman disease) | lysosomal acid lipase |
| 1453 38098_at | LPIN1 | D80010 | lipin 1 | |
| 1454 37542_at | LHFPL2 | D86961 | lipoma HMGIC fusion partner-like 2 | |
| 1455 41209_at | LPL | M15856 | lipoprotein lipase | lipoprotein lipase precursor |
| 1456 1798_at | LIV-1 | U41060 | LIV-1 protein, estrogen regulated liver form; Homo sapiens glycogen phosphorylase (PYGL) gene, exon 20 and complete cds. | estrogen regulated LIV-1 protein |
| 1457 37215_at | PYGL | AF046798 | | glycogen phosphorylase |

Fig 21

| A | B | C | D | E |
|-----------------|-----------|----------|--|--|
| 1458 40493_at | CD44 | L05424 | long tailed isoform; individual exons 6-14 are alternative exons any of which can be spliced out of the mRNA.; putative; long tailed isoform; putative; long tailed isoform; hemopoietic variant; putative; long tailed isoform; epithelial form; putative; Human cell surface glycoprotein CD44 (CD44) gene, 3' end of long tailed isoform. | cell surface glycoprotein CD44 |
| 1459 36194_at | LRPAP1 | M63959 | low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1) | alpha-2-macroglobulin receptor-associated protein |
| 1460 34400_at | QP-C | A1540957 | low molecular mass ubiquitinone-binding protein (9.5kD) | |
| 1461 37025_at | PIG7 | AL120815 | LPS-induced TNF-alpha factor | |
| 1462 39017_at | LSM1 | AJ238094 | Lsm1 protein | Lsm1 protein |
| 1463 38038_at | LUM | U21128 | lumican | lumican |
| 1464 38115_at | FUS1 | AF055479 | lung cancer candidate | lung cancer candidate FUS1 |
| 1465 39428_at | LNK | AF055581 | lymphocyte adaptor protein | adaptor protein Lnk |
| 1466 39396_at | LYPLA1 | AF081281 | lysophospholipase I | lysophospholipase |
| 1467 33788_at | LYSAL1 | AB002390 | lysosomal apyrase-like 1 | lysosomal apyrase-like 1 |
| 1468 39758_f_at | LAMP1 | J04182 | lysosomal-associated membrane protein 1 | lysosomal membrane glycoprotein-1 |
| 1469 38403_at | LAMP2 | X77196 | lysosomal-associated membrane protein 2 | lysosome-associated membrane protein-2 |
| 1470 38402_at | LAMP2 | U36336 | lysosomal-associated membrane protein 2 | lysosome-associated membrane protein-2b |
| 1471 39019_at | LAPTM4A | D14696 | lysosomal-associated membrane protein | lysosomal-associated protein |
| 1472 33127_at | LOXL2 | U89942 | transmembrane 4 alpha | transmembrane 4 alpha |
| 1473 34336_at | KARS | D32053 | lysyl oxidase-like 2 | lysyl oxidase-related protein |
| 1474 32832_at | MAEA | AF084928 | lysyl-tRNA synthetase | Lysyl tRNA Synthetase |
| | | | macrophage erythroblast attacher | erythroblast macrophage protein EMP |
| 1475 36174_at | MACMARCKS | X70326 | macrophage myristoylated alanine-rich C kinase substrate | macrophage myristoylated alanine-rich C kinase substrate |

Fig 21

| A | B | C | D | E |
|-----------------|----------|----------|---|--|
| 1476 1453_at | MADH2 | U68018 | MAD, mothers against decapentaplegic homolog 2 (Drosophila) | mad protein homolog |
| 1477 38944_at | MADH3 | U68019 | MAD, mothers against decapentaplegic homolog 3 (Drosophila) | mad protein homolog |
| 1478 1433_g_at | MADH3 | U68019 | MAD, mothers against decapentaplegic homolog 3 (Drosophila) | mad protein homolog |
| 1479 36953_at | MADH4 | U44378 | MAD, mothers against decapentaplegic homolog 4 (Drosophila) | Dpc4 |
| 1480 1013_at | MADH5 | U59913 | MAD, mothers against decapentaplegic homolog 5 (Drosophila) | Smad5 |
| 1481 1955_s_at | MADH6 | AF035528 | MAD, mothers against decapentaplegic homolog 6 (Drosophila) | Smad6 |
| 1482 1857_at | MADH7 | AF010193 | MAD, mothers against decapentaplegic homolog 7 (Drosophila) | MAD-related gene SMAD7 |
| 1483 41237_at | HLA-A | D32129 | major histocompatibility complex, class I, A | HLA-A26 |
| 1484 41609_at | HLA-DMB | U15085 | major histocompatibility complex, class II, DM beta | HLA-DMB |
| 1485 38096_f_at | HLA-DPB1 | M83664 | major histocompatibility complex, class II, DP beta 1 | HLA-DPB1 |
| 1486 38095_i_at | HLA-DPB1 | M83664 | major histocompatibility complex, class II, DP beta 1 | HLA-DPB1 |
| 1487 37039_at | HLA-DRA | J00194 | major histocompatibility complex, class II, DR alpha | major histocompatibility complex, class II, DR alpha precursor |
| 1488 33261_at | HLA-DRB1 | M16941 | major histocompatibility complex, class II, DR beta 1 | |
| 1489 34425_at | HLALS | AF031469 | major histocompatibility complex, class I-like sequence | MHC class I-related protein 1 isoform D |
| 1490 34003_at | CD4 | U47924 | major receptor for HIV-1; member of immunoglobulin supergene family; T cell surface glycoprotein T4 | protein 'A', isoform 1 |
| 1491 36608_at | MDH1 | D55654 | malate dehydrogenase 1, NAD (soluble) | cytosolic malate dehydrogenase |
| 1492 837_s_at | ME1 | U43944 | malic enzyme 1, NADP(+)-dependent, cytosolic | cytosolic NADP(+)-dependent malic enzyme |

G.S. 21

| A | B | C | D | E |
|---------------|---------------|----------|---|---|
| 1493 36599_at | ME2 | M55905 | malic enzyme 2, NAD(+)-dependent, mitochondrial | mitochondrial NAD(P)+ -dependent malic enzyme |
| 1494 36673_at | MPI | X76057 | mannose phosphate isomerase | phosphomannose isomerase |
| 1495 35299_at | MKNK1 | AB000409 | MAP kinase-interacting serine/threonine kinase 1 | MNK1 |
| 1496 40826_at | MARK3 | M80359 | MAP/microtubule affinity-regulating kinase 3 | protein p78 |
| 1497 41506_at | MAPKAPK5; PRA | AF032437 | MAPK-activated protein kinase; PRK; Homo sapiens mitogen activated protein kinase activated protein kinase gene, complete cds. | mitogen activated protein kinase activated protein kinase |
| 1498 37009_at | CAT | AL035079 | match proteins: Sw:P04040 Sw:P04762 Sw:P24270 Tr:O62839 Sw:P00432 Sw:P17336 Tr:P90682 Tr:Q27487 Sw:O61235 Tr:O18193 Tr:O77229 Tr:Q49133 Sw:P26901 Sw:P55306 Sw:P30263 Tr:P95631 Sw:P44390 Tr:Q27710 Sw:Q96528 Sw:O13289 Sw:P07820 Sw:P30265 Sw:P77872 Tr:Q59602 Tr:P77924 Sw:Q59170 Sw:P15202 Tr:Q59296 Tr:O33613 Sw:Q92405 Sw:Q59635 Sw:P81138 match ESTs: W94164 N28621 match to ESTs AA316181 (NID:g3165221), AA032221 (NID:g1502183), and AI167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7q21, complete sequence. | dJ53C18.1 (Catalase) |
| 1499 40297_at | WUGSC:H_RG04 | AC005053 | | six transmembrane epithelial antigen of the prostate |

C's 21

| A | B | C | D | E |
|-----------------|-------------|----------|--|---|
| 1500 34860_g_at | BCG1 | Z98046 | match: cDNAs X67055 X14690 D89287 X70393 S82800 X16260 M18192 Y11283 D38535 D38595 match: proteins Q06033 P97280 O54882 O35802 Q61704 Q14624 P79263 Q63416 O42141 P19823 O02668 Q61703 P97279 Q29052 match: cDNAs: Em:AL050345 match: ESTs: Em:AA304885 Em:AA447346 Em:AA314213 Em:AA209368 Em:AA209372 Em:T84723 Em:H23039 Em:AA542125 Em:W41686 Em:AA384854 Em:AA492678 | hepatocellular carcinoma associated protein; breast cancer associated gene 1 |
| 1501 35336_at | HS508115A | AL021707 | match: protein O15214 | chromosome 22 open reading frame 2 |
| 1502 32658_at | dJ1033B10.1 | AL031228 | match: protein O15214 | BING4 |
| 1503 31545_at | dJ1033B10.1 | AL031228 | match: protein SPTREMBL; Q14241 | BING4 |
| 1504 36986_at | dJ886K2.1 | AL031295 | match: proteins CE02000 O59733 CE01999; supported by FGENES and GENSCAN | UDP-galactose-4-epimerase |
| 1505 38072_at | dJ465N24.1 | AL031432 | match: proteins O15037 CE16881 supported by GENSCAN possibly this partial gene and dJ281H8.1 are part of one gene | hypothetical protein dJ465N24.2.1 |
| 1506 32478_f_at | dJ281H8.1 | AL031133 | | dJ281H8.2 (PUTATIVE novel protein similar to KIAA0323 and worm C30F12.1) |

Fig 21

| A | B | C | D | E |
|---------------|-----------|----------|--|--|
| 1507 39759_at | dJ51J12.1 | AL031781 | <p>match: proteins O42476 Q94539; match: protein O88972; match: cDNA AF091047; owing to a different in-frame ORF, the translation of the last coding exon (8 C-terminal amino-acids) differs from that in mouse and is terminated more upstream; match: protein Q61110; Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.</p> | dJ51J12.1 (human ortholog of zebrafish Quaking protein homolog ZKQ-1 (isoform 1)); dJ51J12.1.2 (human ortholog of mouse KH Domain RNA Binding protein QKI-7B (isoform 2)); dJ51J12.1.3 (human ortholog of mouse KH Domain RNA Binding protein QKI-7 (isoform 3)) |
| 1508 39760_at | dJ51J12.1 | AL031781 | <p>match: proteins O42476 Q94539; match: protein O88972; match: cDNA AF091047; owing to a different in-frame ORF, the translation of the last coding exon (8 C-terminal amino-acids) differs from that in mouse and is terminated more upstream; match: protein Q61110; Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.</p> | dJ51J12.1 (human ortholog of zebrafish Quaking protein homolog ZKQ-1 (isoform 1)); dJ51J12.1.2 (human ortholog of mouse KH Domain RNA Binding protein QKI-7B (isoform 2)); dJ51J12.1.3 (human ortholog of mouse KH Domain RNA Binding protein QKI-7 (isoform 3)) |
| 1509 32573_at | COX6A | AL021546 | <p>match: proteins P13182 P12074 P10818 P43024 Q02221 P07471 P10817 P43023 P13182 O13085 O13082</p> | cytochrome c oxidase subunit VIa polypeptide 1 |

63 21

| A | B | C | D | E |
|---------------|------------|----------|---|---|
| 1510 33443_at | HSF2 | Z99129 | match: proteins P38533 Q03933 P38530 P41154 Q00613 P38529 P38531 Q63717 P38532 Q99472 | heat shock transcription factor 2 |
| 1511 36133_at | dJ512B11.1 | AL031058 | match: proteins Q14189 P15924 Q03001 P97395 P97396 P97394; Human DNA sequence from clone 512B11 on chromosome 6p24-25. Contains the Desmoplakin I (DPI) gene, ESTs, STSs and GSSs, complete sequence. | dJ512B11.1 (Desmoplakin I (DPI)) |
| 1512 37043_at | E2F-2 | AL021154 | match: proteins Q14209 Q16254 Q35261 O00716 Q61501 Q90977 Q01094 Q27368 | E2F transcription factor 2 |
| 1513 41227_at | OCRL1 | AL022162 | match: proteins Q15774; match: protein Q01968 P32019; Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence. | dJ454M7.1.2 (Lowe Oculocerebrorenal Syndrome protein OCRL-1) (isoform 2); dJ454M7.1.1 (Lowe Oculocerebrorenal Syndrome protein OCRL-1) (isoform 1) |
| 1514 38990_at | dJ341E18.1 | AL031178 | match: proteins Q62726 P20793 Q04859 Q39423 P43294 O49669 | dJ341E18.1 (Serine/Threonine Protein Kinase (presumptive isolog of Rat protein Q62726)) |

F's 21

| A | B | C | D | E |
|-----------------|-------------|----------|---|--|
| 1515 34782_at | JUMONJI | AL021938 | match: proteins Q92833 Q62315; protein Q92833 has a different stop codon 19 aa further downstream because it jumps frame twice, circumventing the stopcodon in this entry. This could be due to a sequence error in the cDNA sequence; Homo sapiens DNA sequence from PAC 232K4 on chromosome 6p22.3. Contains the JUMONJI gene for a hypothetical 141.7 kD protein. Contains ESTs, STSs, a CA repeat polymorphism and genomic marker D6S260', complete sequence. | dJ232K4.1 (hypothetical 141.7 kD protein JUMONJI) |
| 1516 37350_at | dJ889N15.1 | AL031177 | match: proteins Q99795 Q91665 Q91664 O09052 P78310 P97792 Q91667 O60939 P54900 Q62861 Q61148 O00426 P06907 P25189 Q92677 P20938 P27573 P10522 P37301 match: patented sequence 180040 supported by GENSCAN and FGENSES | dJ889N15.1 (novel protein similar to X. laevis Cortical Thymocyte Marker CTX) |
| 1517 39738_at | APOL2 | Z82215 | match: proteins: Sw:Q14791 | apolipoprotein L |
| 1518 31824_at | ME1 | AL049699 | match: proteins: Sw:P06801 Sw:P28227 Sw:Q29558 Sw:P13697 Sw:P40927 Sw:Q16798 Tr:Q16797 Sw:P48163 | dJ747H23.1 (malic enzyme 1, soluble (NADP-dependent malic enzyme, malate oxidoreductase, EC 1.1.1.40)) |
| 1519 32766_at | OTK27 SSFA1 | Z83840 | match: proteins: Sw:P12956 | non-histone chromosome protein 2 (S. cerevisiae)-like 1 |
| 1520 39756_g_at | XBP1 | Z93930 | match: proteins: Sw:P17861 Tr:Q35426; Human DNA sequence from clone CTA-292E10 on chromosome 22q11-12 Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island, complete sequence. | bK292E10.1 (X-box binding protein 1 (TREB5)) |

Fig 21

| A | B | C | D | E |
|---------------|------------|----------|--|--|
| 1521 39755_at | XBP1 | Z93930 | <p>match: proteins: Sw:P17861 Tr:O35426; Human DNA sequence from clone CTA-292E10 on chromosome 22q11-12 Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island, complete sequence.</p> <p>match: proteins: Sw:P26038 Tr:O35763 Sw:P26041 Sw:P26042 Sw:P26044 Sw:P35241 Sw:P26043 Sw:P15311 Sw:P31976 Sw:P26040 Tr:Q26520 Tr:Q24788 Tr:Q24796 Tr:Q94815; Human DNA sequence from clone 376D21 on chromosome Xq11.1-12 Contains the MSN gene for Moesin (Membrane-organizing Extension Spike protein), ESTs, STSs, GSSs, genomic marker DXS8029 and a putative CpG island, complete sequence.</p> | bK292E10.1 (X-box binding protein 1 (TREB5)) |
| 1522 40771_at | MSN | Z98946 | | dJ376D21.1 (Moesin (Membrane-organizing Extension Spike protein)) |
| 1523 31722_at | RPL3 | AL022326 | <p>match: proteins: Sw:P39023 Sw:O16797 Sw:P21531 Sw:P39872 Sw:P27659 Sw:Q92901 Sw:P49149 Sw:P22738 Sw:P35684 Sw:P17094 Wp:CE05598</p> <p>match: proteins: Sw:P50550 Sw:O09181 Tr:O62622 Sw:P40984 Sw:P50623 Tr:Q42551 Tr:O24240 Tr:Q42973 Sw:P52478 Sw:Q02159 Sw:P15732 Sw:O00102 Tr:O76542 Sw:P27949 Sw:P49427 Tr:O17424 Sw:P25867 Sw:P52490</p> | ribosomal protein L3 |
| 1524 33136_at | UBE21 | AL031714 | | C358B7.1 (ubiquitin-conjugating enzyme E2) (homologous to yeast UBC9)) |
| 1525 36607_at | bK250D10.3 | Z99716 | <p>match: proteins: Sw:Q12772 Sw:Q60429 Sw:P36956 Sw:Q60416 Tr:O15352</p> | septin 3 |
| 1526 38399_at | SNRPB2 | AL034428 | <p>match: proteins: Sw:Q28038 Sw:Q16674 Tr:P97591 Sw:Q61865</p> | small nuclear ribonucleoprotein polypeptide B" |

Fig 21

| A | B | C | D | E |
|---------------|---------------|----------|--|--|
| 1527 36711_at | | | match: proteins: Tr:O54791 Sw:Q90595 Sw:Q61827 Sw:Q90596 Tr:O54790 Tr:O15525 Sw:Q90889 Tr:O73679 Tr:O75444 Sw:P54844 Sw:P54843 Sw:Q00056 Sw:Q10060 Sw:Q15427 | chromosome 22 open reading frame 5 |
| 1528 39561_at | HS506A DKFZP5 | AL021977 | match: proteins: Tr:O54793 Tr:O44229 match: proteins: Tr:O75354 Tr:O75356 Tr:Q9QYC8 Tr:Q9WUZ9 Tr:O70214 Tr:Q9QYC9 | chromobox homolog 6 |
| 1529 39876_at | DNAL4 | AL008583 | | dJ738P15.2 (CD39-like 2 (a nucleoside phosphatase)) |
| 1530 37189_at | dJ738P15.1 | AL035252 | match: proteins: Tr:O94136 Sw:Q99798 Sw:P49609 Sw:P20004 Sw:P16276 Tr:O75809 Tr:O74699 Wp:CE00516 Sw:P19414 Tr:O75944 Sw:O13966 | dJ347H13.1 (aconitase 2, mitochondrial (Aconitate Hydratase, EC 4.2.1.3, Citrate Hydrolase)) |
| 1531 41235_at | ACO2 | AL023553 | match: proteins: Tr:P70386 Sw:Q02527 Sw:Q10470 Sw:Q09327 | activating transcription factor 4 |
| 1532 36550_at | TAXREB67 TXRE | AL022312 | match: proteins: Tr:Q00425 Sw:Q13671 Tr:O15010 Tr:P97680 | dJ117516.1 (Ras inhibitor JC265 (Ras association (RalGDS/AF-6) domain containing protein)) |
| 1533 39368_at | dJ117516.1 | AL049538 | match: proteins: Tr:Q14621 Tr:Q64012 Sw:P07910 Sw:P19600 Tr:O60812 Sw:Q14011 Sw:P26686 | RNA-binding protein (autoantigenic) long isoform |
| 1534 33821_at | P542 | AL031668 | match: proteins: Tr:Q9Y3M0 Tr:Q9WU14 Sw:P39540 Tr:Q9Y396 | dJ483K16.1.1 (novel protein (isoform 1)) |
| 1535 39029_at | dJ483K16.1 | AL034374 | maternal G10 transcript | maternal G10 transcript |
| 1536 35145_at | G10 | U11861 | MAX binding protein | ROX protein |
| 1537 39072_at | MNT | X96401 | MAX interacting protein 1 | MAX interacting protein 1, isoform a; MAX interacting protein 1, isoform b |
| 1538 654_at | MX11 | L07648 | MAX interacting protein 1 | MAX interacting protein 1, isoform a; MAX interacting protein 1, isoform b |
| 1539 35312_at | MX11 | L07648 | MAX interacting protein 1 | MAX interacting protein 1, isoform a; MAX interacting protein 1, isoform b |
| 1540 40469_at | MCM2 | D21063 | MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisiae) | |
| | | | MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) associated protein | |
| | MCM3AP | AB011144 | | KIAA0572 protein |

Cs 21

| A | B | C | D | E |
|-----------------|---------|----------|--|---|
| 1541 40117_at | MCM6 | D84557 | MCM6 minichromosome maintenance deficient 6 (MIS5 homolog, <i>S. pombe</i>) (<i>S. cerevisiae</i>) | HsMcm6 |
| 1542 41388_at | MEIS2 | AF017418 | Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) | homeobox protein MEIS2 |
| 1543 37486_f_at | MEIS3 | U68385 | Meis1, myeloid ecotropic viral integration site 1 homolog 3 (mouse) | Meis1-related protein 2 |
| 1544 35340_at | MEL | AI819948 | mel transforming oncogene (derived from cell line NK14)- RAB8 homolog | |
| 1545 36500_at | MAGEA2A | AF027974 | melanoma antigen, family A, 2, copy a; similar to GenBank Accession Number L18920 | melanoma antigen family A2a |
| 1546 41139_at | MAGED1 | W26633 | melanoma antigen, family D, 1 | |
| 1547 39327_at | D2S448 | D86983 | Melanoma associated gene | |
| 1548 38441_s_at | MCP | X59408 | membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen) | membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen) |
| 1549 39471_at | M11S1 | Z48042 | membrane component, chromosome 11, surface marker 1 | GPI-anchored protein p137 |
| 1550 33444_at | M17S2 | D30756 | membrane component, chromosome 17, surface marker 2 (ovarian carcinoma antigen CA125) | membrane component, chromosome 17, surface marker 2 |
| 1551 1389_at | MME | J03779 | membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) | membrane metallo-endopeptidase |
| 1552 40399_r_at | MEOX2 | AI743406 | mesenchyme homeo box 2 (growth arrest-specific homeo box) | |
| 1553 37697_s_at | por | L08666 | Met at bp 326 also used as initiation codon in vitro; Met at bp 248 also used as initiation codon in vitro; Homo sapiens porin (por) mRNA, complete cds and truncated cds. | porin |
| 1554 40244_s_at | MPPE1 | AI743654 | metallo phosphoesterase | |

Fig 21

| A | B | C | D | E |
|-----------------|--------|----------|--|--|
| 1555 31975_at | | X55503 | metallothionein (MT)-like gene; H.sapiens pseudogene for metallothionein and AG/CT repetitive element. | metallothionein |
| 1556 39081_at | MT2A | AI547258 | metallothionein 2A | |
| 1557 38945_at | MTF1 | X78710 | metal-regulatory transcription factor 1 | metal-regulatory transcription factor |
| 1558 1643_g_at | MTA1 | U35113 | metastasis associated 1 | metastasis associated protein |
| 1559 35642_at | MTX2 | AF053551 | metaxin 2 | metaxin 2 |
| 1560 39342_at | MARS | X94754 | methionine-tRNA synthetase | yeast methionyl-tRNA synthetase homolog |
| 1561 37619_at | METAP1 | D42084 | methionyl aminopeptidase 1 | |
| 1562 41828_at | MBD1 | Y10746 | methyl-CpG binding domain protein 1 | methyl-CpG binding protein |
| 1563 33905_at | MBD2 | AF072242 | methyl-CpG binding domain protein 2 | methyl-CpG binding protein MBD2 |
| 1564 34386_at | MBD4 | AF072250 | methyl-CpG binding domain protein 4 | methyl-CpG binding protein MBD4 |
| 1565 40074_at | MTHFD2 | X16396 | methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase | methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase, precursor |
| 1566 674_g_at | MTHFD1 | J04031 | methylene tetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase | methylene tetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase |
| 1567 40105_at | MUT | M65131 | methylmalonyl Coenzyme A mutase | methylmalonyl-CoA mutase |
| 1568 35937_at | MICB | U65416 | MHC class I chain-related gene B; cDNA sequence deposited under GenBank Accession Number X91625; Human MHC class I molecule (MICB) gene, complete cds. | MHC class I molecule |
| 1569 36535_at | MFAP1 | U04209 | microfibrillar-associated protein 1 | associated microfibrillar protein |
| 1570 38228_g_at | MITF | AB006909 | microphthalmia-associated transcription factor | A-type microphthalmia associated transcription factor |
| 1571 820_at | MGST2 | U77604 | microsomal glutathione S-transferase 2 | microsomal glutathione S-transferase 2 |
| 1572 38704_at | MACF1 | AB007934 | microtubule-actin crosslinking factor 1 | KIAA0465 protein |
| 1573 35917_at | MAP1A | W26631 | microtubule-associated protein 1A | |
| 1574 33850_at | MAP4 | W26892 | microtubule-associated protein 4 | |

6's 21

| | A | B | C | D | E |
|------|------------|-------------|----------|--|---|
| 1575 | 33456_at | MAPRE1 | U24166 | microtubule-associated protein, RP/EB family, member 1 | EB1 |
| 1576 | 39370_at | MAP1A/1BLC3 | W28807 | microtubule-associated proteins 1A/1B light chain 3 | |
| 1577 | 34296_at | MID1 | AFO41210 | midline 1 (Opitz/BBB syndrome) | midline 1 fetal kidney isoform 3 |
| 1578 | 34403_at | MFGES | U58516 | milk fat globule-EGF factor 8 protein | BA46 |
| 1579 | 40027_at | ATPW | W52999 | mitochondrial ATP synthase regulatory component factor B | |
| 1580 | 37174_at | MRPL19 | D14660 | mitochondrial ribosomal protein L19 | mitochondrial ribosomal protein L19 |
| 1581 | 37726_at | MRPL3 | X06323 | mitochondrial ribosomal protein L3 | mitochondrial ribosomal protein L3 |
| 1582 | 39717_g_at | MRPL33 | AI597616 | mitochondrial ribosomal protein L33 | |
| 1583 | 32221_at | MRPS18B | AL050361 | mitochondrial ribosomal protein S18B | mitochondrial ribosomal protein S18B |
| 1584 | 38899_s_at | MFN1 | U95822 | mitofusin 1 | putative transmembrane GTPase |
| 1585 | 34369_at | MFN2 | D86987 | mitofusin 2 | KIAA0214 protein |
| 1586 | 36577_at | MIG2 | Z24725 | mitogen-inducible 2 | mitogen-inducible gene mig-2 |
| 1587 | 37733_at | MAPK14 | L35263 | mitogen-activated protein kinase 14 | CSAids binding protein |
| 1588 | 36926_at | MAPK6 | X80692 | mitogen-activated protein kinase 6 | p97mapk |
| 1589 | 38431_at | MAPK9 | U09759 | mitogen-activated protein kinase 9 | protein kinase |
| 1590 | 1238_at | MAPK9 | U09759 | mitogen-activated protein kinase 9 | protein kinase |
| 1591 | 1130_at | MAP2K1 | L11284 | mitogen-activated protein kinase kinase 1 | mitogen-activated protein kinase kinase 1 |
| 1592 | 1327_s_at | MAP3K5 | U67156 | mitogen-activated protein kinase kinase kinase 5 | mitogen-activated kinase kinase kinase 5 |
| 1593 | 36905_at | MAP3K7 | AB009356 | mitogen-activated protein kinase kinase kinase 7 | TGF-beta activated kinase 1a |
| 1594 | 38980_at | MAP3K7IP2 | AB018276 | mitogen-activated protein kinase kinase kinase 7 interacting protein 2 | KIAA0733 protein |
| 1595 | 35694_at | MAP4K4 | AB014587 | mitogen-activated protein kinase kinase kinase 4 | KIAA0687 protein |
| 1596 | 36179_at | MAPKAPK2 | U12779 | mitogen-activated protein kinase-activated protein kinase 2 | MAP kinase activated protein kinase 2 |
| 1597 | 1637_at | MAPKAPK3 | U09578 | mitogen-activated protein kinase-activated protein kinase 3 | MAPKAP kinase |
| 1598 | 41220_at | MSF | AB023208 | MLL septin-like fusion | KIAA0991 protein |
| 1599 | 38437_at | MLN51 | X80199 | MLN51 protein | MLN51 protein |

GIS 21

| | A | B | C | D | E |
|------|------------|-----------|----------|--|--|
| 1600 | 35273_at | MMS19L | AF007151 | MMS19-like (MET18 homolog, <i>S. cerevisiae</i>) | MMS19 (MET18 <i>S. cerevisiae</i>)-like |
| 1601 | 34767_at | MAP-1 | A1670788 | modulator of apoptosis 1 | |
| 1602 | 41771_g_at | MAOA | AA420624 | monoamine oxidase A | |
| 1603 | 41772_at | MAOA | M68840 | monoamine oxidase A | monoamine oxidase A |
| 1604 | 41770_at | MAOA | AA420624 | monoamine oxidase A | |
| 1605 | 37628_at | MAOB | M69177 | monoamine oxidase B | monoamine oxidase B |
| 1606 | 37565_at | MMD | X85750 | monocyte to macrophage differentiation-associated | monocyte to macrophage differentiation-associated, precursor |
| 1607 | 40861_at | MRGX | D14812 | MORF-related gene X | MORF-related gene X |
| 1608 | 33797_at | MPHOSPH10 | X98494 | M-phase phosphoprotein 10 (U3 small nuclear ribonucleoprotein) | M phase phosphoprotein 10 |
| 1609 | 34306_at | MBNL | AB007888 | muscleblind-like (Drosophila) | muscleblind (Drosophila)-like |
| 1610 | 35992_at | MSC | AF087036 | musculin (activated B-cell factor-1) | musculin |
| 1611 | 31884_at | MLH3 | L40399 | mutL homolog 3 (E. coli) | mutL homolog 3 |
| 1612 | 860_at | MSH2 | U03911 | mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli) | mutS homolog 2 |
| 1613 | 2003_s_at | MSH6 | U28946 | mutS homolog 6 (E. coli) | G/T mismatch binding protein |
| 1614 | 33769_at | MPZL1 | AF087020 | myelin protein zero-like 1 | protein zero related protein |
| 1615 | 33146_at | MCL1 | L08246 | myeloid cell leukemia sequence 1 (BCL2-related) | myeloid cell leukemia sequence 1 (BCL2-related) |
| 1616 | 277_at | MCL1 | L08246 | myeloid cell leukemia sequence 1 (BCL2-related) | myeloid cell leukemia sequence 1 (BCL2-related) |
| 1617 | 39037_at | MLLT2 | L13773 | myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2 | myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2 |
| 1618 | 41637_at | MYLE | AF108145 | MYLE protein | DEXI |
| 1619 | 41439_at | MYO1B | AJ001381 | myosin IB | myh-1c |
| 1620 | 35729_at | MYO1D | AB018270 | myosin ID | KIAA0727 protein |
| 1621 | 37631_at | MYO1E | U14391 | myosin IE | myosin-IC |
| 1622 | 38251_at | MLC1SA | AI127424 | myosin light chain 1 slow a | myosin regulatory light chain |
| 1623 | 41187_at | MLC-B | U26162 | myosin regulatory light chain | myosin regulatory light chain |
| 1624 | 35362_at | MYO10 | AB018342 | myosin X | KIAA0799 protein |
| 1625 | 33447_at | MLCB | X54304 | myosin, light polypeptide, regulatory, non-sarcomeric (20kD) | myosin, light polypeptide, regulatory, non-sarcomeric (20kD) |
| 1626 | 35739_at | MTMR3 | AB002369 | myotubularin related protein 3 | myotubularin related protein 3 |

Fig 21

| | A | B | C | D | E |
|------|------------|--------|----------|---|---|
| 1627 | 39707_at | MTMR4 | AB014547 | myotubularin related protein 4 | KIAA0647 protein |
| 1628 | 38035_at | MTMR6 | AF072928 | myotubularin related protein 6 | myotubularin related protein 6 |
| 1629 | 39607_at | MTMR8 | AL080178 | myotubularin related protein 8 | hypothetical protein |
| 1630 | 36692_at | MTMR8 | AF052099 | myotubularin related protein 8 | |
| 1631 | 32434_at | MARCKS | D10522 | myristoylated alanine-rich protein kinase C substrate | 80K-L protein |
| 1632 | 39267_at | AGM1 | AF102265 | N-acetylglucosamine-phosphate mutase | N-acetylglucosamine-phosphate mutase |
| 1633 | 36938_at | ASAH | U70063 | N-acylsphingosine amidohydrolase (acid ceramidase) | acid ceramidase |
| 1634 | 461_at | ASAH | U70063 | N-acylsphingosine amidohydrolase (acid ceramidase) | acid ceramidase |
| 1635 | 36169_at | NDUFA1 | N47307 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 (7.5kD, MWFE) | |
| 1636 | 40546_s_at | NDUFA2 | AF047185 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8) | NADH-ubiquinone oxidoreductase subunit C1B8 |
| 1637 | 38462_at | NDUFA5 | U64028 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (13kD, B13) | NADPH:ubiquinone oxidoreductase subunit B13 |
| 1638 | 32752_at | NDUFA7 | W72440 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (14.5kD, B14.5a) | |
| 1639 | 38605_at | NDUFB1 | AI345944 | NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1 (7kD, MNLL) | |
| 1640 | 38981_at | NDUFB3 | AA203354 | NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3 (12kD, B12) | |
| 1641 | 32232_at | NDUFB5 | AF047181 | NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (16kD, SGDh) | NADH-ubiquinone oxidoreductase subunit C1SGDH |
| 1642 | 32774_at | NDUFB8 | AI541050 | NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1) | |
| 1643 | 38485_at | NDUFC1 | AA760866 | NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1 (6kD, KFYI) | |
| 1644 | 38395_at | NDUFS1 | X61100 | NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) | 75 kDa subunit NADH dehydrogenase precursor |
| 1645 | 38695_at | NDUFS4 | AA203303 | NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase) | |

Fig 21

| | A | B | C | D | E |
|------|------------|---------------|----------|--|---|
| 1646 | 38060_at | NDUFS5 | AI541336 | NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase) | |
| 1647 | 34893_at | NDUFV2 | AI557064 | NADH dehydrogenase (ubiquinone) flavoprotein 2 (24kD) | |
| 1648 | 34519_at | NPR3 | M59305 | natriuretic peptide receptor C/guanylate cyclase C (atrial natriuretic peptide receptor C) | atrial natriuretic peptide clearance receptor |
| 1649 | 34234_f_at | NKTR | AI688640 | natural killer-tumor recognition sequence | |
| 1650 | 41795_at | NCK1 | X17576 | NCK adaptor protein 1 | NCK adaptor protein 1 |
| 1651 | 33357_at | NCKAP1 | AB011159 | NCK-associated protein 1 | KIAA0587 protein |
| 1652 | 36073_at | NDN | U35139 | nectin homolog (mouse) | NECDIN related protein |
| 1653 | 34202_at | DKFZP566B0846 | AL050071 | nectin 3 | hypothetical protein |
| 1654 | 34264_at | NESCA | AB026894 | nesca protein | NESCA |
| 1655 | 38719_at | NSF | U03985 | N-ethylmaleimide-sensitive factor | N-ethylmaleimide-sensitive factor |
| 1656 | 39356_at | NEDD4L | AB007899 | neural precursor cell expressed, developmentally down-regulated 4-like | ubiquitin-protein ligase NEDD4-like |
| 1657 | 40281_at | NEDD5 | D63878 | neural precursor cell expressed, developmentally down-regulated 5 | neural precursor cell expressed, developmentally down-regulated 5 |
| 1658 | 1695_at | NEDD8 | D23662 | neural precursor cell expressed, developmentally down-regulated 8 | ubiquitin-like protein |
| 1659 | 37005_at | NBL1 | D28124 | neuroblastoma, suppression of tumorigenicity 1 | neuroblastoma, suppression of tumorigenicity 1 |
| 1660 | 31896_at | NAG | AL050281 | neuroblastoma-amplified protein | hypothetical protein |
| 1661 | 37286_at | NRCAM | AB002341 | neuronal cell adhesion molecule | neuronal cell adhesion molecule |
| 1662 | 37673_at | NSMAF | X96586 | neutral sphingomyelinase (N-SMase) | FAN protein |
| 1663 | 38692_at | NAB1 | AF045451 | activation associated factor | transcriptional regulatory protein p54 |
| 1664 | 34835_at | NCSTN | D87442 | NGF1-A binding protein 1 (EGR1 binding protein 1) | |
| 1665 | 37032_at | NNMT | U08021 | nicastrin | nicotinamide N-methyltransferase |
| 1666 | 41722_at | NNT | U40490 | nicotinamide N-methyltransferase | nicotinamide N-methyltransferase |
| 1667 | 35366_at | NID | M30269 | nicotinamide nucleotide transhydrogenase | nicotinamide nucleotide transhydrogenase |
| 1668 | 753_at | NID2 | D86425 | nidogen (enactin) | nidogen |
| | | | | nidogen 2 | osteonidogen |

Fig 21

| | A | B | C | D | E |
|------|------------|----------|----------|--|-------------------------------------|
| 1669 | 37047_at | NPC1 | AF002020 | Niemann-Pick disease, type C1 | Niemann-Pick C disease protein |
| 1670 | 980_at | NPC1 | AF002020 | Niemann-Pick disease, type C1 | Niemann-Pick C disease protein |
| 1671 | 39345_at | NPC2 | AI525834 | Niemann-Pick disease, type C2 | |
| 1672 | 35153_at | NBS1 | AF058696 | Nijmegen breakage syndrome 1 (nibrin) | cell cycle regulatory protein p95 |
| 1673 | 36047_at | NEK1 | AL050385 | NIMA (never in mitosis gene a)-related kinase 1 | |
| 1674 | 35843_at | Nek8 | L40402 | NIMA-related kinase Nek8 | |
| 1675 | 40866_at | NIPSNAP1 | AJ001258 | nipsnap homolog 1 (C. elegans) | NIPSNAP1 protein |
| 1676 | 33916_at | NISCH | AB023192 | nischarin | KIAA0975 protein |
| 1677 | 39165_at | NIFU | U47101 | nitrogen fixation cluster-like | NifU-like protein |
| 1678 | 36472_at | NMI | U32849 | N-myc (and STAT) interactor | Nmi |
| 1679 | 36933_at | NDRG1 | D87953 | N-myc downstream regulated gene 1 | RTP |
| 1680 | 41656_at | NMT2 | AF043325 | N-myristoyltransferase 2 | N-myristoyltransferase 2 |
| 1681 | 39040_at | NCUBE1 | W28360 | non-canonical ubiquitin conjugating enzyme 1 | |
| 1682 | 39039_s_at | NCUBE1 | AI557497 | non-canonical ubiquitin conjugating enzyme 1 | |
| 1683 | 1521_at | NME1 | X17620 | non-metastatic cells 1, protein (NM23A) expressed in | Nm23 protein |
| 1684 | 33415_at | NME2 | X58965 | non-metastatic cells 2, protein (NM23B) expressed in | NM23-H2 protein |
| 1685 | 1980_s_at | NME2 | X58965 | non-metastatic cells 2, protein (NM23B) expressed in | NM23-H2 protein |
| 1686 | 38527_at | NONO | U02493 | non-POU domain containing, octamer-binding | 54 kDa protein |
| 1687 | 38750_at | NOTCH3 | U97669 | Notch homolog 3 (Drosophila) | Notch3 |
| 1688 | 34781_at | WS-3 | D84145 | novel RGD-containing protein | novel RGD-containing protein |
| 1689 | 40122_at | NSAP1 | AF037448 | NS1-associated protein 1 | Gry-rbp |
| 1690 | 33752_at | NS1-BP | AB020657 | NS1-binding protein | KIAA0850 protein |
| 1691 | 35626_at | SGSH | U30894 | N-sulfoglucosamine sulfohydrolase (sulfamidase) | N-sulphoglucosamine sulphonydrolase |
| 1692 | 37352_at | SP100 | M60618 | nuclear antigen Sp100 | nuclear autoantigen |
| 1693 | 37353_g_at | SP100 | M60618 | nuclear antigen Sp100 | nuclear autoantigen |
| 1694 | 40901_at | GS2NA | U17989 | nuclear autoantigen | GS2NA |
| 1695 | 32789_at | NCBP2 | AA149428 | nuclear cap binding protein subunit 2, 20kD | |

Fig 2.1

| A | B | C | D | E |
|---------------|-----------------|----------|---|---|
| 1696 35836_at | NUDC | AB019408 | nuclear distribution gene C homolog (A. nidulans) | nuclear distribution gene C (A. nidulans) homolog |
| 1697 39782_at | C1D | X95592 | nuclear DNA-binding protein | C1D protein |
| 1698 40063_at | NDP52 | U22897 | nuclear domain 10 protein | NDP52 |
| 1699 853_at | NFE2L2 | S74017 | nuclear factor (erythroid-derived 2)-like 2 | Nrf2 |
| 1700 38354_at | CEBPB; LAP; CRI | X52560 | nuclear factor NF-IL6 (AA 1-345); Human gene for nuclear factor NF-IL6. | CCAAT/enhancer binding protein (C/EBP), beta |
| 1701 40822_at | NFATC3 | L41067 | nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 | nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 |
| 1702 38438_at | NFKB1 | M58603 | nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) | nuclear factor kappa-B DNA binding subunit |
| 1703 1377_at | NFKB1 | M58603 | nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) | nuclear factor kappa-B DNA binding subunit |
| 1704 1461_at | NFKBIA | M69043 | nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha | nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha |
| 1705 37544_at | NFIL3 | X64318 | nuclear factor, interleukin 3 regulated | nuclear factor, interleukin 3 regulated |
| 1706 38648_at | CIZ | U80760 | nuclear matrix transcription factor 4 | CAGH1 alternate open reading frame |
| 1707 40816_at | PWP1 | L07758 | nuclear phosphoprotein similar to S. cerevisiae PWP1 | IEF SSP 9502 |
| 1708 34312_at | NCOA2 | A1040324 | nuclear receptor coactivator 2 | Amplified in Breast Cancer |
| 1709 33381_at | NCOA3 | AF012108 | nuclear receptor coactivator 3 | Ret fused gene |
| 1710 39174_at | NCOA4 | X77548 | nuclear receptor coactivator 4 | nuclear factor RIP140 |
| 1711 40088_at | NRIP1 | X84373 | nuclear receptor interacting protein 1 | |
| 1712 39397_at | NR2F2 | M64497 | nuclear receptor subfamily 2, group F, member 2 | apolipoprotein A1 regulatory protein-1 |
| 1713 36690_at | NR3C1 | M10901 | nuclear receptor subfamily 3, group C, member 1 | nuclear receptor subfamily 3, group C, member 1 |
| 1714 35302_at | NXF1 | AJ132712 | nuclear RNA export factor 1 | nuclear RNA export factor 1 |
| 1715 37928_at | NFYB | AA621555 | nuclear transcription factor Y, beta | |
| 1716 34667_at | NFX1 | U15306 | nuclear transcription factor, X-box binding 1 | NFX1 |
| 1717 33413_at | PRL-1 | AF051160 | nuclear; Homo sapiens tyrosine phosphatase (PRL-1) gene, complete cds. | tyrosine phosphatase |

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| A | B | C | D | E |
|-----------------|-----------|----------|---|--|
| 1718 32340_s_at | NSEP1 | M85234 | nuclease sensitive element binding protein 1 | nuclease sensitive element binding protein-1 |
| 1719 35643_at | NUCB2 | X76732 | nucleobindin 2 | NEFA protein |
| 1720 36597_at | NOLC1 | D21262 | nucleolar and coiled-body phosphoprotein 1 | ORF |
| 1721 37520_at | HSA6591 | AJ006591 | nucleolar cysteine-rich protein | cysteine-rich protein |
| 1722 36930_at | HUMAUNTIG | L05425 | nucleolar GTPase | nucleolar GTPase |
| 1723 39390_at | NUP133 | AF052123 | nucleoporin 133kD | |
| 1724 32850_at | NUP153 | Z25535 | nucleoporin 153kD | nuclear pore complex protein hnup153 |
| 1725 39024_at | NUP98 | AF042357 | nucleoporin 98kD | |
| 1726 571_at | NAP1L1 | M86667 | nucleosome assembly protein 1-like 1 | nucleosome assembly protein 1-like 1 |
| 1727 743_at | NAP1L3 | D50370 | nucleosome assembly protein 1-like 3 | nucleosome assembly protein |
| 1728 32575_at | NAP1L4 | U77456 | nucleosome assembly protein 1-like 4 | nucleosome assembly protein 2 |
| 1729 36127_g_at | NBP | U18919 | nucleotide binding protein | nucleotide binding protein |
| 1730 41584_at | NUDT3 | AF062529 | nudix (nucleoside diphosphate linked moiety X)-type motif 3 | diphosphoinositol polyphosphate phosphohydrolase |
| 1731 37693_at | NUMB | L40393 | numb homolog (Drosophila) | numb homolog |
| | | | ob15e02.s1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1323770 3' similar to SW:ROA3_HUMAN P51991 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A3 ; mRNA sequence. | |
| 1732 35916_s_at | INHBC | AA877215 | oculocerebrorenal syndrome of Lowe | ocr11 |
| 1733 34169_s_at | OCRL | U57627 | olfactory receptor, Human olfactory receptor (OLF3) gene, complete cds. | |
| 1734 31921_at | OLF3 | U56421 | O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase) | HsOLF3 |
| 1735 39507_at | OGT | AL050366 | opioid growth factor receptor | hypothetical protein |
| 1736 40332_at | OGFR | AF109134 | optic atrophy 1 (autosomal dominant) | Jul-60 |
| 1737 39745_at | OPA1 | AB011139 | optineurin | KIAA0567 protein |
| 1738 41744_at | OPTN | AF070533 | OR11-3; olfactory receptor; Homo sapiens OR7E12P pseudogene, complete sequence. | optineurin |
| 1739 34539_at | OR7E12P | AF065854 | | |

Fig-21

| | A | B | C | D | E |
|------|----------------|-------------|----------|--|---|
| 1740 | AFFX-BioC-3_at | bioA | J04423 | ORF 1 | 7,8-diamino-pelargonic acid aminotransferase |
| 1741 | AFFX-BioB-M_at | bioA | J04423 | ORF 1 | 7,8-diamino-pelargonic acid aminotransferase |
| 1742 | AFFX-BioDn-5_a | bioA | J04423 | ORF 1 | 7,8-diamino-pelargonic acid aminotransferase |
| 1743 | AFFX-BioDn-3_a | bioA | J04423 | ORF 1 | 7,8-diamino-pelargonic acid aminotransferase |
| 1744 | AFFX-BioC-5_at | bioA | J04423 | ORF 1 | 7,8-diamino-pelargonic acid aminotransferase |
| 1745 | 32412_at | RPS14 | M13934 | ORF; putative; Human ribosomal protein S14 gene, complete cds. | unknown protein; ribosomal protein S14 |
| 1746 | 1315_at | OAZ1 | D78361 | ORF1; ORF 2; no start codon; Human mRNA for ornithine decarboxylase antizyme, ORF 1 and ORF 2. | ornithine decarboxylase antizyme 1 |
| 1747 | 32800_at | RXRA; NR2B1 | U66306 | ORF-2; ORF-3; Human retinoid X receptor alpha mRNA, 3' UTR, partial sequence. | retinoid X receptor, alpha |
| 1748 | 38155_at | ORC5L | U92538 | origin recognition complex, subunit 5-like (yeast) | origin recognition complex subunit 5 homolog |
| 1749 | 36636_at | OAT | M12267 | ornithine aminotransferase (gyrate atrophy) | ornithine aminotransferase |
| 1750 | 1959_at | OAZIN | D88674 | ornithine decarboxylase antizyme inhibitor | antizyme inhibitor |
| 1751 | 33367_s_at | OAZIN | D88674 | ornithine decarboxylase antizyme inhibitor | antizyme inhibitor |
| 1752 | 1081_at | ODC1 | M33764 | ornithine decarboxylase; Human ornithine decarboxylase gene, complete cds. | ornithine decarboxylase 1 |
| 1753 | 31700_at | GPR35 | AF027957 | orphan G protein-coupled receptor; Homo sapiens G protein-coupled receptor (GPR35) gene, complete cds. | G protein-coupled receptor |
| 1754 | 1451_s_at | OSF-2 | D13666 | osteoblast specific factor 2 (fascilin l-like) | osteoblast specific factor 2 |
| 1755 | 39774_at | OXA1L | X80695 | oxidase (cytochrome c) assembly 1-like | oxidase (cytochrome c) assembly 1-like |

Fig-21

| A | B | C | D | E |
|-----------------|----------------|----------|---|--|
| 1756 39136_at | OSR1 | AB017642 | oxidative-stress responsive 1 | oxidative-stress responsive 1 |
| 1757 41438_at | OSBPL8 | AL049923 | oxysterol binding protein-like 8 | oxysterol-binding protein-like protein 8 |
| 1758 34329_at | PAK2 | N25547 | p21 (CDKN1A)-activated kinase 2 | |
| 1759 39710_at | P311 | U30521 | P311 protein | P311 HUM |
| 1760 36136_at | PIG11 | AF010315 | p53-induced protein | Pig11 |
| 1761 40441_g_at | PAI-RBP1 | AL080119 | PAI-1 mRNA-binding protein | hypothetical protein |
| 1762 40440_at | PAI-RBP1 | AL080119 | PAI-1 mRNA-binding protein | hypothetical protein |
| 1763 32001_s_at | PACE4 | M80482 | paired basic amino acid cleaving system 4 | subtilisin-like protease |
| 1764 121_at | PAX8 | X69699 | paired box gene 8 | paired box gene 8, isoform PAX8A; paired box gene 8, isoform PAX8B; paired box gene 8, isoform PAX8C; paired box gene 8, isoform PAX8D; paired box gene 8, isoform PAX8E |
| 1765 40127_at | PMX1 | M95929 | paired mesoderm homeo box 1 | homeobox protein |
| 1766 41191_at | KIAA0992 | AB023209 | palladin | KIAA0992 protein |
| 1767 40504_at | PON2 | AF001601 | paraoxonase 2 | paraoxonase |
| 1768 36032_at | dJ167A19.1 | AL031427 | partially supported by FGENES and GENSCAN | hypothetical protein |
| 1769 39243_s_at | PSIP2 | U94319 | PC4 and SFRS1 interacting protein 2 | DFS70 |
| 1770 41665_at | PCF11 | AB020631 | PCF11p homolog | KIAA0824 protein |
| 1771 38758_at | PDAP1 | R98910 | PDGFA associated protein 1 | |
| 1772 36937_s_at | PDLIM1 | U90878 | PDZ and LIM domain 1 (elfin) | carboxyl terminal LIM domain protein |
| 1773 32026_s_at | PDZ-GEF1 | AB002311 | PDZ domain containing guanine nucleotide exchange factor(GEF)1 | PDZ domain containing guanine nucleotide exchange factor(GEF)1 |
| 1774 34745_at | PDZ-GEF1 | AF070570 | PDZ domain containing guanine nucleotide exchange factor(GEF)1 | |
| 1775 40856_at | SERPINF1; PEDF | U29953 | PEDF; Human pigment epithelium-derived factor gene, complete cds. | pigment epithelium-derived factor |
| 1776 1491_at | PTX3 | M31166 | pentaxin-related gene, rapidly induced by IL-1 beta | tumor necrosis factor |
| 1777 38465_at | PAM | M37721 | peptidylglycine alpha-amidating monooxygenase | peptidylglycine alpha-amidating monooxygenase |
| 1778 35823_at | PPIB | M63573 | peptidylprolyl isomerase B (cyclophilin B) | secreted cyclophilin-like protein |

fig-21

| A | B | C | D | E |
|-----------------|----------------|----------|---|---|
| 1779 37422_at | PPIC | S71018 | peptidylprolyl isomerase C (cyclophilin C) | cyclophilin C |
| 1780 37385_at | PPIG | U40763 | peptidyl-prolyl isomerase G (cyclophilin G) | CARS-Cyp |
| 1781 36829_at | PER1 | AF022991 | period homolog 1 (Drosophila) | Rigul |
| 1782 35835_at | PDL-108 | AB019409 | periodontal ligament fibroblast protein | |
| 1783 32806_at | BZRP; MBR; PBR | M36035 | peripheral benzodiazepine receptor; Human peripheral benzodiazepine receptor (hpbs) mRNA, complete cds. | peripheral benzodiazepine receptor; peripheral benzodiazepine receptor short form |
| 1784 36653_at | PMP22 | D11428 | peripheral myelin protein 22 | PMP-22(PAS-11/5R13/Gas-3) |
| 1785 41213_at | PRDX1 | X67951 | peroxiredoxin 1 | peroxiredoxin 1 |
| 1786 36631_at | PRDX3 | D49396 | peroxiredoxin 3 | Aop1_Human, MER5(Aop1_Mouse)-like protein |
| 1787 38435_at | PRDX4 | U25182 | peroxiredoxin 4 | antioxidant enzyme AOE37-2 |
| 1788 37900_at | PEX11B | AF093670 | peroxisomal biogenesis factor 11B | peroxisomal biogenesis factor |
| 1789 36864_at | PEX3 | AJ001625 | peroxisomal biogenesis factor 3 | Pex3 protein |
| 1790 36625_at | ZAP128 | L40401 | peroxisomal long-chain acyl-coA thioesterase | peroxisomal long-chain acyl-coA thioesterase |
| 1791 33265_at | PXMP3 | M86852 | peroxisomal membrane protein 3 (35kD, Zellweger syndrome) | peroxisome assembly factor-1 |
| 1792 36502_at | PFTK1 | AB020641 | PFTAIRE protein kinase 1 | KIAA0834 protein |
| 1793 37694_at | PHF3 | D87685 | PHD finger protein 3 | PHD finger protein 3 |
| 1794 39381_at | XAP135 | AF055030 | PHD zinc finger protein XAP135 | PHD zinc finger protein XAP135, isoform a; PHD zinc finger protein XAP135, isoform b |
| 1795 1434_at | PTEN | U92436 | phosphatase and tensin homolog (mutated in multiple advanced cancers 1) | MMAC1 |
| 1796 34797_at | PPAP2A | AF014402 | phosphatidic acid phosphatase type 2A | type-2 phosphatidic acid phosphatase alpha- 1 |
| 1797 33862_at | PPAP2B | AF017786 | phosphatidic acid phosphatase type 2B | phosphatidic acid phosphohydrolase homolog |
| 1798 40783_s_at | PIK4CA | L36151 | phosphatidylinositol 4-kinase, catalytic, alpha polypeptide | phosphatidylinositol 4-kinase |
| 1799 37685_at | PICALM | U45976 | phosphatidylinositol binding clathrin assembly protein | CALM |

Fig-21

| A | B | C | D | E |
|-----------------|---------|----------|--|--|
| 1800 39993_at | PIGA | D11466 | phosphatidylinositol glycan, class A (paroxysmal nocturnal hemoglobinuria) | PIG-A protein |
| 1801 314_at | PIGB | D42138 | phosphatidylinositol glycan, class B | PIG-B |
| 1802 751_at | PIGC | D85418 | phosphatidylinositol glycan, class C | phosphatidylinositol-glycan-class C (PIG-C) |
| 1803 776_at | PIGF | D13435 | phosphatidylinositol glycan, class F | PIG-F |
| 1804 40629_at | PIGH | L19783 | phosphatidylinositol glycan, class H | phosphatidylinositol glycan, class H |
| 1805 38297_at | PITPNM | X98654 | phosphatidylinositol transfer protein, membrane-associated | homologue of Drosophila retinal degeneration B gene |
| 1806 35741_at | PIP5K2B | U85245 | phosphatidylinositol-4-phosphate 5-kinase, type II, beta | phosphatidylinositol-4-phosphate 5-kinase type II beta |
| 1807 37320_at | PTDSS1 | D14694 | phosphatidylserine synthase 1 | phosphatidylserine synthase 1 |
| 1808 33705_at | PDE4B | L20971 | phosphodiesterase 4B, cAMP-specific (Drosophila) | phosphodiesterase |
| 1809 39422_at | PDE4DIP | AB007923 | phosphodiesterase 4D interacting protein (myomegalin) | KIAA0454 protein |
| 1810 37676_at | PDE8A | AF056490 | phosphodiesterase 8A | cAMP-specific phosphodiesterase 8A |
| 1811 37188_at | PCK2 | X92720 | phosphoenolpyruvate carboxykinase 2 (mitochondrial) | phosphoenolpyruvate carboxykinase (GTP) |
| 1812 39175_at | PFKP | D25328 | phosphofructokinase, platelet | platelet-type phosphofructokinase |
| 1813 32210_at | PGM1 | M83088 | phosphoglucomutase 1 | phosphoglucomutase 1 |
| 1814 36963_at | PGD | U30255 | phosphogluconate dehydrogenase | phosphogluconate dehydrogenase |
| 1815 37677_at | PGK1 | V00572 | phosphoglycerate kinase 1 | phosphoglycerate kinase 1 |
| 1816 41221_at | PGAM1 | J04173 | phosphoglycerate mutase 1 (brain) | phosphoglycerate mutase 2 |
| 1817 35665_at | PIK3C3 | Z46973 | phosphoinositide-3-kinase, class 3 | phosphatidylinositol 3-kinase |
| 1818 1269_at | PIK3R1 | M61906 | phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha) | |
| 1819 37961_at | PIK3R3 | U90907 | phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma) | |
| 1820 32775_r_at | PLSCR1 | AB006746 | phospholipid scramblase 1 | phospholipid scramblase 1 |
| 1821 32260_at | PEA15 | X86809 | phosphoprotein enriched in astrocytes 15 | |
| 1822 36489_at | PRPS1 | D00860 | phosphoribosyl pyrophosphate synthetase 1 | phosphoribosyl pyrophosphate synthetase subunit 1 |

Fig-21

| A | B | C | D | E |
|-----------------|----------|----------|--|---|
| 1823 37338_at | PRPSAP1 | D61391 | phosphoribosyl pyrophosphate synthetase-associated protein 1 | phosphoribosyl pyrophosphate synthetase-associated protein 39 |
| 1824 39056_at | PAICS | X53793 | phosphoribosylaminoimidazole carboxylase, | phosphoribosylaminoimidazole carboxylase, |
| 1825 37392_at | PHKB | X84908 | phosphoribosylaminoimidazole succinocarboxamide synthetase | phosphoribosylaminoimidazole succinocarboxamide synthetase |
| 1826 36667_at | PYGB | U47025 | phosphorylase kinase, beta | phosphorylase kinase |
| 1827 32724_at | PHYH | AF023462 | phosphorylase, glycogen; brain | glycogen phosphorylase B |
| 1828 33543_s_at | PNN | U77718 | phytanoyl-CoA hydroxylase (Reisum disease) | peroxisomal phytanoyl-CoA alpha-hydroxylase |
| 1829 39003_at | PTTG1IP | Z50022 | pinin, desmosome associated protein | pinin |
| 1830 34793_s_at | PLS3 | M22299 | pituitary tumor-transforming 1 interacting protein | putative surface glycoprotein |
| 1831 32569_at | PAFAH1B1 | L13385 | platelet-activating factor acetylhydrolase, isoform 1b, alpha subunit (45kD) | Miller-Dieker lissencephaly protein |
| 1832 1731_at | PDGFRA | M21574 | platelet-derived growth factor receptor, alpha polypeptide | platelet-derived growth factor receptor A chain |
| 1833 38666_at | PSCD1 | M85169 | pleckstrin homology, Sec7 and coiled/coiled domains 1 (cytohesin 1) | cytohesin 1, isoform 1; cytohesin 1, isoform 2 |
| 1834 38741_at | PSCD2 | U70728 | pleckstrin homology, Sec7 and coiled/coiled domains 2 (cytohesin-2) | cytohesin-2 |
| 1835 36943_r_at | PLAGL1 | U81992 | pleiomorphic adenoma gene-like 1 | C2H2 zinc finger protein PLAGL1 |
| 1836 34780_at | PLXNB2 | AB002313 | plexin B2 | plexin B2 |
| 1837 32193_at | PLXNC1 | AF030339 | plexin C1 | VESPR |
| 1838 38270_at | PARG | AF005043 | poly (ADP-ribose) glycohydrolase | poly(ADP-ribose) glycohydrolase |
| 1839 31951_s_at | PABPC1 | Z48501 | poly(A) binding protein, cytoplasmic 1 | polyadenylate binding protein II |
| 1840 31950_at | PABPC1 | Y00345 | poly(A) binding protein, cytoplasmic 1 | poly(A) binding protein, cytoplasmic 1 |
| 1841 36003_at | PARN | AJ005698 | poly(A)-specific ribonuclease (deadenylation nuclease) | poly(A)-specific ribonuclease |
| 1842 34305_at | PCBP1 | Z29505 | poly(rC) binding protein 1 | sub2.3 |
| 1843 35746_r_at | PCBP2 | X78136 | poly(rC) binding protein 2 | hnRNP-E2 |
| 1844 35745_f_at | PCBP2 | X78136 | poly(rC) binding protein 2 | hnRNP-E2 |
| 1845 39868_at | PCBP3 | AL046394 | poly(rC) binding protein 3 | |

Fig. 21

| | A | B | C | D | E |
|------|----------------|--------|----------|--|--|
| 1846 | 38120_at | PKD2 | U50928 | polycystic kidney disease 2 (autosomal dominant) | polycystin 2 |
| 1847 | 33380_at | POLS | AB005754 | polymerase (DNA directed) sigma | LAK-1 |
| 1848 | 38702_at | POLE3 | AF070640 | polymerase (DNA directed), epsilon 3 (p17 subunit) | polymerase (DNA directed), epsilon 3 (p17 subunit) |
| 1849 | 40791_at | POLR2A | X63564 | polymerase (RNA) II (DNA directed) polypeptide A (220kD) | RNA polymerase II largest subunit |
| 1850 | 39746_at | POLR2B | X63563 | polymerase (RNA) II (DNA directed) polypeptide B (140kD) | RNA polymerase II 140 kDa subunit |
| 1851 | 36027_at | POLR2F | AA418779 | polymerase (RNA) II (DNA directed) polypeptide F | |
| 1852 | 35631_at | POLR2H | U37689 | polymerase (RNA) II (DNA directed) polypeptide H | RNA polymerase II subunit |
| 1853 | 1248_at | POLR2H | U37689 | polymerase (RNA) II (DNA directed) polypeptide H | RNA polymerase II subunit |
| 1854 | 503_at | POLR2L | U37690 | polymerase (RNA) II (DNA directed) polypeptide L (7.6kD) | RNA polymerase II subunit |
| 1855 | 35841_at | POLR2L | N24355 | polymerase (RNA) II (DNA directed) polypeptide L (7.6kD) | |
| 1856 | 34320_at | PTRF | AL050224 | polymerase I and transcript release factor | |
| 1857 | 34005_at | PIGR | X73079 | polymeric immunoglobulin receptor | Polymeric immunoglobulin receptor |
| 1858 | 40593_at | PTBP1 | X66975 | polypyrimidine tract binding protein 1 | nuclear ribonucleoprotein |
| 1859 | 31600_s_at | PMS2L1 | D38435 | postmeiotic segregation increased 2-like 1 | |
| 1860 | AFFX-CreX-5_at | | | pot. ORF1 (aa 1-73); ORF2, put. cre protein (aa 1-343); Bacteriophage P1 cre gene for recombinase protein. | |
| 1861 | AFFX-CreX-3_at | | X03453 | pot. ORF1 (aa 1-73); ORF2, put. cre protein (aa 1-343); Bacteriophage P1 cre gene for recombinase protein. | |
| 1862 | 315_at | PRDM2 | D45132 | PR domain containing 2, with ZNF domain | zinc-finger DNA-binding protein |
| 1863 | 32696_at | PBX3 | X59841 | pre-B-cell leukemia transcription factor 3 | homeobox protein |

Fig. 21

| | A | B | C | D | E |
|-----------------|---|--------|----------|--|--|
| 1864 36666_at | | P4HB | M22806 | precursor; Human prolyl 4-hydroxylase beta-subunit and disulfide isomerase (P4HB) gene, exon 11, clones 6B-(1,3,5,6). | prolyl 4-hydroxylase beta-subunit |
| 1865 34321_i_at | | GS3786 | D87120 | predicted osteoblast protein | GS3786 |
| 1866 41003_at | | PFDN4 | U41816 | prefoldin 4 | C-1 |
| 1867 38698_at | | PREI3 | AL080070 | preimplantation protein 3 | hypothetical protein |
| 1868 40269_at | | PRP18 | U51990 | pre-mRNA processing factor 18 | hPrp18 |
| 1869 38291_at | | PENK | J00123 | preproenkephalin (; Human enkephalin gene: exon 3 and 3'flank. | proenkephalin |
| 1870 641_at | | PSN1 | L76517 | presenilin 1 (Alzheimer disease 3) | presenilin 1 |
| 1871 40621_at | | PAWR | U63809 | PRKC, apoptosis, WT1, regulator | prostate apoptosis response protein par-4 |
| 1872 41773_at | | PCOLN3 | U58048 | procollagen (type III) N-endopeptidase | PRSM1 |
| 1873 31609_s_at | | PCOLCE | L33799 | procollagen C-endopeptidase enhancer | procollagen C-proteinase enhancer protein |
| 1874 34795_at | | PLOD2 | U84573 | procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2 | lysyl hydroxylase isoform 2 |
| 1875 36184_at | | PLOD | L06419 | procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) | lysyl hydroxylase |
| 1876 37037_at | | P4HA1 | M24486 | procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I | procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I |
| 1877 34390_at | | P4HA2 | U90441 | procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II | prolyl 4-hydroxylase alpha (II) subunit |
| 1878 691_g_at | | P4HB | J02783 | procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55) | procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55) |
| 1879 38840_s_at | | PFN2 | L10678 | profilin 2 | profilin II |
| 1880 38839_at | | PFN2 | AL096719 | profilin 2 | profilin 2 isoform b; profilin 2 isoform a |
| 1881 38802_at | | PGRMC1 | Y12711 | progesterone receptor membrane component 1 | putative progesterone binding protein |
| 1882 38821_at | | PGRMC2 | AJ002030 | progesterone receptor membrane component 2 | progesterone binding protein |

fig. 21

| A | B | C | D | E |
|-----------------|---------|----------|---|---|
| 1883 39035_at | DD5 | AF006010 | progesterone induced protein | progesterone induced protein |
| 1884 39036_g_at | DD5 | AF006010 | progesterone induced protein | progesterone induced protein |
| 1885 35218_at | PDCD10 | AF022385 | programmed cell death 10 | TFAR15 |
| 1886 37569_at | PDCD6 | AF035606 | programmed cell death 6 | calcium binding protein |
| 1887 32212_at | PDCD8 | AL049703 | programmed cell death 8 (apoptosis-inducing factor) | hypothetical protein |
| 1888 36592_at | PHB | S85655 | prohibitin | prohibitin |
| 1889 1884_s_at | PCNA | M15796 | proliferating cell nuclear antigen | proliferating cell nuclear antigen |
| 1890 41600_at | PA2G4 | U59435 | proliferation-associated 2G4, 38kD | cell cycle protein p38-2G4 homolog |
| 1891 35978_at | PRRG1 | AF009242 | proline-rich Gla (G-carboxyglutamic acid) polypeptide 1 | proline-rich Gla protein 1 |
| 1892 36023_at | PRH1 | AI864120 | proline-rich protein Haelll subfamily 1 | pro-oncogene receptor inducing membrane injury gene |
| 1893 40803_at | PORIMIN | AL050161 | pro-oncogene receptor inducing membrane injury gene | Propionyl-Coenzyme A carboxylase, alpha polypeptide precursor |
| 1894 1348_s_at | PCCA | S79219 | propionyl Coenzyme A carboxylase, alpha polypeptide | propionyl-CoA carboxylase |
| 1895 36561_at | PCCB | X73424 | propionyl Coenzyme A carboxylase, beta polypeptide | protease PC6 isoform A |
| 1896 41032_at | PCSK5 | U56387 | proprotein convertase subtilisin/kexin type 5 | protease PC6 isoform A |
| 1897 36795_at | PSAP | J03077 | prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) | prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) |
| 1898 38406_f_at | PTGDS | AI207842 | prostaglandin D2 synthase (21kD, brain) | |
| 1899 828_at | PTGER2 | U19487 | prostaglandin E receptor 2 (subtype EP2), 53kD | prostaglandin E2 receptor |
| 1900 1890_at | PLAB | AB000584 | prostate differentiation factor | TGF-beta superfamily protein |
| 1901 32611_at | PBP | X75252 | prostatic binding protein | phosphatidylethanolamine binding protein |
| 1902 719_g_at | PRSS11 | D87258 | protease, serine, 11 (IGF binding) | serin protease with IGF-binding motif |
| 1903 718_at | PRSS11 | D87258 | protease, serine, 11 (IGF binding) | serin protease with IGF-binding motif |
| 1904 33368_at | PRSS15 | X76040 | protease, serine, 15 | Lon protease-like protein |
| 1905 40078_at | SPUVE | AF015287 | protease, serine, 23 | serine protease |
| 1906 39845_at | PRSS25 | AF020760 | protease, serine, 25 | serine protease |
| 1907 688_at | PSMC1 | L02426 | proteasome (prosome, macropain) 26S subunit, ATPase, 1 | 26S protease (S4) regulatory subunit |

Fig. 21

| A | B | C | D | E |
|-----------------|--------|----------|--|--|
| 1908 35353_at | PSMC2 | D11094 | proteasome (prosome, macropain) 26S subunit, ATPase, 2 | MSS1 protein |
| 1909 592_at | PSMC3 | M34079 | proteasome (prosome, macropain) 26S subunit, ATPase, 3 | proteasome (prosome, macropain) 26S subunit, ATPase, 3 |
| 1910 37766_s_at | PSMC5 | AF035309 | proteasome (prosome, macropain) 26S subunit, ATPase, 5 | |
| 1911 949_s_at | PSMC6 | D78275 | proteasome (prosome, macropain) 26S subunit, ATPase, 6 | proteasome subunit p42 |
| 1912 1314_at | PSMD1 | D44466 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 | proteasome subunit p112 |
| 1913 1192_at | PSMD12 | AB003103 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 | 26S proteasome subunit p55 |
| 1914 32240_at | PSMD5 | D31889 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 |
| 1915 945_at | PSMD7 | D50063 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog) | proteasome subunit p40 / Mov34 protein |
| 1916 40276_at | PSMD7 | D50063 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog) | proteasome subunit p40 / Mov34 protein |
| 1917 32584_at | PSMD8 | D38047 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 8 | 26S proteasome subunit p31 |
| 1918 36492_at | PSMD9 | A1347155 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 9 | |
| 1919 41171_at | PSME2 | D45248 | proteasome (prosome, macropain) activator subunit 2 (PA28 beta) | proteasome activator hPA28 suunit beta |
| 1920 1184_at | PSME2 | D45248 | proteasome (prosome, macropain) activator subunit 2 (PA28 beta) | proteasome activator hPA28 suunit beta |
| 1921 36974_at | PSMF1 | D88378 | proteasome (prosome, macropain) inhibitor subunit 1 (Pi31) | proteasome inhibitor hPi31 subunit |
| 1922 38371_at | PSMA1 | M64992 | proteasome (prosome, macropain) subunit, alpha type, 1 | prosomeal protein P30-33K |
| 1923 1446_at | PSMA2 | D00760 | proteasome (prosome, macropain) subunit, alpha type, 2 | proteasome (prosome, macropain) subunit, alpha type, 2 |
| 1924 1448_at | PSMA3 | D00762 | proteasome (prosome, macropain) subunit, alpha type, 3 | proteasome (prosome, macropain) subunit, alpha type, 3 |

Fig. 21

| | A | B | C | D | E |
|------|-----------|---------|----------|--|---|
| 1925 | 1450_g_at | PSMA4 | D00763 | proteasome (prosome, macropain) subunit, alpha type, 4 | proteasome (prosome, macropain) subunit, alpha type, 4 |
| 1926 | 1449_at | PSMA4 | D00763 | proteasome (prosome, macropain) subunit, alpha type, 4 | proteasome (prosome, macropain) subunit, alpha type, 4 |
| 1927 | 37046_at | PSMA5 | A1246726 | proteasome (prosome, macropain) subunit, alpha type, 5 | |
| 1928 | 36122_at | PSMA6 | X59417 | proteasome (prosome, macropain) subunit, alpha type, 6 | prosome P27K protein |
| 1929 | 1447_at | PSMB1 | D00761 | proteasome (prosome, macropain) subunit, beta type, 1 | proteasome (prosome, macropain) subunit, beta type, 1 |
| 1930 | 1310_at | PSMB2 | D26599 | proteasome (prosome, macropain) subunit, beta type, 2 | proteasome subunit HsC7-l |
| 1931 | 33154_at | PSMB4 | D26600 | proteasome (prosome, macropain) subunit, beta type, 4 | proteasome subunit HsN3 |
| 1932 | 1311_at | PSMB4 | D26600 | proteasome (prosome, macropain) subunit, beta type, 4 | proteasome subunit HsN3 |
| 1933 | 37666_at | PSMB5 | D29011 | proteasome (prosome, macropain) subunit, beta type, 5 | proteasome subunit X |
| 1934 | 941_at | PSMB6 | D29012 | proteasome (prosome, macropain) subunit, beta type, 6 | proteasome subunit Y |
| 1935 | 39060_at | PSMB7 | D38048 | proteasome (prosome, macropain) subunit, beta type, 7 | proteasome subunit z |
| 1936 | 1313_at | PSMB7 | D38048 | proteasome (prosome, macropain) subunit, beta type, 7 | proteasome subunit z |
| | | | | proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2) | |
| 1937 | 38287_at | PSMB9 | AA808961 | | |
| 1938 | 41750_at | P5 | D49489 | protein disulfide isomerase-related protein | human P5 |
| 1939 | 32558_at | PIAS3 | AB021868 | protein inhibitor of activated STAT3 | protein inhibitor of activated STAT3 |
| 1940 | 34376_at | PKIG | AB019517 | protein kinase (cAMP-dependent, catalytic) inhibitor gamma | protein kinase inhibitor gamma |
| 1941 | 36957_at | PRKCBP1 | W22296 | protein kinase C binding protein 1 | |
| 1942 | 1602_at | PRKCI | L33881 | protein kinase C, iota | protein kinase C iota |
| 1943 | 1603_g_at | PRKCI | L33881 | protein kinase C, iota | protein kinase C iota |
| 1944 | 36835_at | PRKCL2 | U33052 | protein kinase C-like 2 | PRK2 |

fig. 21

| | A | B | C | D | E |
|------|----------|----------|----------|--|--|
| 1945 | 41768_at | PRKAR1A | M33336 | protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1) | cAMP-dependent protein kinase type I-alpha subunit |
| 1946 | 227_g_at | PRKAR1A | M33336 | protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1) | cAMP-dependent protein kinase type I-alpha subunit |
| 1947 | 226_at | PRKAR1A | M33336 | protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1) | cAMP-dependent protein kinase type I-alpha subunit |
| 1948 | 32205_at | PRKRA | AF072860 | protein kinase, interferon-inducible double stranded RNA dependent activator | protein activator of the interferon-induced protein kinase |
| 1949 | 37725_at | PPP1CC | X74008 | protein phosphatase 1, catalytic subunit, gamma isoform | serine /threonine specific protein phosphatase |
| 1950 | 40438_at | PPP1R12A | D87930 | protein phosphatase 1, regulatory (inhibitor) subunit 12A | myosin phosphatase target subunit 1 |
| 1951 | 39366_at | PPP1R3C | N36638 | protein phosphatase 1, regulatory (inhibitor) subunit 3C | |
| 1952 | 41540_at | PPP1R7 | Z50749 | protein phosphatase 1, regulatory subunit 7 | yeast sds22 homolog |
| 1953 | 857_at | PPM1A | S87759 | protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform | protein phosphatase 2C alpha |
| 1954 | 36501_at | PPM1A | S87759 | protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform | protein phosphatase 2C alpha |
| 1955 | 37107_at | PPM1D | U78305 | protein phosphatase 1D magnesium-dependent, delta isoform | Wip1 |
| 1956 | 924_s_at | PPP2CB | J03805 | protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform | |
| 1957 | 41167_at | PPP2R2A | M64929 | protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform | protein phosphatase-2A subunit-alpha |
| 1958 | 1383_at | PPP2R2A | M64929 | protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform | protein phosphatase-2A subunit-alpha |
| 1959 | 32734_at | PPP2R5E | L76703 | protein phosphatase 2, regulatory subunit B (B56), epsilon isoform | protein phosphatase B56-epsilon |

Fig-21

| | A | B | C | D | E |
|------|------------|---------|----------|--|--|
| 1960 | 40786_at | PPP2R5C | U37352 | protein phosphatase 2, regulatory subunit B (B56), gamma isoform | protein phosphatase 2A B'alpha1 regulatory subunit |
| 1961 | 176_at | PPP2R5C | U37352 | protein phosphatase 2, regulatory subunit B (B56), gamma isoform | protein phosphatase 2A B'alpha1 regulatory subunit |
| 1962 | 39127_f_at | PPP2R4 | X73478 | protein phosphatase 2A, regulatory subunit B' (PR 53) | phosphotyrosyl phosphatase activator |
| 1963 | 38277_at | PPP3CB | M29550 | protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta) | protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta) |
| 1964 | 32541_at | PPP3CC | S46622 | protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma) | calcineurin A catalytic subunit |
| 1965 | 34371_at | PPP4R1 | U79267 | protein phosphatase 4, regulatory subunit 1 | |
| 1966 | 37581_at | PPP6C | X92972 | protein phosphatase 6, catalytic subunit | protein phosphatase 6 |
| 1967 | 35752_s_at | PROS1 | M15036 | protein S (alpha) | protein S (alpha) |
| 1968 | 32564_at | SEC61B | AA083129 | protein translocation complex beta | |
| 1969 | 1064_at | PTK9 | U02680 | protein tyrosine kinase 9 | protein tyrosine kinase |
| 1970 | 843_at | PTP4A1 | U48296 | protein tyrosine phosphatase type IVA, member 1 | protein tyrosine phosphatase PTPCAAX1 |
| 1971 | 38415_at | PTP4A2 | U14603 | protein tyrosine phosphatase type IVA, member 2 | protein-tyrosine phosphatase |
| 1972 | 1241_at | PTP4A2 | U14603 | protein tyrosine phosphatase type IVA, member 2 | protein-tyrosine phosphatase |
| 1973 | 40137_at | PTPN1 | M31724 | protein tyrosine phosphatase, non-receptor type 1 | protein tyrosine phosphatase, non-receptor type 1 |
| 1974 | 1463_at | PTPN12 | M93425 | protein tyrosine phosphatase, non-receptor type 12 | protein tyrosine phosphatase |
| 1975 | 34198_at | PTPN13 | U12128 | protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase) | protein tyrosine phosphatase 1E |
| 1976 | 1496_at | PTPRA | M34668 | protein tyrosine phosphatase, receptor type, A | protein tyrosine phosphatase, receptor type, A, isoform 1 precursor; protein tyrosine phosphatase, receptor type, A, isoform 2 precursor |

Fig. 21

| | A | B | C | D | E |
|------|------------|----------|----------|---|--|
| 1977 | 36204_at | PTPRF | Y00815 | protein tyrosine phosphatase, receptor type, F | put. LAR preprotein (AA -16 to 1881) |
| 1978 | 41780_at | PPF1A1 | U22816 | protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 | LAR-interacting protein 1b |
| 1979 | 1488_at | PTPRK | L77886 | protein tyrosine phosphatase, receptor type, K | protein tyrosine phosphatase |
| 1980 | 995_g_at | PTPRM | X58288 | protein tyrosine phosphatase, receptor type, M | protein-tyrosine phosphatase |
| 1981 | 31892_at | PTPRM | X58288 | protein tyrosine phosphatase, receptor type, M | protein-tyrosine phosphatase |
| 1982 | 41141_at | PRKRIR | AL049970 | protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor) | hypothetical protein |
| 1983 | 37737_at | PCMT1 | D25547 | protein-L-isoaspartate (D-aspartate) O-methyltransferase | PIMT isozyme I |
| 1984 | 37736_at | PCMT1 | D13892 | protein-L-isoaspartate (D-aspartate) O-methyltransferase | carboxyl methyltransferase |
| 1985 | 32227_at | PRG1 | X17042 | proteoglycan 1, secretory granule | proteoglycan 1, secretory granule |
| 1986 | 38590_r_at | PTMA | M14630 | prothymosin, alpha (gene sequence 28) | prothymosin, alpha (gene sequence 28) |
| 1987 | 38589_i_at | PTMA | M14630 | prothymosin, alpha (gene sequence 28) | prothymosin, alpha (gene sequence 28) |
| 1988 | 37936_at | HPRP4P | A1184802 | PRP4/STKWD splicing factor | |
| 1989 | 31697_s_at | FTHP1 | J04755 | pseudoferritin H protein; Human ferritin H processed pseudogene, complete cds. | |
| 1990 | 36117_at | PTK2 | L13616 | PTK2 protein tyrosine kinase 2 | focal adhesion kinase |
| 1991 | 40048_at | PUM1 | D43951 | pumilio homolog 1 (Drosophila) | KIAA0099 protein |
| 1992 | 35359_at | PUM2 | D87078 | pumilio homolog 2 (Drosophila) | KIAA0235 protein |
| 1993 | 35221_at | PURA | X91648 | purine-rich element binding protein A | |
| 1994 | 33341_at | GNB1 | X04526 | put. ORFX (AA 1-75); beta subunit (AA 1-340); Human liver mRNA for beta-subunit signal transducing proteins Gs/Gi (beta-G). | guanine nucleotide-binding protein, beta-1 subunit |
| 1995 | 33720_at | LOC56902 | L48692 | putative 28 kDa protein | |
| 1996 | 39363_at | BC-2 | AF042384 | putative breast adenocarcinoma marker (32kD) | BC-2 protein |

Fig. 21

| | A | B | C | D | E |
|------|------------|----------|----------|--|--|
| 1997 | 39884_g_at | HSA9761 | AF091078 | putative dimethyladenosine transferase | putative dimethyladenosine transferase |
| 1998 | 38841_at | GDBR1 | AF068195 | putative glioblastoma cell differentiation-related | putative glioblastoma cell differentiation-related protein |
| 1999 | 41188_at | LC27 | W28186 | putative integral membrane transporter | |
| | | | | putative L-type neutral amino acid transporter | |
| 2000 | 38984_at | KIAA0436 | AB007896 | putative membrane protein | |
| 2001 | 39116_at | LOC54499 | AF070626 | | |
| 2002 | 35286_r_at | RY1 | X76302 | putative nucleic acid binding protein RY-1 | nucleic acid binding protein |
| 2003 | 36852_at | N33 | U42349 | Putative prostate cancer tumor suppressor | |
| | | | | putative protein similar to nussy (Drosophila) | C3f |
| 2004 | 33710_at | C3F | U72515 | putative translation initiation factor | putative translation initiation factor |
| 2005 | 40203_at | SUI1 | AJ012375 | putative transmembrane protein | putative transmembrane protein |
| 2006 | 37678_at | NMA | U23070 | putative transmembrane protein; homolog of yeast Golgi membrane protein Yfi1p (Yip1p-interacting factor) | 54TMp |
| 2007 | 35326_at | 54TM | AF004876 | putative; Homo sapiens PTS gene, complete cds. | 6-pyruvoyltetrahydropterin synthase |
| 2008 | 35697_at | PTS | L76259 | putative; originally identified as an 'oncogene', product renamed by NCBI staff; Homo sapiens longation factor 1-alpha 1 (PTI-1) mRNA, complete cds. | longation factor 1-alpha 1 |
| 2009 | 40887_g_at | PTI-1 | L41498 | putative; originally identified as an 'oncogene', product renamed by NCBI staff; Homo sapiens longation factor 1-alpha 1 (PTI-1) mRNA, complete cds. | longation factor 1-alpha 1 |
| 2010 | 40886_at | PTI-1 | L41498 | pVHL-interacting deubiquitinating enzyme 1 | KIAA1097 protein |
| 2011 | 33219_at | VDU1 | AB029020 | Pyruvate dehydrogenase complex, lipoyl-containing component X; E3-binding protein | pyruvate dehydrogenase complex protein X subunit precursor |
| 2012 | 36164_at | PDX1 | U82328 | pyruvate kinase, muscle | pyruvate kinase, muscle |
| 2013 | 32378_at | PKM2 | M26252 | quinoid dihydropteridine reductase | quinoid dihydropteridine reductase |
| 2014 | 260_at | QDPR | M16447 | | |

Fig. 21

| | A | B | C | D | E |
|------|------------|---------|----------|--|--|
| 2015 | 36610_at | R3HDM | D21852 | R3H domain (binds single-stranded nucleic acids) containing | KIAA0029 protein |
| 2016 | 39030_at | RABAC1 | AJ133534 | Rab acceptor 1 (prenylated) | prenylated Rab acceptor 1 (PRA1) |
| 2017 | 37703_at | RABGGTB | Y08201 | Rab geranylgeranyltransferase, beta subunit | rab geranylgeranyl transferase |
| 2018 | 38264_at | RABIF | U74324 | RAB interacting factor | guanine nucleotide exchange factor mss4 |
| 2019 | 36660_at | RAB11A | AF000231 | RAB11A, member RAS oncogene family | rab11a |
| 2020 | 35325_at | RAB14 | AF052113 | RAB14, member RAS oncogene family | |
| 2021 | 34393_r_at | RAB1A | AL050268 | RAB1A, member RAS oncogene family | hypothetical protein |
| 2022 | 34392_s_at | RAB1A | AL050268 | RAB1A, member RAS oncogene family | hypothetical protein |
| 2023 | 33326_at | RAB21 | D42087 | RAB21, member RAS oncogene family | RAB21, member RAS oncogene family |
| 2024 | 809_at | RAB27A | U57094 | RAB27A, member RAS oncogene family | Rab27a |
| 2025 | 33371_s_at | RAB31 | U59877 | RAB31, member RAS oncogene family | low-Mr GTP-binding protein Rab31 |
| 2026 | 36110_at | RAB5A | M28215 | RAB5A, member RAS oncogene family | GTP-binding protein |
| 2027 | 35289_at | GAPCEN | AJ011679 | rab6 GTPase activating protein (GAP and centrosome-associated) | Rab6 GTPase activating protein, GAPCenA |
| 2028 | 35304_at | RAB6A | AF052130 | RAB6A, member RAS oncogene family | |
| 2029 | 39628_at | RAB9A | AI671547 | RAB9A, member RAS oncogene family | |
| 2030 | 41716_at | RC3 | AB020663 | rabconnectin-3 | KIAA0856 protein |
| 2031 | 37543_at | ARHGEF6 | D25304 | Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 | |
| 2032 | 36857_at | RAD1 | AF084513 | RAD1 homolog (S. pombe) | DNA repair exonuclease |
| 2033 | 38114_at | RAD21 | D38551 | RAD21 homolog (S. pombe) | RAD21 homolog |
| 2034 | 1874_at | RAD23B | D21090 | RAD23 homolog B (S. cerevisiae) | XP-C repair complementing protein (p58/HHR23B) |
| 2035 | 32757_at | RAE1 | U84720 | RAE1 RNA export 1 homolog (S. pombe) | mRNA export protein |
| 2036 | 1524_at | | U46194 | RAGE-4 ORF2; one of 2 possible coding regions; RAGE-4 ORF3; one of 2 possible coding regions; Human renal cell carcinoma antigen RAGE-4 mRNA, complete putative cds. | |
| 2037 | 36628_at | RALBP1 | L42542 | ralA binding protein 1 | RLP76 protein |
| 2038 | 37539_at | RGL | AB023176 | RaGDS-like gene | KIAA0959 protein |

Fig. 21

| | A | B | C | D | E |
|------|-----------|----------|----------|---|---|
| 2039 | 41342_at | RANBP1 | D38076 | RAN binding protein 1 | Ran-BP1(Ran-binding protein 1) |
| 2040 | 40824_at | RANBP16 | AB018288 | RAN binding protein 16 | KIAA0745 protein |
| 2041 | 41174_at | RANBP2L1 | AF012086 | RAN binding protein 2-like 1 | Ran binding protein 2 |
| 2042 | 35255_at | RANBP7 | AF098799 | RAN binding protein 7 | RanBP7/importin 7 |
| 2043 | 32602_at | RAP1GDS1 | X63465 | RAP1, GTP-GDP dissociation stimulator 1 | smg GDS |
| 2044 | 1848_at | RAP1A | M22995 | RAP1A, member of RAS oncogene family | ras-related protein |
| 2045 | 40146_at | RAP1B | AL080212 | RAP1B, member of RAS oncogene family | hypothetical protein |
| 2046 | 39601_at | RASSF1 | AF061836 | Ras association (RalGDS/AF-6) domain family 1 | putative tumor suppressor protein |
| 2047 | 37598_at | RASSF2 | D79990 | Ras association (RalGDS/AF-6) domain family 2 | Ras association (RalGDS/AF-6) domain family 2 |
| 2048 | 1659_s_at | RHEB2 | D78132 | Ras homolog enriched in brain 2 | ras-related GTP-binding protein |
| 2049 | 37309_at | ARHA | L09159 | ras homolog gene family, member A | multidrug resistance protein |
| 2050 | 1394_at | ARHA | L25080 | ras homolog gene family, member A | GTP-binding protein |
| 2051 | 35803_at | ARHE | S82240 | ras homolog gene family, member E | RhoE |
| 2052 | 36935_at | RASA1 | M23379 | RAS p21 protein activator (GTPase activating protein) 1 | GTPase-activating protein |
| 2053 | 1675_at | RASA1 | M23379 | RAS p21 protein activator (GTPase activating protein) 1 | GTPase-activating protein |
| 2054 | 35793_at | G3BP2 | AB014560 | Ras-GTPase activating protein SH3 domain-binding protein 2 | KIAA0660 protein |
| 2055 | 40864_at | RAC1 | D25274 | ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1) | |
| 2056 | 2050_s_at | RAC1 | M29870 | ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1) | ras-related C3 botulinum toxin substrate 1 isoform Rac1; ras-related C3 botulinum toxin substrate 1 isoform Rac1b |
| 2057 | 35316_at | RAGA | U41654 | Ras-related GTP-binding protein | adenovirus E3-14.7K interacting protein 1 |
| 2058 | 33234_at | BCAA | AA887480 | RBP1-like protein | |
| 2059 | 41407_at | RDBP | L03411 | RD RNA-binding protein | RD protein |
| 2060 | 34684_at | RECQL | L36140 | RecQ protein-like (DNA helicase Q1-like) | DNA helicase |

Fig. 21

| A | B | C | D | E |
|-----------------|------------|----------|--|--|
| 2061 34685_at | RECQL | AI685944 | RecQ protein-like (DNA helicase Q1-like) regulated at the translational level; contains l-mfa domain; utilizes unique GTG start codon; Homo sapiens HIC protein isoform p40 and HIC protein isoform p32 mRNAs, complete cds. | HIC protein isoform p40; HIC protein isoform p32 |
| 2062 37842_at | HIC | AF054589 | regulator of G-protein signalling 19 | |
| 2063 35756_at | RGS19IP1 | AF089816 | interacting protein 1 | RGS-GAIP interacting protein GIPC |
| 2064 37701_at | RGS2 | L13463 | regulator of G-protein signalling 2, 24kD | helix-loop-helix phosphoprotein |
| 2065 35722_at | RENT2 | AL080198 | regulator of nonsense transcripts 2 | hypothetical protein |
| 2066 32827_at | RRAS2 | AI365215 | related RAS viral (r-ras) oncogene homolog 2 | |
| 2067 34845_at | dJ796117.4 | AL035398 | remainder of gene in clone 549K18 (AL023654) | CGI-51 protein |
| 2068 1055_g_at | RFC4 | M87339 | replication factor C (activator 1) 4 (37kD) | replication factor C, 37-kDa subunit |
| 2069 38481_at | RPA1 | M63488 | replication protein A1 (70kD) | replication protein A, 70-kDa subunit |
| 2070 652_g_at | RPA3 | L07493 | replication protein A3 (14kD) | replication protein A 14kDa subunit |
| 2071 37651_at | RCOR | D31888 | REST corepressor | REST corepressor |
| 2072 34350_at | RSN | X64838 | restin (Reed-Steinberg cell-expressed intermediate filament-associated protein) | restin |
| 2073 31851_at | RFP2 | AJ224819 | ret finger protein 2 | tumor suppressor |
| 2074 40556_at | RCN1 | D42073 | reticulocalbin 1, EF-hand calcium binding domain | reticulocalbin |
| 2075 37727_l_at | RCN2 | X78669 | reticulocalbin 2, EF-hand calcium binding domain | EF-hand protein |
| 2076 37728_r_at | RCN2 | X78669 | reticulocalbin 2, EF-hand calcium binding domain | EF-hand protein |
| 2077 31536_at | RTN4 | AB020693 | reticulon 4 | KIAA0886 protein |
| 2078 39964_at | RP2 | AJ007590 | retinitis pigmentosa 2 (X-linked recessive) | XRP2 protein |
| 2079 38164_at | RPGR | U57629 | retinitis pigmentosa GTPase regulator | retinitis pigmentosa GTPase regulator |
| 2080 2044_s_at | RB1 | M15400 | retinoblastoma 1 (including osteosarcoma) | retinoblastoma 1 (including osteosarcoma) |

Fig-21

| | A | B | C | D | E |
|------|------------|---------------|----------|---|---|
| 2081 | 35227_at | RBBP8 | U72066 | retinoblastoma binding protein 8 | CBP interacting protein CtIP |
| 2082 | 33860_at | RBAF600 | AB007931 | retinoblastoma-associated factor 600 | KIAA0462 protein |
| 2083 | 32597_at | RBL2 | X76061 | retinoblastoma-like 2 (p130) | 130K protein |
| 2084 | 35848_at | RAI17 | AL049432 | retinoic acid induced 17 | |
| | | | | retropseudogene; Human | |
| 2085 | 31672_g_at | RBMS1P; MSSP1 | D82351 | retropseudogene MSSP-1 DNA, complete cds. | MSSP-1 |
| 2086 | 39908_s_at | REV3L | AL096744 | REV3-like, catalytic subunit of DNA polymerase zeta (yeast) | hypothetical protein |
| 2087 | 35236_g_at | RECK | AA099265 | reversion-inducing-cysteine-rich protein with kazal motifs | |
| 2088 | 35235_at | RECK | AA099265 | reversion-inducing-cysteine-rich protein with kazal motifs | |
| 2089 | 35234_at | RECK | D50406 | reversion-inducing-cysteine-rich protein with kazal motifs | RECK protein precursor |
| 2090 | 553_g_at | ARHGAP1 | U02570 | Rho GTPase activating protein 1 | CDC42 GTPase-activating protein |
| 2091 | 39700_at | ARHGAP1 | A1961929 | Rho GTPase activating protein 1 | |
| 2092 | 34180_at | ARHGEF10 | AB002292 | Rho guanine nucleotide exchange factor (GEF) 10 | Rho guanine nucleotide exchange factor 10 |
| 2093 | 40828_at | ARHGEF7 | D63476 | Rho guanine nucleotide exchange factor (GEF) 7 | PAK-interacting exchange factor beta |
| 2094 | 40100_at | ARHGEF2 | U72206 | rho/rac guanine nucleotide exchange factor (GEF) 2 | guanine nucleotide regulatory factor |
| 2095 | 36537_at | P114-RHO-GEF | AB011093 | Rho-specific guanine nucleotide exchange factor p114 | KIAA0521 protein |
| 2096 | 41040_at | RPP38 | U77664 | ribonuclease P (38kD) | RNaseP protein P38 |
| 2097 | 32664_at | RNASE4 | D37931 | ribonuclease, RNase A family, 4 | RNase 4 |
| 2098 | 36187_at | RNH | X13973 | ribonuclease/angiogenin inhibitor | ribonuclease/angiogenin inhibitor |
| 2099 | 34314_at | RRM1 | X59543 | ribonucleotide reductase M1 polypeptide | M1 subunit of ribonucleotide reductase |
| 2100 | 2016_s_at | RPL10 | M64241 | ribosomal protein L10 | Wilm's tumor-related protein |
| 2101 | 41178_at | RPL11 | X79234 | ribosomal protein L11 | ribosomal protein L11 |
| 2102 | 33668_at | RPL12 | AF037643 | ribosomal protein L12 | |
| 2103 | 31509_at | RPL13 | X64707 | ribosomal protein L13 | ribosomal protein L13 |
| 2104 | 35119_at | RPL13A | X56932 | ribosomal protein L13a | 23 kD highly basic protein |
| 2105 | 31907_at | RPL14 | D87735 | ribosomal protein L14 | ribosomal protein L14 |

fig. 21

| | A | B | C | D | E |
|------|------------|--------|----------|------------------------|---|
| 2106 | 32432_f_at | RPL15 | L25899 | ribosomal protein L15 | ribosomal protein L10 |
| 2107 | 32440_at | RPL17 | X53777 | ribosomal protein L17 | ribosomal protein L17 |
| 2108 | 31546_at | RPL18 | L11566 | ribosomal protein L18 | ribosomal protein L18 |
| 2109 | 33614_at | RPL18A | X80822 | ribosomal protein L18a | ribosomal protein L18a |
| 2110 | 32435_at | RPL19 | X63527 | ribosomal protein L19 | ribosomal protein L19 |
| 2111 | 32337_at | RPL21 | U25789 | ribosomal protein L21 | ribosomal protein L21 |
| 2112 | 33451_s_at | RPL22 | A1526079 | ribosomal protein L22 | |
| 2113 | 32395_r_at | RPL23 | X55954 | ribosomal protein L23 | HL23 ribosomal protein |
| 2114 | 32394_s_at | RPL23 | X55954 | ribosomal protein L23 | HL23 ribosomal protein |
| 2115 | 32341_f_at | RPL23A | U37230 | ribosomal protein L23a | ribosomal protein L23a |
| 2116 | 33677_at | RPL24 | M94314 | ribosomal protein L24 | ribosomal protein L30 |
| 2117 | 32444_at | RPL26 | X69392 | ribosomal protein L26 | ribosomal protein L26 |
| 2118 | 39830_at | RPL27 | AA044823 | ribosomal protein L27 | |
| 2119 | 32436_at | RPL27A | U14968 | ribosomal protein L27a | ribosomal protein L27a |
| 2120 | 31708_at | RPL30 | L05095 | ribosomal protein L30 | ribosomal protein L30 |
| 2121 | 33676_at | RPL31 | X15940 | ribosomal protein L31 | ribosomal protein L31 |
| 2122 | 32276_at | RPL32 | X03342 | ribosomal protein L32 | ribosomal protein L32 |
| 2123 | 33657_at | RPL34 | L38941 | ribosomal protein L34 | ribosomal protein L34 |
| 2124 | 41765_at | RPL35 | A1541285 | ribosomal protein L35 | |
| 2125 | 41152_f_at | RPL36A | T89651 | ribosomal protein L36a | |
| 2126 | 33656_at | RPL37 | D23661 | ribosomal protein L37 | ribosomal protein L37 |
| 2127 | 31962_at | RPL37A | L06499 | ribosomal protein L37a | ribosomal protein L37a |
| 2128 | 34085_at | RPL38 | Z26876 | ribosomal protein L38 | ribosomal protein |
| 2129 | 33485_at | RPL4 | D23660 | ribosomal protein L4 | ribosomal protein |
| 2130 | 32466_at | RPL41 | Z12982 | ribosomal protein L41 | human homologue to yeast ribosomal protein YL41 |
| 2131 | 33660_at | RPL5 | U14966 | ribosomal protein L5 | ribosomal protein L5 |
| 2132 | 31952_at | RPL6 | X69391 | ribosomal protein L6 | ribosomal protein L6 |
| 2133 | 36333_at | RPL7 | X57958 | ribosomal protein L7 | ribosomal protein L7 |
| 2134 | 31505_at | RPL8 | Z28407 | ribosomal protein L8 | ribosomal protein L8 |
| 2135 | 31568_at | RPS10 | U14972 | ribosomal protein S10 | ribosomal protein S10 |
| 2136 | 32330_at | RPS11 | X06617 | ribosomal protein S11 | ribosomal protein S11 |
| 2137 | 33116_f_at | RPS12 | AA977163 | ribosomal protein S12 | |
| 2138 | 33619_at | RPS13 | L01124 | ribosomal protein S13 | ribosomal protein S13 |
| 2139 | 34317_g_at | RPS15A | W52024 | ribosomal protein S15a | ribosomal protein S15a |
| 2140 | 38061_at | RPS16 | A1541256 | ribosomal protein S16 | |

Fig. 21

| A | B | C | D | E |
|-----------------|-----------|----------|---|---------------------------------------|
| 2141 34593_g_at | RPS17 | M13932 | ribosomal protein S17 | ribosomal protein S17 |
| 2142 34592_at | RPS17 | M13932 | ribosomal protein S17 | ribosomal protein S17 |
| 2143 31330_at | RPS19 | M81757 | ribosomal protein S19 | S19 ribosomal protein |
| 2144 31527_at | RPS2 | X17206 | ribosomal protein S2 | ribosomal protein S2 |
| 2145 32438_at | RPS20 | L06498 | ribosomal protein S20 | ribosomal protein S20 |
| 2146 347_s_at | RPS23 | D14530 | ribosomal protein S23 | ribosomal protein |
| 2147 32315_at | RPS24 | M31520 | ribosomal protein S24 | ribosomal protein S24 |
| 2148 31573_at | RPS25 | M64716 | ribosomal protein S25 | ribosomal protein |
| 2149 32748_at | RPS27 | A1557852 | ribosomal protein S27 (metalloprotein) | |
| 2150 34570_at | RPS27A | S79522 | ribosomal protein S27a | ubiquitin carboxyl extension protein |
| 2151 39798_at | RPS28 | R87876 | ribosomal protein S28 | |
| 2152 34645_at | RPS3 | X55715 | ribosomal protein S3 | ribosomal protein S3 |
| 2153 1653_at | RPS3A | M84711 | ribosomal protein S3A | v-fos transformation effector protein |
| 2154 34643_at | RPS4X | M58458 | ribosomal protein S4, X-linked | ribosomal protein S4X isoform |
| 2155 32437_at | RPS5 | U14970 | ribosomal protein S5 | ribosomal protein S5 |
| 2156 31511_at | RPS9 | U14971 | ribosomal protein S9 | ribosomal protein S9 |
| 2157 31538_at | RPLP0 | M17885 | ribosomal protein, large, P0 | ribosomal protein P0 |
| 2158 31956_f_at | RPLP1 | M17886 | ribosomal protein, large, P1 | ribosomal protein P1 |
| 2159 31957_r_at | RPLP1 | M17886 | ribosomal protein, large, P1 | ribosomal protein P1 |
| 2160 33213_g_at | RRBP1 | AF006751 | ribosome binding protein 1 homolog 180kD (dog) | ES/130 |
| 2161 38331_at | RIT | Y07566 | Ric-like, expressed in many tissues (Drosophila) | Ric-like, expressed in many tissues |
| 2162 35656_at | RNF6 | AJ010346 | ring finger protein (C3H2C3 type) 6 | RING-H2 |
| 2163 39150_at | RNF11 | U69559 | ring finger protein 11 | |
| 2164 35811_at | RNF13 | AF037204 | ring finger protein 13 | RING zinc finger protein |
| 2165 33343_at | RNF14 | AB022663 | ring finger protein 14 | ring finger protein 14 |
| 2166 33484_at | RNF2 | Y10571 | ring finger protein 2 | ring finger protein 2 |
| 2167 37964_at | RNF3 | W25793 | ring finger protein 3 | |
| 2168 35777_at | RNF4 | AB000468 | ring finger protein 4 | zinc finger protein |
| | | | ring zinc-finger protein; escapes X chromosome inactivation; Human ring zinc finger protein (ZNF127-Xp) gene and 5' flanking sequence. | |
| 2169 37650_at | ZNF127-Xp | U41315 | | ZNF127-Xp |
| 2170 37732_at | RYBP | AL049940 | RING1 and YY1 binding protein | |

Fig. 21

| A | B | C | D | E |
|-----------------|----------|----------|--|---|
| 2171 38073_at | RNMT | AB007858 | RNA (guanine-7-) methyltransferase | RNA (guanine-7-) methyltransferase |
| 2172 41460_at | RBM14 | AF080561 | RNA binding motif protein 14 | SYT interacting protein SIP |
| 2173 41741_at | RBM3 | U28686 | RNA binding motif protein 3 | RNPL |
| 2174 35351_at | RBM4 | U89505 | RNA binding motif protein 4 | Hlark |
| 2175 32804_at | RBM5 | AF091263 | RNA binding motif protein 5 | RNA binding motif protein 5 |
| 2176 40870_g_at | RBM6 | AF069517 | RNA binding motif protein 6 | RNA binding protein DEF-3 |
| 2177 40260_g_at | RBM9 | AL009266 | RNA binding motif protein 9 | hypothetical protein |
| 2178 39731_at | RBMX | Z23064 | RNA binding motif protein, X chromosome | hnRNP G protein |
| 2179 33867_s_at | RBMS1 | X77494 | RNA binding motif, single stranded interacting protein 1 | RNA binding motif, single stranded interacting protein 1, isoform a |
| 2180 36186_at | RNPS1 | L37368 | RNA binding protein S1, serine-rich domain | RNA-binding protein |
| 2181 35202_at | RNGTT | AF025654 | RNA guanylyltransferase and 5'-phosphatase | mRNA capping enzyme |
| 2182 33237_at | KIAA0801 | AB018344 | RNA helicase | KIAA0801 protein |
| 2183 36045_at | RNAH | AJ223948 | RNA helicase family | RNA helicase |
| 2184 38762_at | RNAHP | AF083255 | RNA helicase-related protein | RNA helicase-related protein |
| 2185 38049_g_at | BPMS | D84110 | RNA-binding protein gene with multiple splicing | RBP-MS/type 4 |
| 2186 38047_at | BPMS | D84109 | RNA-binding protein gene with multiple splicing | RBP-MS/type 3 |
| 2187 38974_at | DJ-1 | AF021819 | RNA-binding protein regulatory subunit | RNA-binding protein regulatory subunit |
| 2188 39725_at | RNPC2 | L10910 | RNA-binding region (RNP1, RRM) containing 2 | splicing factor |
| 2189 38011_at | RMP | AB006572 | RPB5-mediated protein | RPB5 mediating protein |
| 2190 35195_at | RTCD1 | Y11651 | RTC domain containing 1 | phosphate cyclase |
| 2191 943_at | RUNX1 | D43968 | run-related transcription factor 1 (acute myeloid leukemia 1; am1 oncogene) | AML1b protein |
| 2192 40124_at | RUVBL1 | Y18418 | RuvB-like 1 (E. coli) | erythrocyte cytosolic protein of 54 kDa, ECP-54 |
| 2193 35758_at | RUVBL2 | AB024301 | RuvB-like 2 (E. coli) | RuvB-like DNA helicase TIP49b |
| 2194 39338_at | S100A10 | AI201310 | S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)) | |

Fig-21

| | A | B | C | D | E |
|------|------------|----------|----------|---|---|
| 2195 | 36089_at | SAC2 | AB023183 | Sac domain-containing inositol phosphatase 2 | KIAA0966 protein |
| 2196 | 41101_at | SAC3 | D87464 | Sac domain-containing inositol phosphatase 3 | KIAA0274 gene product |
| 2197 | 36511_at | SACM1L | AB020658 | SAC1 suppressor of actin mutations 1-like (yeast) | KIAA0851 protein |
| 2198 | 34792_at | AHCYL1 | AL049954 | S-adenosylhomocysteine hydrolase-like 1 | hypothetical protein |
| 2199 | 41302_at | AHCYL1 | R59606 | S-adenosylhomocysteine hydrolase-like 1 | |
| 2200 | 36685_at | AMD1 | W63793 | S-adenosylmethionine decarboxylase 1 | |
| 2201 | 263_g_at | AMD1 | M21154 | S-adenosylmethionine decarboxylase 1 | S-adenosylmethionine decarboxylase 1 precursor |
| 2202 | 41449_at | SGCE | AJ000534 | sarcoglycan, epsilon | epsilon-sarcoglycan |
| 2203 | 36083_at | SAS | U01160 | sarcoma amplified sequence | SAS |
| 2204 | 36536_at | SCHIP1 | AF070614 | schwannomin interacting protein 1 | schwannomin interacting protein 1 |
| 2205 | 33423_g_at | SEC13L1 | AF052155 | SEC13-like 1 (S. cerevisiae) | SEC13 (S. cerevisiae)-like 1 |
| 2206 | 33422_at | SEC13L1 | AF052155 | SEC13-like 1 (S. cerevisiae) | SEC13 (S. cerevisiae)-like 1 |
| 2207 | 36207_at | SEC14L1 | D67029 | SEC14-like 1 (S. cerevisiae) | SEC14 (S. cerevisiae)-like 1 |
| 2208 | 39099_at | SEC23A | X97064 | SEC23 homolog A (S. cerevisiae) | SEC23 protein |
| 2209 | 34199_at | SEC24A | AJ131244 | SEC24 related gene family, member A (S. cerevisiae) | Sec24A protein |
| 2210 | 35845_at | SEC24B | AJ131245 | SEC24 related gene family, member B (S. cerevisiae) | Sec24B protein |
| 2211 | 32770_at | SEC24D | AB018298 | SEC24 related gene family, member D (S. cerevisiae) | |
| 2212 | 34349_at | SEC63L | AJ011779 | SEC63 protein | KIAA0755 protein |
| 2213 | 32521_at | SFRP1 | AF056087 | secreted frizzled-related protein 1 | SEC63 protein |
| | | | | secreted phosphoprotein 1 (osteopontin, bone sialoprotein 1, early T-lymphocyte activation 1) | secreted frizzled related protein |
| 2214 | 34342_s_at | SPP1 | AF052124 | secreted protein, acidic, cysteine-rich (osteonectin) | osteopontin |
| 2215 | 671_at | SPARC | J03040 | secretory granule, neuroendocrine protein 1 (7B2 protein) | secreted protein, acidic, cysteine-rich (osteonectin) |
| 2216 | 34265_at | SGNE1 | Y00757 | selenium binding protein 1 | secretory granule, neuroendocrine protein 1 (7B2 protein) |
| 2217 | 37405_at | SELENBP1 | U29091 | | selenium-binding protein |

fig. 21

| A | B | C | D | E |
|-----------------|----------|----------|--|--|
| 2218 39078_at | SPS2 | U43286 | selenophosphate synthetase 2 | selenophosphate synthetase 2 |
| 2219 34363_at | SEPP1 | Z11793 | selenoprotein P, plasma, 1 | selenoprotein P |
| 2220 377_g_at | SEMA3C | AB000220 | sema domain, immunoglobulin domain (lg), short basic domain, secreted, (semaphorin) 3C | semaphorin E |
| 2221 376_at | SEMA3C | AB000220 | sema domain, immunoglobulin domain (lg), short basic domain, secreted, (semaphorin) 3C | semaphorin E |
| 2222 35666_at | SEMA3F | U38276 | sema domain, immunoglobulin domain (lg), short basic domain, secreted, (semaphorin) 3F | semaphorin III family homolog |
| 2223 38826_at | 2-Sep | D50918 | sepin 6 | sepin 2 |
| 2224 40898_at | SQSTM1 | U46751 | sequestosome 1 | phosphotyrosine independent ligand for the Lck SH2 domain p62 |
| 2225 34789_at | SERPINE6 | S69272 | serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6 | cytoplasmic antiproteinase |
| 2226 38125_at | SERPINE1 | M14083 | serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1 | serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1 |
| 2227 39167_r_at | SERPINE2 | D83174 | serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 2 | collagen binding protein 2 |
| 2228 38818_at | SPTLC1 | Y08685 | serine palmitoyltransferase, long chain base subunit 1 | serine palmitoyltransferase, subunit I |
| 2229 40966_at | STK39 | AF099989 | serine threonine kinase 39 (STE20/SPS1 homolog, yeast) | Ste-20 related kinase SPAK |
| 2230 41737_at | SRRM1 | AF048977 | serine/arginine repetitive matrix 1 | Ser/Arg-related nuclear matrix protein |
| 2231 36019_at | STK19 | L26260 | serine/threonine kinase 19 | RP protein |
| 2232 40473_at | STK24 | AF024636 | serine/threonine kinase 24 (STE20 homolog, yeast) | STE20-like kinase 3 |
| 2233 32142_at | STK3 | U26424 | serine/threonine kinase 3 (STE20 homolog, yeast) | MST2 |
| 2234 32784_at | PRP4 | AB011108 | serine/threonine-protein kinase PRP4 homolog | KIAA0536 protein |

fig. 21

| A | | B | C | D | | E | |
|------|----------|---------|----------|--|---|---|---|
| | | | | serum response factor (c-fos serum response element-binding transcription factor) | serum response factor (c-fos serum response element-binding transcription factor) | serum response factor (c-fos serum response element-binding transcription factor) | serum response factor (c-fos serum response element-binding transcription factor) |
| 2235 | 40109_at | SRF | J03161 | | | | |
| 2236 | 1409_at | SRF | J03161 | | | | |
| 2237 | 41544_at | SNK | AF059617 | serum-inducible kinase | | serum-inducible kinase | |
| 2238 | 34849_at | SARS | X91257 | seryl-tRNA synthetase | | seryl-tRNA synthetase | |
| 2239 | 40189_at | SET | M93651 | SET translocation (myeloid leukemia-associated) | | SET translocation (myeloid leukemia-associated) | |
| 2240 | 32160_at | SIAH1 | U76247 | seven in absentia homolog 1 (Drosophila) | | hSIAH1 | |
| 2241 | 33799_at | SIAH2 | U76248 | seven in absentia homolog 2 (Drosophila) | | hSIAH2 | |
| 2242 | 39088_at | NIFIE14 | Y18007 | seven transmembrane domain protein | | seven transmembrane domain protein | |
| 2243 | 39747_at | rpb-7 | U52427 | seventh largest subunit; Human RNA polymerase II seventh subunit (rpb-7) gene, complete cds. | | RNA polymerase II seventh subunit | |
| 2244 | 38518_at | SCML2 | Y18004 | sex comb on midleg-like 2 (Drosophila) | | SCML2 protein | |
| 2245 | 36040_at | SH3BGR | AI337192 | SH3 domain binding glutamic acid-rich protein | | SH3 domain binding glutamic acid-rich-like protein | |
| 2246 | 39714_at | SH3BGRL | AF042081 | SH3 domain binding glutamic acid-rich protein like | | SH3 binding protein | |
| 2247 | 38968_at | SH3BP5 | AB005047 | SH3-domain binding protein 5 (BTK-associated) | | SH3-containing protein SH3GLB1 | |
| 2248 | 39691_at | SH3GLB1 | AB007960 | SH3-domain GRB2-like endophilin B1 | | | |
| 2249 | 38118_at | SHC1 | U73377 | SHC (Src homology 2 domain containing) transforming protein 1 | | p66shc | |
| 2250 | 34256_at | SIAT9 | AB018356 | sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) | | GM3 synthase | |
| 2251 | 39139_at | SPC18 | AI357653 | signal peptidase complex (18kD) | | | |
| 2252 | 41194_at | SRP14 | AI525652 | signal recognition particle 14kD (homologous Alu RNA binding protein) | | | |
| 2253 | 35231_at | SRP19 | X12791 | signal recognition particle 19kD | | signal recognition particle 19kD | |
| 2254 | 36060_at | SRP54 | U51920 | signal recognition particle 54kD | | signal recognition particle | |

fig-21

| A | B | C | D | E |
|-------------------|-------|----------|--|--|
| 2255 33837_at | SRP72 | AF069765 | signal recognition particle 72kD | signal recognition particle 72 |
| 2256 36981_at | SRP9 | AF070649 | signal recognition particle 9kD | |
| 2257 36679_at | SRPR | X06272 | signal recognition particle receptor ('docking protein') | signal recognition particle receptor ('docking protein') |
| 2258 AFFX-HUMISGF | STAT1 | M97935 | signal transducer and activator of transcription 1, 91kD | transcription factor ISGF-3 |
| 2259 32860_g_at | STAT1 | M97935 | signal transducer and activator of transcription 1, 91kD | transcription factor ISGF-3 |
| 2260 32859_at | STAT1 | M97935 | signal transducer and activator of transcription 1, 91kD | transcription factor ISGF-3 |
| 2261 33338_at | STAT1 | M97936 | signal transducer and activator of transcription 1, 91kD | |
| 2262 39708_at | STAT3 | L29277 | signal transducer and activator of transcription 3 (acute-phase response factor) | DNA-binding protein |
| 2263 160_at | STAM | U43899 | signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 | STAM |
| 2264 35804_at | ASH2L | AB022785 | similar to Drosophila ash2 gene; Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene. | |
| 2265 41552_g_at | RER1 | AW044624 | similar to S. cerevisiae RER1 | |
| 2266 41551_at | RER1 | AW044624 | similar to S. cerevisiae RER1 | |
| 2267 33632_g_at | DIM1 | AF023612 | similar to S. pombe dim1+ | Dim1p homolog |
| 2268 35083_at | G1L | AL031670 | similar to SW:GOLI DROME Q06003 GOLIATH PROTEIN | ring finger protein 24 |
| 2269 37178_at | na | M74089 | similar to TB1 | |
| 2270 40787_at | WIRE | U90911 | similar to Wiskott-Aldrich syndrome protein interacting protein | |
| 2271 34705_at | BET3 | AJ224335 | similar to yeast BET3 (S. cerevisiae) | hBET3 protein |
| 2272 39131_at | UPF3A | N36842 | similar to yeast Upf3, variant A | |
| 2273 41277_at | SAP18 | AW021542 | sin3-associated polypeptide, 18kD | sin3 associated polypeptide p18 |
| 2274 33859_at | SAP18 | U96915 | sin3-associated polypeptide, 18kD | mSin3A associated polypeptide p30 |
| 2275 40992_s_at | SAP30 | AF055993 | sin3-associated polypeptide, 30kD | sine oculis homeobox (Drosophila) homolog 1 |
| 2276 40004_at | SIX1 | X91868 | sine oculis homeobox homolog 1 (Drosophila) | |

12.5

| A | B | C | D | E |
|-----------------|-------------|----------|---|---|
| 2277 39070_at | SNL | U03057 | singed-like (fascin homolog, sea urchin) (Drosophila) | actin bundling protein |
| 2278 39086_g_at | SSBP1 | AA768912 | single-stranded DNA binding protein | hypothetical protein |
| 2279 32668_at | SSBP2 | AL080076 | single-stranded DNA binding protein 2 | 60kD Ro/SSA autoantigen |
| 2280 35294_at | SSA2 | M25077 | Sjogren syndrome antigen A2 (60kD, ribonucleoprotein autoantigen SS-A/Ro) | 60kD Ro/SSA autoantigen |
| 2281 35295_g_at | SSA2 | M25077 | Sjogren syndrome antigen A2 (60kD, ribonucleoprotein autoantigen SS-A/Ro) | 60kD Ro/SSA autoantigen |
| 2282 38450_at | SSB | X69804 | Sjogren syndrome antigen B (autoantigen La) | Sjogren syndrome antigen B (autoantigen La) |
| 2283 37715_at | SNW1 | AF045184 | SKI-interacting protein | nuclear receptor coactivator NCoA-62 |
| 2284 37389_at | IMAGE145052 | AI346580 | small acidic protein | |
| 2285 40875_s_at | SNRP70 | X06815 | small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen) | hU1-70K-like protein (216 AA) |
| 2286 38679_g_at | SNRPE | AA733050 | small nuclear ribonucleoprotein polypeptide E | |
| 2287 37337_at | SNRPG | AI803447 | small nuclear ribonucleoprotein polypeptide G | |
| 2288 34842_at | SNRPN | U41303 | small nuclear ribonucleoprotein polypeptide N | small nuclear ribonucleoprotein particle N |
| 2289 35247_at | SNAPC5 | AI557062 | small nuclear RNA activating complex, polypeptide 5, 19kD | |
| 2290 32172_at | SHARP | AL096858 | SMART/HDAC1 associated repressor protein | hypothetical protein |
| 2291 32849_at | SMC1L1 | D80000 | SMC1 structural maintenance of chromosomes 1-like 1 (yeast) | |
| 2292 38738_at | SMT3H1 | X99584 | SMT3 suppressor of mif two 3 homolog 1 (yeast) | SMT3A protein |
| 2293 41185_f_at | SMT3H2 | AI971724 | SMT3 suppressor of mif two 3 homolog 2 (yeast) | |
| 2294 38288_at | SNAI2 | U69196 | snail homolog 2 (Drosophila) | |
| 2295 38659_at | SHOC2 | AB020669 | soc-2 suppressor of clear homolog (C. elegans) | KIAA0862 protein |
| 2296 40928_at | WSB1 | W26496 | SOCS box-containing WD protein SWIP-1 | |

fig. 21

| A | B | C | D | E |
|-----------------|---------|----------|---|---|
| 2297 36809_at | SLC1A3 | D26443 | solute carrier family 1 (glial high affinity glutamate transporter), member 3 | glutamate transporter |
| 2298 35320_at | SLC11A2 | AB004857 | solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 | NRAMP2 |
| 2299 33143_s_at | SLC16A3 | U81800 | solute carrier family 16 (monocarboxylic acid transporters), member 3 | monocarboxylate transporter |
| 2300 39260_at | SLC16A4 | U59185 | solute carrier family 16 (monocarboxylic acid transporters), member 4 | solute carrier family 16 (monocarboxylic acid transporters), member 4 |
| 2301 36979_at | SLC2A3 | M20681 | solute carrier family 2 (facilitated glucose transporter), member 3 | solute carrier family 2 (facilitated glucose transporter), member 3 |
| 2302 32084_at | SLC22A5 | AF057164 | solute carrier family 22 (organic cation transporter), member 5 | organic cation transporter OCTN2 |
| 2303 38122_at | SLC23A1 | D87075 | solute carrier family 23 (nucleobase transporters), member 1 | |
| 2304 32822_at | SLC25A4 | J02966 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4 |
| 2305 37740_r_at | SLC25A5 | J02683 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 |
| 2306 40436_g_at | SLC25A6 | J03592 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6 | |
| 2307 40435_at | SLC25A6 | J03592 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6 | |
| 2308 37675_at | SLC25A3 | X60036 | solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3 | phosphate carrier protein |
| 2309 33901_at | SLC29A1 | U81375 | solute carrier family 29 (nucleoside transporters), member 1 | equilibrative nucleoside transporter 1 |
| 2310 40364_at | SLC31A1 | U83460 | solute carrier family 31 (copper transporters), member 1 | high-affinity copper uptake protein |

Fig. 21

| A | B | C | D | E |
|-----------------|---------|----------|--|--|
| 2311 34749_at | SLC31A2 | U83461 | solute carrier family 31 (copper transporters), member 2 | putative copper uptake protein |
| 2312 37895_at | SLC35A1 | D87969 | solute carrier family 35 (CMP-sialic acid transporter), member 1 | CMP-sialic acid transporter |
| 2313 38208_at | SLC35A3 | AB021981 | solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3 | UDP-N-acetylglucosamine transporter |
| 2314 34936_at | SLC4A7 | AB012130 | solute carrier family 4, sodium bicarbonate cotransporter, member 7 | sodium bicarbonate cotransporter2 |
| 2315 34166_at | SLC6A7 | S80071 | solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 | brain-specific L-proline transporter |
| 2316 32186_at | SLC7A5 | M80244 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 |
| 2317 39533_at | SLC7A6 | D87432 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 |
| 2318 32681_at | SLC9A1 | S68616 | solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na+/H+, amiloride sensitive) | Na+/H+ exchanger NHE-1 isoform |
| 2319 36542_at | SLC9A6 | AF030409 | solute carrier family 9 (sodium/hydrogen exchanger), isoform 6 | sodium-hydrogen exchanger 6 |
| 2320 39097_at | SON | X63753 | SON DNA binding protein | SON DNA-binding protein |
| 2321 32857_at | SOS2 | L13858 | son of sevenless homolog 2 (Drosophila) | guanine nucleotide exchange factor |
| 2322 41462_at | SNX2 | AF065482 | sorting nexin 2 | sorting nexin 2 |
| 2323 39360_at | SNX3 | AF034546 | sorting nexin 3 | sorting nexin 3 |
| 2324 40605_at | SNX4 | AA524345 | sorting nexin 4 | |
| 2325 37808_at | SNX7 | AL049989 | sorting nexin 7 | hypothetical protein |
| 2326 33352_at | H2A | X57985 | Source: H.sapiens genes for histones H2B.1 and H2A. | histone H2A |
| 2327 36112_r_at | SC-35 | X75755 | Source: H.sapiens PR264 gene. | splicing factor, arginine/serine-rich 2 |
| 2328 36111_s_at | SC-35 | X75755 | Source: H.sapiens PR264 gene. | splicing factor, arginine/serine-rich 2 |

fig. 21

| | A | B | C | D | E |
|------|------------|-----------|--------------|--|--|
| 2329 | 1173_g_at | | HG172-HT3924 | Source: Homo sapiens chromosome 10 clone RP11-96B5, WORKING DRAFT SEQUENCE, 8 unordered pieces. | |
| 2330 | 40617_at | 44M2.1 | AC004381 | Source: Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence. | hypothetical protein FLJ20274 |
| | | | | Source: Homo sapiens clk2 kinase (CLK2), propin1, cote1, glucocerebrosidase (GBA), and metaxin genes, complete cds; metaxin pseudogene and glucocerebrosidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds. | |
| 2331 | 33740_at | COTE1 | AF023268 | Source: Homo sapiens hJTB gene, complete cds. | chromosome 1 open reading frame 2 |
| 2332 | 41834_g_at | HJTB PAR | AB016492 | Source: Homo sapiens hJTB gene, complete cds. | jumping translocation breakpoint |
| 2333 | 41833_at | HJTB PAR | AB016492 | Source: Homo sapiens hJTB gene, complete cds. | jumping translocation breakpoint |
| 2334 | 32335_r_at | UbC2 | AB009010 | Source: Homo sapiens mRNA for polyubiquitin UbC, complete cds. | polyubiquitin UbC |
| 2335 | 32334_f_at | UbC2 | AB009010 | Source: Homo sapiens mRNA for polyubiquitin UbC, complete cds. | polyubiquitin UbC |
| 2336 | 32194_at | CBF | M37197 | Source: Human CCAAT-box-binding factor (CBF) mRNA, complete cds. | CCAAT-box-binding transcription factor |
| 2337 | 229_at | CBF | M37197 | Source: Human CCAAT-box-binding factor (CBF) mRNA, complete cds. | CCAAT-box-binding transcription factor |
| 2338 | 41791_at | 101F10.3 | AC002550 | Source: Human Chromosome 16 BAC clone CIT987SK-A-101F10, complete sequence. | hypothetical protein |
| 2339 | 41488_at | A-211C6.1 | AC002394 | Source: Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence. | hypothetical protein A-211C6.1 |
| 2340 | 35742_at | A-362G6.1 | U95740 | Source: Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete sequence. | hypothetical protein A-362G6.1 |

Fig-21

| | A | B | C | D | E |
|------|------------|---------------------|----------|--|---|
| 2341 | 41733_at | 61E3.1 | AC003007 | Source: Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence. | Unknown gene product (partial) |
| 2342 | 36894_at | | AL031846 | Source: Human DNA sequence from clone RP4-742C19 on chromosome 22, complete sequence. | |
| 2343 | 37383_f_at | HLA class I - locus | X58536 | Source: Human mRNA for HLA class I locus C heavy chain. | HLA class I heavy chain |
| 2344 | 39778_at | GLYT1 GLCNAC | M55621 | Source: Human N-acetylglucosaminyltransferase I (GlcNAc-TI) mRNA, complete cds. | mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase |
| 2345 | 41573_at | SP3 | X68560 | Sp3 transcription factor | |
| 2346 | 32102_at | SACS | AB018273 | spastic ataxia of Charlevoix-Saguenay (sacsin) | KIAA0730 protein |
| 2347 | 35171_at | SPG4 | AB029006 | spastic paraplegia 4 (autosomal dominant; spastin) | KIAA1083 protein |
| 2348 | 39423_f_at | SPOP | AJ000644 | speckle-type POZ protein | SPOP |
| 2349 | 38924_s_at | SSH3BP1 | AF001628 | spectrin SH3 domain binding protein 1 | interactor protein AbiBP4 |
| 2350 | 33886_at | SSH3BP1 | AF006516 | spectrin SH3 domain binding protein 1 | e3B1 |
| 2351 | 39556_at | SPTBN1 | M96803 | spectrin, beta, non-erythrocytic 1 | beta-spectrin |
| 2352 | 34304_s_at | SAT | AL050290 | spermidine/spermine N1-acetyltransferase | |
| 2353 | 32574_at | SMPD1 | X59960 | sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase) | sphingomyelin phosphodiesterase |
| 2354 | 36142_at | SCA1 | X79204 | spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1) | ataxin-1 |
| 2355 | 36998_s_at | SCA2 | Y08262 | spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant, ataxin 2) | ataxin 2 |
| 2356 | 38040_at | SPF30 | AF107463 | splicing factor 30, survival of motor neuron-related | splicing factor |
| 2357 | 36973_at | SF3B2 | U41371 | splicing factor 3b, subunit 2, 145kD | spliceosome associated protein |

Fig. 21

| | A | B | C | D | E |
|------|------------|---------------|----------|--|---|
| 2358 | 36224_g_at | SFPQ | A1827895 | splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) | |
| 2359 | 40638_at | SFPQ | X70944 | splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) | PTB-associated splicing factor |
| 2360 | 36098_at | SFRS1 | M72709 | splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor) | splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor) |
| 2361 | 140_s_at | SFRS10 | U68063 | splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila) | transformer-2 beta |
| 2362 | 32183_at | SFRS11 | M74002 | splicing factor, arginine/serine-rich 11 | arginine-rich nuclear protein |
| 2363 | 35258_f_at | SFRS2IP | AF030234 | splicing factor, arginine/serine-rich 2, interacting protein | splicing factor Sip1 |
| 2364 | 40457_at | SFRS3 | AF038250 | splicing factor, arginine/serine-rich 3 | |
| 2365 | 36991_at | SFRS4 | L14076 | splicing factor, arginine/serine-rich 4 | pre-mRNA splicing factor |
| 2366 | 40453_s_at | SFRS5 | U30826 | splicing factor, arginine/serine-rich 5 | SRp40-1 |
| 2367 | 40262_at | SRP46 | AF031166 | Splicing factor, arginine/serine-rich, 46kD | SRp46 splicing factor |
| 2368 | 35839_at | SOLE | D78130 | squalene epoxidase | squalene epoxidase |
| 2369 | 39047_at | SART3 | AB020880 | squamous cell carcinoma antigen recognised by T cells 3 | squamous cell carcinoma antigen SART-3 |
| 2370 | 41784_at | DKFZp56480769 | AL080186 | SR rich protein | hypothetical protein |
| 2371 | 36091_at | SCAP2 | AF051323 | src family associated phosphoprotein 2 | Src-associated adaptor protein |
| 2372 | 41354_at | STC1 | U25997 | stanniocalcin 1 | stanniocalcin precursor |
| 2373 | 32043_at | STC2 | AF098462 | stanniocalcin 2 | stanniocalcin-related protein |
| 2374 | 41295_at | STARD7 | AL041780 | START domain containing 7 | |
| 2375 | 38800_at | STMN2 | D45352 | stathmin-like 2 | |
| 2376 | 41823_at | STAU | AJ132258 | staufen, RNA binding protein (Drosophila) | staufen protein |
| 2377 | 38669_at | SLK | D86959 | Ste20-related serine/threonine kinase | KIAA0204 protein |
| 2378 | 37147_at | SCGF | AF020044 | stem cell growth factor; lymphocyte secreted C-type lectin | lymphocyte secreted C-type lectin precursor |
| 2379 | 36913_at | SLBP | U75679 | stem-loop (histone) binding protein | histone stem-loop binding protein |
| 2380 | 38034_at | STS | M16505 | steroid sulfatase (microsomal), arylsulfatase C, isozyme S | steroid sulfatase (microsomal), arylsulfatase C, isozyme S |

Fig. 21

| A | B | C | D | E |
|-----------------|----------|--------------------|--|--|
| 2381 589_at | SRD5A1 | | steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-4-dehydrogenase alpha 1) | steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1) |
| 2382 33369_at | SC4MOL | M32313 A1535653 | sterol-C4-methyl oxidase-like | |
| 2383 33421_s_at | SC5DL | AB016247 | sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like | sterol-C5-desaturase |
| 2384 40419_at | EPB72 | X85116 | stomatin; H.sapiens epb72 gene exon 1. | band 7 integral membrane protein |
| 2385 33322_i_at | SFN | X57348 | stratiffin | stratiffin |
| | | | stress-associated endoplasmic reticulum protein 1; ribosome associated membrane protein 4 | |
| 2386 37035_at | SERP1 | A1557272 | | stromal cell derived factor receptor 1 isoform b; stromal cell derived factor receptor 1 isoform a |
| 2387 35747_at | SDFR1 | AF035287 | stromal cell derived factor receptor 1 | intercrine-alpha |
| 2388 32666_at | SDF1 | U19495 | stromal cell-derived factor 1 | pre-B cell stimulating factor homologue |
| 2389 33834_at | SDF1 | L36033 | stromal cell-derived factor 1 | SDF2 |
| 2390 41627_at | SDF2 | D50645 | stromal cell-derived factor 2 | succinate dehydrogenase flavoprotein subunit |
| 2391 34826_at | SDHA | L21936 | succinate dehydrogenase complex, subunit A, flavoprotein (Fp) | |
| | | | succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD | integral membrane protein CII-3 |
| 2392 34385_at | SDHC | U57877 | succinate dehydrogenase complex, subunit D, integral membrane protein | cytochrome b small subunit of complex II |
| 2393 40467_at | SDHD | AB006202 | succinate-CoA ligase, ADP-forming, beta subunit | ATP-specific succinyl-CoA synthetase beta subunit |
| 2394 40893_at | SUCLA2 | AF058953 | sulfatase FP | KIAA1077 protein |
| 2395 35832_at | KIAA1077 | AB029000 | sulfotransferase family 4A, member 1 | |
| 2396 33712_at | SULT4A1 | N63574 | SUMO-1 activating enzyme subunit 2 | |
| 2397 34814_at | UBA2 | AL041443 | superkiller viralicidic activity 2-like (S. cerevisiae) | helicase-like protein |
| 2398 37998_at | SKIV2L | U09877 | superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult)) | superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult)) |
| 2399 36620_at | SOD1 | X02317 | supervillin | supervillin |
| 2400 40069_at | SVIL | AF051850 | supported by FGENESH | growth hormone releasing hormone |
| 2401 36676_at | GHRF GRF | AL031659 | | |

Fig. 21

| A | B | C | D | E |
|-----------------|----------------|----------|---|---|
| 2402 33297_at | CBF-B HAP2 NF- | AL031778 | supported by GENEWISE, GENSCAN and FGENES | nuclear transcription factor Y, alpha, isoform 1 |
| 2403 34825_at | TTRAP | AL031775 | supported by GENSCAN | TRAF and TNF receptor-associated protein |
| 2404 1640_at | ST13 | U17714 | suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein) | putative tumor suppressor ST13 |
| 2405 37745_s_at | ST5 | U15780 | suppression of tumorigenicity 5 | p82 |
| 2406 37805_at | SRPUL | AF060567 | sushi-repeat protein | sushi-repeat protein |
| 2407 31855_at | SRPX | U61374 | sushi-repeat-containing protein, X chromosome | |
| 2408 31869_at | KIAA0640 | AB014540 | SWAP-70 protein | KIAA0640 protein |
| 2409 40213_at | SMARCA1 | M88163 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 | transcription activator |
| 2410 40961_at | SMARCA2 | X72889 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 | HBRM |
| 2411 32579_at | SMARCA4 | U29175 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 | transcriptional activator |
| 2412 39132_at | SMARCA5 | AB010882 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 | hSNF2H |
| 2413 34753_at | SYBL1 | X92396 | synaptobrevin-like 1 | synaptobrevin-like 1 |
| 2414 41692_at | SYNJ1 | AB020717 | synaptotagmin 1 | KIAA0910 protein |
| 2415 38075_at | SYPL | X68194 | synaptophysin-like protein | synaptophysin-like protein |
| 2416 36452_at | KIAA1029 | AB028952 | synaptopodin | KIAA1029 protein |
| 2417 32178_r_at | SNAP23 | AJ011915 | synaptosomal-associated protein, 23kD | synaptosome associated protein of 23 kilodaltons, isoform A |
| 2418 39757_at | SDC2 | J04621 | syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan) | |
| 2419 32092_at | SDC3 | AB007937 | syndecan 3 (N-syndecan) | KIAA0468 protein |
| 2420 38110_at | SDCBP | AF000652 | syndecan binding protein (syntenin) | syntenin |
| 2421 38685_at | STX12 | AL035306 | syntaxin 12 | hypothetical protein |
| 2422 38381_at | STX3A | U32315 | syntaxin 3A | syntaxin 3 |

Fig. 2

| A | B | C | D | E |
|-----------------|---------------------|----------|--|--|
| 2423 38774_at | STX7 | U77942 | syntaxin 7 | syntaxin 7 |
| 2424 37510_at | STX8 | AF036715 | syntaxin 8 | syntaxin 8 |
| 2425 33942_s_at | STXBP1 | AF004563 | syntaxin binding protein 1 | hUNC18b |
| 2426 37962_r_at | STXBP3 | D63506 | syntaxin binding protein 3 | unc-18homologue |
| 2427 33315_at | | M29204 | Synthetic construct chimeric DNA-binding factor mRNA, complete cds. | chimeric DNA-binding factor |
| 2428 192_at | TAF7 | U18062 | TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55 kD | TFIID subunit TAFII55 |
| 2429 193_at | TAF9 | U21858 | TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32 kD | TAFII32 precursor |
| 2430 37620_at | TAF12; TAF2J; TAF15 | U57693 | TAFII20; contains homology to histone H2B; TFIID subunit; TAFII15; contains homology to histone H2B; TFIID subunit; Human TFIID subunits TAF20 and TAF15 mRNA, complete cds. | TAF20; TAF15 |
| 2431 32166_at | TLN1 | AB028950 | taln 1 | KIAA1027 protein |
| 2432 39765_at | TLN2 | AB002318 | taln 2 | |
| 2433 41168_at | TAPBP | AF029750 | TAP binding protein (tapasin) | tapasin |
| 2434 39779_at | TARBP1 | U38847 | TAR (HIV) RNA binding protein 1 | TAR RNA loop binding protein |
| 2435 32241_at | TARDBP | AL050265 | TAR DNA binding protein | hypothetical protein |
| 2436 39416_at | TIP-1 | U90913 | Tax interaction protein 1 | Tax interaction protein 1 |
| 2437 498_at | TAX1BP1 | U33821 | Tax1 (human T-cell leukemia virus type I) binding protein 1 | tax1-binding protein TXBP151 |
| 2438 35279_at | TAX1BP1 | U33821 | Tax1 (human T-cell leukemia virus type I) binding protein 1 | tax1-binding protein TXBP151 |
| 2439 36702_at | TBX19 | AJ010277 | T-box 19 | TBX19 protein |
| 2440 32196_at | TIP120A | AB020636 | TBP-interacting protein | KIAA0829 protein |
| 2441 34791_at | TCP1 | X52882 | t-complex 1 | t-complex 1 |
| 2442 36921_at | TCTE1L | U02556 | t-complex-associated-testis-expressed 1-like | t-complex-associated-testis-expressed 1-like |
| 2443 946_at | TCTEL1 | D50663 | t-complex-associated-testis-expressed 1-like 1 | t-complex-associated-testis-expressed 1-like 1 |

Fig. 21

| A | B | C | D | E |
|-----------------|--------------------------|----------|---|--|
| 2444 38374_at | TIEG; EGRA; KLF AF050110 | | TEIG; EGRA; Homo sapiens TGFb inducible early protein and early growth response protein alpha genes, complete cds. | TGFb inducible early protein; early growth response protein alpha |
| 2445 32255_i_at | TERF1 | U40705 | telomeric repeat binding factor (NIMA-interacting) 1 | telomeric repeat binding factor 1, isoform 2; telomeric repeat binding factor 1, isoform 1 |
| 2446 32134_at | TES | AL050162 | testis derived transcript (3 LIM domains) | hypothetical protein |
| 2447 33988_at | TEGT | X75861 | testis enhanced gene transcript (BAX inhibitor 1) | testis enhanced gene transcript (BAX inhibitor 1) |
| 2448 32080_at | TETRA | L11669 | tetracycline transporter-like protein | tetracycline transporter-like protein |
| 2449 38612_at | TSPAN-3 | M69023 | tetraspan 3 | |
| 2450 37321_at | TTC1 | U46570 | tetratricopeptide repeat domain 1 | tetratricopeptide repeat protein |
| 2451 39065_s_at | TTC3 | D83077 | tetratricopeptide repeat domain 3 | TPRD |
| 2452 224_at | TIEG | S81439 | TGFB inducible early growth response | zinc finger transcription factor |
| 2453 38805_at | TGIF | X89750 | TGFB-induced factor (TALE family homeobox) | TGIF protein |
| | | | The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds. | growth factor-binding protein-3 precursor |
| 2454 37319_at | IGFBP3 | M35878 | The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds. | growth factor-binding protein-3 precursor |
| 2455 1586_at | IGFBP3 | M35878 | | growth factor-binding protein-3 precursor |

Fig. 21

| A | B | C | D | E |
|-----------------|------------------|----------|--|--|
| | | | The first in-frame ATG codon is located at nucleotides 17-19, followed by a second ATG codon 52 codons downstream. And the second ATG codon is potential initiation point for translation of NPPase.; Human mRNA for nucleotide pyrophosphatase, complete cds. | NPPase |
| 2456 342_at | ENPP1; M6S1; NPP | D12485 | thioredoxin | |
| 2457 36992_at | TXN | AI653621 | thioredoxin domain-containing | hypothetical protein |
| 2458 34768_at | TXNDC | AL080080 | | |
| 2459 31508_at | TXNIP | S73591 | thioredoxin interacting protein | brain-expressed HHCPA78 homolog VDUP1 |
| 2460 39425_at | TXNRD1 | X91247 | thioredoxin reductase 1 | thioredoxin reductase (NADPH) |
| 2461 32214_at | TXNL | AF003938 | thioredoxin-like, 32kD | thioredoxin-like protein |
| 2462 38473_at | TARS | M63180 | threonyl-tRNA synthetase | threonyl-tRNA synthetase |
| 2463 659_g_at | THBS2 | L12350 | thrombospondin 2 | thrombospondin 2 |
| 2464 658_at | THBS2 | L12350 | thrombospondin 2 | thrombospondin 2 |
| 2465 40865_at | TDG | U51166 | thymine-DNA glycosylase | G/T mismatch-specific thymine DNA glycosylase |
| 2466 31557_at | TMSB4X | M17733 | thymosin, beta 4, X chromosome | thymosin, beta 4 |
| 2467 32654_g_at | SMAP | AW020536 | thyroid hormone receptor coactivating protein | |
| 2468 39699_at | TRIP12 | D28476 | thyroid hormone receptor interactor 12 | thyroid hormone receptor interactor 12 |
| 2469 41251_at | TRIP3 | L40410 | thyroid hormone receptor interactor 3 | thyroid receptor interactor |
| 2470 39341_at | TRIP6 | AJ001902 | thyroid hormone receptor interactor 6 | TRIP6 |
| 2471 37348_s_at | TRIP7 | AA845349 | thyroid hormone receptor interactor 7 | |
| 2472 41625_at | TRAP240 | AB011165 | thyroid hormone receptor-associated protein, 240 kDa subunit | KIAA0593 protein |
| 2473 34323_at | TRIP15 | AF084260 | thyroid receptor interacting protein 15 | signalosome subunit 2 |
| 2474 33852_at | TIA1 | M77142 | TIA1 cytotoxic granule-associated RNA binding protein | TIA1 protein, isoform 1; TIA1 protein, isoform 2 |
| 2475 41763_g_at | TIAL1 | D64015 | TIA1 cytotoxic granule-associated RNA binding protein-like 1 | T-cluster binding protein |
| 2476 36655_at | TJP2 | L27476 | tight junction protein 2 (zona occludens 2) | tight junction protein 2 (zona occludens 2) |
| 2477 37801_at | TJ6 | AF112972 | TJ6 protein | TJ6 |

Fig-21

| A | B | C | D | E |
|----------------|----------|----------|--|---|
| 2478 35238_at | TRAF5 | AB000509 | TNF receptor-associated factor 5 | TRAF5 |
| 2479 33243_at | GG2-1 | AF099935 | TNF-induced protein | MDC-3.13 isoform 2 |
| 2480 40310_at | TLR2 | AF051152 | toll-like receptor 2 | Toll/interleukin-1 receptor-like protein 4 |
| 2481 1030_s_at | TOP1 | U07806 | topoisomerase (DNA) I | DNA topoisomerase I |
| 2482 36571_at | TOP2B | X68060 | topoisomerase (DNA) II beta (180kD) | DNA topoisomerase II |
| 2483 32233_at | TOR1B | AF007872 | torsin family 1, member B (torsin B) | torsinB |
| 2484 32219_at | TLK1 | D50927 | tousled-like kinase 1 | KIAA0137 protein |
| 2485 35321_at | TLK2 | AB004884 | tousled-like kinase 2 | PKU-alpha |
| 2486 39742_at | TANK | U59863 | TRAF family member-associated NFKB activator | I-TRAF |
| 2487 40051_at | KIAA0057 | D31762 | TRAM-like protein | TRAM-like protein |
| 2488 1073_at | TCEA1 | M81601 | transcription elongation factor A (SII), 1 | transcription elongation factor SII |
| 2489 38317_at | TCEAL1 | M99701 | transcription elongation factor A (SII)-like 1 | transcription elongation factor A (SII)-like 1 |
| 2490 1399_at | TCEB1 | L34587 | transcription elongation factor B (SIII), polypeptide 1 (15kD, elongin C) | RNA polymerase II elongation factor SIII, p15 subunit |
| 2491 41759_at | TCEB1L | Z47087 | transcription elongation factor B (SIII), polypeptide 1-like | RNA polymerase II elongation factor-like protein |
| 2492 39426_at | TCERG1 | AF017789 | transcription elongation regulator 1 (CA150) | putative transcription factor CA150 |
| 2493 33348_at | TCF12 | M80627 | transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) | helix-loop-helix protein |
| 2494 1373_at | TCF3 | M31523 | transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47) | |
| 2495 33440_at | TCF8 | U19969 | transcription factor 8 (represses interleukin 2 expression) | ZEB |
| 2496 39638_at | TFAP4 | S73885 | transcription factor AP-4 (activating enhancer binding protein 4) | AP-4 |
| 2497 37757_at | TFDP1 | L23959 | transcription factor Dp-1 | E2F-related transcription factor |
| 2498 32578_at | TCFL4 | AW005997 | transcription factor-like 4 | |
| 2499 35614_at | TCFL5 | AB012124 | transcription factor-like 5 (basic helix-loop-helix) | transcription factor-like 5 |
| 2500 35749_at | TADA3L | AF069733 | transcriptional adaptor 3-like | ADA3-like protein |

Fig. 21

| | A | B | C | D | E |
|------|------------|-----------|----------|--|---|
| 2501 | 35297_at | GGA2 VEAR | AC002400 | Transcriptional coactivator P15 like | KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2 |
| 2502 | 33876_at | TAZ | AL050107 | transcriptional co-activator with PDZ-binding motif (TAZ) | hypothetical protein |
| 2503 | 39358_at | SMRT | U37146 | transcriptional co-repressor; Human silencing mediator of retinoid and thyroid hormone action (SMRT) mRNA, complete cds. | silencing mediator of retinoid and thyroid hormone action |
| 2504 | 37312_at | TRIP-Br2 | D50917 | transcriptional regulator interacting with the PHS-bromodomain 2 | KIAA0127 gene product |
| 2505 | 40631_at | TOB1 | D38305 | transducer of ERBB2, 1 | Tob |
| 2506 | 32554_s_at | TBL1 | Y12781 | transducin (beta)-like 1 | transducin (beta) like 1 protein |
| 2507 | 37324_at | TFRC | X01060 | transferrin receptor (p90, CD71) | transferrin receptor (p90, CD71) |
| 2508 | 39344_at | HSU53209 | U53209 | transformer-2 alpha (hira-2 alpha) | transformer-2 alpha |
| 2509 | 39032_at | TSC22 | AJ222700 | transforming growth factor beta-stimulated protein TSC-22 | TSC-22 |
| 2510 | 41445_at | TGFB1 | X02812 | transforming growth factor, beta 1 (Camurati-Engelmann disease) | transforming growth factor, beta 1 (Camurati-Engelmann disease) |
| 2511 | 1815_g_at | TGFBR2 | D50683 | transforming growth factor, beta receptor II (70-80kD) | TGF-betaIIIR alpha |
| 2512 | 1814_at | TGFBR2 | D50683 | transforming growth factor, beta receptor II (70-80kD) | TGF-betaIIIR alpha |
| 2513 | 1385_at | TGFB1 | M77349 | transforming growth factor, beta-induced, 68kD | transforming growth factor induced protein |
| 2514 | 40841_at | TACC1 | AF049910 | transforming, acidic coiled-coil containing protein 1 | TACC1 |
| 2515 | 38816_at | TACC2 | AF095791 | transforming, acidic coiled-coil containing protein 2 | TACC2 protein |
| 2516 | 36931_at | TAGLN | M95787 | transgelin | smooth muscle protein |
| 2517 | 36678_at | TAGLN2 | D21261 | transgelin 2 | transgelin 2 |
| 2518 | 31829_r_at | TGOLN2 | AF027515 | trans-golgi network protein 2 | hTGN48 |
| 2519 | 39124_r_at | TRPC1 | X89066 | transient receptor potential cation channel, subfamily C, member 1 | TRPC1 protein |
| 2520 | 39123_s_at | TRPC1 | X89066 | transient receptor potential cation channel, subfamily C, member 1 | TRPC1 protein |

Fig. 21

| A | B | C | D | E |
|-----------------|---------------|----------|--|---|
| 2525 41051_at | TSNAX | X95073 | translin-associated factor X | Translin associated protein X |
| 2526 32831_at | TIMM17A | AA453183 | translocase of inner mitochondrial membrane 17 homolog A (yeast) | |
| 2527 36198_at | TOMM20-PENDIN | D13641 | translocase of outer mitochondrial membrane 20 (yeast) homolog | mitochondrial outer membrane protein 19 |
| 2528 37050_r_at | TOMM34 | AI130910 | translocase of outer mitochondrial membrane 34 | |
| 2529 32853_at | TOMM70A | AB018262 | translocase of outer mitochondrial membrane 70 homolog A (yeast) | KIAA0719 protein |
| 2530 34796_at | TRAM | X63679 | translocating chain-associating membrane protein | TRAM protein |
| 2531 38100_at | TLOC1 | D87127 | translocation protein 1 | translocation protein-1 |
| 2532 950_at | TLOC1 | D87127 | translocation protein 1 | translocation protein-1 |
| 2533 41531_at | TM4SF1 | AI445461 | transmembrane 4 superfamily member 1 | |
| 2534 39362_r_at | TM4SF6 | AF043906 | transmembrane 4 superfamily member 6 | T245 protein |
| 2535 32083_at | TM7SF1 | AF027826 | transmembrane 7 superfamily member 1 (upregulated in kidney) | putative seven pass transmembrane protein |
| 2536 38835_at | TM9SF1 | U94831 | transmembrane 9 superfamily member 1 | multispanning membrane protein |
| 2537 34307_at | TM9SF2 | U81006 | transmembrane 9 superfamily member 2 | p76 |
| 2538 37955_at | TMEM4 | AB015631 | transmembrane protein 4 | type II membrane protein |
| 2539 37445_at | TMEM5 | AB015633 | transmembrane protein 5 | type II membrane protein |
| 2540 36128_at | TMP21 | L40397 | transmembrane trafficking protein | |
| 2541 38982_at | RAP1 | W28865 | TRF2-interacting telomeric RAP1 protein | |
| 2542 39382_at | TRIM2 | AB011089 | tripartite motif-containing 2 | KIAA0517 protein |
| 2543 36825_at | TRIM22 | X82200 | tripartite motif-containing 22 | gpStat50 |
| 2544 38537_at | TRIM32 | U18543 | tripartite motif-containing 32 | zinc-finger protein |
| 2545 32635_at | TRIM33 | AB029036 | tripartite motif-containing 33 | KIAA1113 protein |
| 2546 33107_at | TRIM37 | AB020705 | tripartite motif-containing 37 | KIAA0898 protein |
| 2547 40461_at | TIX1 | AB007855 | triple homeobox 1 | |
| 2548 36791_g_at | TPM1 | M19267 | tropomyosin 1 (alpha) | tropomyosin 1 (alpha) |
| 2549 36790_at | TPM1 | M19267 | tropomyosin 1 (alpha) | tropomyosin 1 (alpha) |

Fig-21

| A | B | C | D | E |
|---------------|-------|----------|---|--|
| | | | <p>RETICULUM ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN) (VCP); Human homolog of spIQ01853TERA_MOUSE TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN) (VCP) pirlS25197 transitional endoplasmic reticulum ATPase - mouse gil55217 (Z14044) murine valosin-containing protein; 99% identical to mouse, rat, and pig homologs; X-ray cross-complementing gene 9; Putative DNA repair protein; Hypothetical 96.6 kDa putative membrane protein; Most similar to hypothetical proteins in fission and budding yeast, and C. elegans: (AB004539) ORF YLL031c [Schizosaccharomyces pombe] producing hypothetical protein (AL021766) [Schizosaccharomyces pombe]; probable membrane protein YLL031c - yeast (Saccharomyces cerevisiae) gnllPIDe245463 (Z73136) ORF YLL031c [Saccharomyces cerevisiae]; (AF003137) C27A12.9 [Caenorhabditis elegans]; Hypothetical 38.8 kDa putative membrane protein; Most similar to hypothetical proteins: PIDe276130 (Z81072) F30A10.5 [Caenorhabditis elegans]; spIP72655IYB28 translation factor sul1 homolog translation initiation factor IF2</p> | <p>TERA_HUMAN; XRCC9; P1.11659_3; P1.11659_4; P1.11659_5 GC20 protein KIAA0741 protein</p> |
| 2521 34380_at | XRCC9 | AC004472 | | |
| 2522 33351_at | GC20 | AF064607 | | |
| 2523 40537_at | IF2 | AB018284 | | |
| 2524 32173_at | UK114 | X95384 | translational inhibitor protein p14.5 | 14.5 kDa translational inhibitor protein, p14.5 |

Fig. 21

| A | B | C | D | E |
|-----------------|-----------|----------|--|--------------------------------------|
| 2550 36792_at | TPM1 | Z24727 | tropomyosin 1 (alpha) | tropomyosin isoform |
| 2551 32313_at | TPM2 | M12125 | tropomyosin 2 (beta) | tropomyosin 2 (beta) |
| 2552 32777_at | WRB | Y12478 | tryptophan rich basic protein | congenital heart disease 5 protein |
| 2553 38121_at | WARS | X59892 | tryptophanyl-tRNA synthetase | 471 aa polypeptide (gamma2) |
| 2554 39867_at | TUFM | S75463 | Tu translation elongation factor, mitochondrial | P43 |
| 2555 31944_at | TULP3 | AI028290 | tubby like protein 3 | |
| 2556 32272_at | K-ALPHA-1 | K00558 | tubulin, alpha, ubiquitous | tubulin, alpha, ubiquitous |
| 2557 39332_at | TUBB | AF035316 | tubulin, beta polypeptide | |
| 2558 39331_at | TUBB | X79535 | tubulin, beta polypeptide | beta tubulin |
| 2559 33346_r_at | TUBG1 | M61764 | tubulin, gamma 1 | gamma-tubulin |
| 2560 36176_at | TBCC | U61234 | tubulin-specific chaperone c | cofactor C |
| 2561 35159_at | TBCE | U61232 | tubulin-specific chaperone e | cofactor E |
| 2562 37007_at | TDE1 | U49188 | tumor differentially expressed 1 | tumor differentially expressed 1 |
| 2563 34892_at | TNFRSF10B | AF016266 | tumor necrosis factor receptor superfamily, member 10b | TRAIL receptor 2 |
| 2564 41190_at | TNFRSF12 | U83598 | tumor necrosis factor receptor superfamily, member 12 (translocating chain-association membrane protein) | death domain receptor 3 soluble form |
| 2565 1563_s_at | TNFRSF1A | M58286 | tumor necrosis factor receptor superfamily, member 1A | tumor necrosis factor receptor |
| 2566 35150_at | TNFRSF5 | X60592 | tumor necrosis factor receptor superfamily, member 5 | CDw40 |
| 2567 37643_at | TNFRSF6 | X63717 | tumor necrosis factor receptor superfamily, member 6 | APO-1 cell surface antigen precursor |
| 2568 36988_at | TNFAIP1 | M80783 | tumor necrosis factor, alpha-induced protein 1 (endothelial) | B12 protein |
| 2569 38631_at | TNFAIP2 | M92357 | tumor necrosis factor, alpha-induced protein 2 | B94 protein |
| 2570 595_at | TNFAIP3 | M59465 | tumor necrosis factor, alpha-induced protein 3 | A20 |
| 2571 40076_at | TPD52L2 | AF004430 | tumor protein D52-like 2 | hD54+ins2 isoform |
| 2572 1711_at | TP53BP1 | U09477 | tumor protein p53 binding protein, 1 | p53-binding protein |
| 2573 34822_at | TP53BP2 | U58334 | tumor protein p53 binding protein, 2 | Bbp/53BP2 |
| 2574 38568_at | TP53BP1 | U82939 | tumor protein p53-binding protein | p53 binding protein |

Fig-21

| A | B | C | D | E |
|-----------------|--------|----------|---|--|
| 2575 31584_at | TPT1 | X16064 | tumor protein, translationally-controlled 1 | tumor protein, translationally-controlled 1 |
| 2576 31888_s_at | TSSC3 | AF001294 | tumor suppressing subtransferable candidate 3 | IPL |
| 2577 147_at | TSG101 | U82130 | tumor susceptibility gene 101 | tumor susceptibility protein |
| 2578 40328_at | TWIST | X99268 | twist homolog (acrocephalosyndactyl 3; Saethre-Chotzen syndrome) (Drosophila) | B-HLH DNA binding protein |
| 2579 2086_s_at | TYRO3 | D17517 | TYRO3 protein tyrosine kinase | Sky |
| 2580 35246_at | TYRO3 | U18934 | TYRO3 protein tyrosine kinase | receptor tyrosine kinase |
| 2581 32324_at | YWHAB | X57346 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide |
| 2582 409_at | YWHAQ | X56468 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide | 14.3.3 protein |
| 2583 32530_at | YWHAQ | X56468 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide | 14.3.3 protein |
| 2584 1235_at | YWHAZ | M86400 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide | phospholipase A2 |
| 2585 32718_at | TPST1 | AF038009 | tyrosylprotein sulfotransferase 1 | tyrosylprotein sulfotransferase-1 |
| 2586 35172_at | TPST2 | AF049891 | tyrosylprotein sulfotransferase 2 | tyrosylprotein sulfotransferase-2 |
| 2587 38977_at | YARS | U89436 | tyrosyl-tRNA synthetase | tyrosyl-tRNA synthetase |
| 2588 36517_at | U2AF1 | M96982 | U2(RNU2) small nuclear RNA auxiliary factor 1 | U2 snRNP auxiliary factor small subunit |
| 2589 32858_at | UBN1 | A1341565 | ubiquitin 1 | ubiquitin 2 |
| 2590 34824_at | UBQLN2 | AB015344 | ubiquitin 2 | ubiquitin 2 |
| 2591 38451_at | UQCR | T58471 | ubiquinol-cytochrome c reductase (6.4kD) subunit | |
| 2592 39427_at | UQCRB | T79616 | ubiquinol-cytochrome c reductase binding protein | |
| 2593 40854_at | UQCRC2 | J04973 | ubiquinol-cytochrome c reductase core protein II | ubiquinol-cytochrome c reductase core protein II |

Fig-21

| A | B | C | D | E |
|----------------|--------|----------|---|--|
| 2594 36104_at | UQCRH | AA526497 | ubiquinol-cytochrome c reductase hinge protein | |
| 2595 1366_i_at | UBC | M26880 | ubiquitin C | ubiquitin C |
| 2596 1367_f_at | UBC | M26880 | ubiquitin C | ubiquitin C |
| 2597 36990_at | UCHL1 | X04741 | ubiquitin carboxyl-terminal esterase L1 (ubiquitin thioesterase) | ubiquitin carboxyl-terminal esterase L1 (ubiquitin thioesterase) |
| 2598 811_at | UFD1L | U64444 | ubiquitin fusion degradation 1-like | ubiquitin fusion-degradation 1 like protein |
| 2599 40623_at | UBE3B | A1749193 | ubiquitin protein ligase | |
| | | | ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) | E6-associated protein E6-AP/ubiquitin-protein ligase |
| 2600 41205_at | UBE3A | U84404 | | ubiquitin specific protease |
| 2601 34383_at | USP1 | AB014458 | ubiquitin specific protease 1 | |
| 2602 37683_at | USP10 | D80012 | ubiquitin specific protease 10 | |
| 2603 162_at | USP11 | U44839 | ubiquitin specific protease 11 | UHX1 protein |
| 2604 36982_at | USP14 | U30888 | ubiquitin specific protease 14 (tRNA-guanine transglycosylase) | tRNA-Guanine Transglycosylase |
| 2605 39866_at | USP22 | AB028986 | ubiquitin specific protease 22 | KIAA1063 protein |
| 2606 35847_at | USP24 | AB028980 | ubiquitin specific protease 24 | KIAA1057 protein |
| 2607 1357_at | USP4 | U20657 | ubiquitin specific protease 4 (proto-oncogene) | ubiquitin protease |
| 2608 34405_at | USP5 | U47927 | ubiquitin specific protease 5 (isopeptidase T) | isopeptidase T |
| 2609 37672_at | USP7 | Z72499 | ubiquitin specific protease 7 (herpes virus-associated) | herpesvirus associated ubiquitin-specific protease (HAUSP) |
| 2610 39794_at | USP8 | D29956 | ubiquitin specific protease 8 | ubiquitin specific protease 8 |
| 2611 32572_at | USP9X | X98296 | ubiquitin specific protease 9, X chromosome (fat facets-like Drosophila) | ubiquitin hydrolase |
| 2612 40066_at | UBE1C | AF046024 | ubiquitin-activating enzyme E1C (UBA3 homolog, yeast) | UBA3 |
| 2613 36579_at | UBE4A | D50916 | ubiquitination factor E4A (UFD2 homolog, yeast) | ubiquitination factor E4A (UFD2 homolog, yeast) |
| 2614 41339_at | UBE4B | AF043117 | ubiquitination factor E4B (UFD2 homolog, yeast) | ubiquitin-fusion degradation protein 2 |
| 2615 36959_at | UBE2V1 | U49278 | ubiquitin-conjugating enzyme E2 variant 1 | UEV-1 |

Fig. 21

| A | B | C | D | E |
|-----------------|---------|----------|--|---|
| 2616 890_at | UBE2A | M74524 | ubiquitin-conjugating enzyme E2A (RAD6 homolog) | ubiquitin-conjugating enzyme E2A (RAD6 homolog) |
| 2617 37826_at | UBE2D1 | AF020761 | ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast) | |
| 2618 38705_at | UBE2D2 | AI310002 | ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast) | |
| 2619 832_at | UBE2D2 | U39317 | ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast) | UbcH5B |
| 2620 39083_at | UBE2D3 | U39318 | ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast) | UbcH5C |
| 2621 504_at | UBE2D3 | U39318 | ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast) | UbcH5C |
| 2622 34850_at | UBE2E3 | AB017644 | ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) | ubiquitin-conjugating enzyme E2 |
| 2623 32236_at | UBE2G2 | AF032456 | ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast) | ubiquitin conjugating enzyme G2 |
| 2624 38480_s_at | UBE2I | U66867 | ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast) | ubiquitin conjugating enzyme 9 |
| 2625 838_s_at | UBE2I | U45328 | ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast) | ubiquitin-conjugating enzyme |
| 2626 223_at | UBE2L3 | S81003 | ubiquitin-conjugating enzyme E2L 3 | L-UBC |
| 2627 40505_at | UBE2L6 | AA883502 | ubiquitin-conjugating enzyme E2L 6 | |
| 2628 36604_at | UBE2N | D83004 | ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast) | ubiquitin-conjugating enzyme E2 Ubch-ben |
| 2629 457_s_at | UBL1 | U67122 | ubiquitin-like 1 (septrin) | SUMO-1 |
| 2630 155_s_at | UBL1 | U61397 | ubiquitin-like 1 (septrin) | ubiquitin-homology domain protein PIC1 |
| 2631 40839_at | UBL3 | AL080177 | ubiquitin-like 3 | hypothetical protein |
| 2632 37336_at | UBXD2 | D87684 | UBX domain-containing 2 | KIAA0242 protein |
| 2633 40960_at | B4GALT1 | D29805 | UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1 | beta-1,4-galactosyltransferase |
| 2634 34177_at | B4GALT2 | AF038660 | UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 2 | beta-1,4-galactosyltransferase |
| 2635 39445_at | B4GALT3 | AF038661 | UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3 | beta-1,4-galactosyltransferase |
| 2636 40215_at | UGCG | D50840 | UDP-glucose ceramide glucosyltransferase | ceramide glucosyltransferase |

fig. 21

| A | B | C | D | E |
|-----------------|------------|----------|--|--|
| 2637 35214_at | UGDH | AF061016 | UDP-glucose dehydrogenase | UDP-glucose dehydrogenase |
| 2638 37373_at | UGP2 | U27460 | UDP-glucose pyrophosphorylase 2 | uridine diphosphoglucose pyrophosphorylase |
| 2639 38041_at | GALNT1 | U41514 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) | UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase |
| 2640 36515_at | GNE | AJ238764 | UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase | UDP-N-acetylglucosamine-2-epimerase / N-acetylmannosamine kinase |
| 2641 41242_at | UAP1 | AB011004 | UDP-N-acetylglucosamine pyrophosphorylase 1 | UDP-N-acetylglucosamine pyrophosphorylase |
| 2642 34827_at | ULK1 | AF045458 | unc-51-like kinase 1 (C. elegans) | serine/threonine kinase ULK1 |
| 2643 37315_f_at | BM036 | AI057607 | uncharacterized bone marrow protein BM036 | |
| 2644 35750_at | HT010 | AL049948 | uncharacterized hypothalamus protein HT010 | |
| 2645 41058_g_at | HT012 | AI760162 | uncharacterized hypothalamus protein HT012 | |
| 2646 41057_at | HT012 | AI760162 | uncharacterized hypothalamus protein HT012 | |
| 2647 38610_s_at | KRT10; KPP | X14487 | unnamed protein product; Human gene for acidic (type I) cytokeratin 10. | keratin 10 |
| 2648 34402_at | UNRIP | AB024327 | unr-interacting protein | WD-40 repeat protein |
| 2649 34372_at | UREB1 | AB002310 | upstream regulatory element binding protein 1 | upstream regulatory element binding protein 1 |
| 2650 37686_s_at | UNG | Y09008 | uracil-DNA glycosylase | uracil-DNA glycosylase |
| 2651 33815_at | UMPS | J03626 | uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) | uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) |
| 2652 41859_at | UST | AB020316 | uronyl-2-sulfotransferase | dermatan/chondroitin sulfate 2-sulfotransferase |
| 2653 39429_at | UVRAG | X99050 | UV Radiation Resistance Associated Gene; H.sapiens mRNA; UV Radiation Resistance Associated Gene. | p63 (processed form) |

Fig-21

| A | B | C | D | E |
|-----------------|----------------|----------|---|--|
| | | | v-abl Abelson murine leukemia viral oncogene homolog 1 | v-abl Abelson murine leukemia viral oncogene homolog 1 isoform a; v-abl Abelson murine leukemia viral oncogene homolog 1 isoform b |
| 2654 39730_at | ABL1 | X16416 | | |
| 2655 35779_at | VPS45A | AJ133421 | vacuolar protein sorting 45A (yeast) | vacuolar protein sorting |
| 2656 38801_at | VAPA | AI742846 | VAMP (vesicle-associated membrane protein)-associated protein A (33kD) | |
| | | | | vascular cell adhesion molecule 1, isoform a precursor; vascular cell adhesion molecule 1, isoform b precursor |
| 2657 583_s_at | VCAM1 | M30257 | vascular cell adhesion molecule 1 | |
| 2658 1953_at | VEGF | AF024710 | vascular endothelial growth factor | vascular endothelial growth factor |
| 2659 36100_at | VEGF | AF022375 | vascular endothelial growth factor | vascular endothelial growth factor |
| | | | | VEGF related factor isoform VRF186 |
| 2660 37268_at | VEGFB | U43368 | vascular endothelial growth factor B | precursor |
| 2661 159_at | VEGFC | U43142 | vascular endothelial growth factor C | vascular endothelial growth factor related protein |
| | | | VDAC protein; similar to mouse VDAC 3; Homo sapiens voltage dependent anion channel protein mRNA, complete cds. | voltage dependent anion channel protein |
| 2662 36102_at | VDAC3; HD-VDAC | AF038962 | | vesicle amine transport protein 1 |
| 2663 40147_at | VATI | U18009 | vesicle amine transport protein 1 | KIAA0917 protein |
| 2664 33930_at | RA410 | AB020724 | vesicle transport-related protein | |
| | | | vesicle-associated membrane protein 2 (synaptobrevin 2) | |
| 2665 32254_at | VAMP2 | AL050223 | vesicle-associated membrane protein 3 (cellubrevin) | |
| 2666 35783_at | VAMP3 | H93123 | villin 2 (ezrin) | villin 2 |
| 2667 40103_at | VIL2 | X51521 | vimentin | vimentin |
| 2668 34091_s_at | VIM | Z19554 | vinculin | vinculin isoform VCL; VCL isoform meta-VCL |
| 2669 36601_at | VCL | M33308 | vitamin A responsive; cytoskeleton related | JWA protein |
| 2670 39091_at | JWA | AF070523 | vitamin D (1,25-dihydroxyvitamin D3) receptor | vitamin D (1,25-dihydroxyvitamin D3) receptor |
| 2671 1388_g_at | VDR | J03258 | v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog | K-ras oncogene protein |
| 2672 1940_at | KRAS2 | M54968 | | |

fig-21

| A | B | C | D | E |
|-----------------|-------|----------|---|--|
| 2673 41504_s_at | MAF | AF055376 | v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) | short form transcription factor C-MAF |
| 2674 32835_at | MAFF | AA725102 | v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian) | |
| 2675 40198_at | VDAC1 | L06132 | voltage-dependent anion channel 1 | voltage-dependent anion channel |
| 2676 37696_at | VDAC2 | L06328 | voltage-dependent anion channel 2 | voltage-dependent anion channel |
| 2677 171_at | GBP1 | U56833 | von Hippel-Lindau binding protein 1 | VHL binding protein-1 |
| 2678 38743_f_at | RAF1 | X06409 | v-raf-1 murine leukemia viral oncogene homolog 1 | |
| 2679 32776_at | RALB | M35416 | v-raf simian leukemia viral oncogene homolog B (ras related; GTP binding protein) | v-raf simian leukemia viral oncogene homolog B |
| 2680 36645_at | RELA | L19067 | v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian) | NF-kappa-B transcription factor subunit |
| 2681 1295_at | RELA | L19067 | v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian) | NF-kappa-B transcription factor subunit |
| 2682 1674_at | YES1 | M15990 | v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 | v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 |
| 2683 1402_at | LYN | M16038 | v-yes-1 Yamaguchi sarcoma viral related oncogene homolog | v-yes-1 Yamaguchi sarcoma viral related oncogene homolog |
| 2684 1058_at | WASF3 | S69790 | WAS protein family, member 3 | |
| 2685 38736_at | WDR1 | AL050108 | WD repeat domain 1 | hypothetical protein |
| 2686 41430_at | WDR7 | AB011113 | WD repeat domain 7 | KIAA0541 protein |
| 2687 36009_at | CL683 | AF091092 | weakly similar to glutathione peroxidase 2 | weakly similar to glutathione peroxidase 2 |
| 2688 36909_at | WEE1 | X62048 | WEE1+ homolog (S. pombe) | wee1 tyrosine kinase |
| 2689 41212_r_at | WBSR1 | D26068 | Williams-Beuren syndrome chromosome region 1 | eukaryotic translation initiation factor 4H, isoform 1; eukaryotic translation initiation factor 4H, isoform 2 |
| 2690 41635_at | WTAP | D14661 | Wilms' tumour 1-associating protein | Wilms' tumour 1-associating protein |
| 2691 31862_at | WNT5A | L20861 | wingless-type MMTV integration site family, member 5A | wingless-type MMTV integration site family, member 5A precursor |

Fig-21

| A | B | C | D | E |
|-----------------|----------|----------|--|--|
| 2692 34225_at | WHSC2 | AF101434 | Wolf-Hirschhorn syndrome candidate 2 | Wolf-Hirschhorn syndrome candidate 2 protein |
| 2693 33438_at | WBP2 | AL049981 | WW domain binding protein 2 | |
| 2694 35213_at | WBP4 | AF071185 | WW domain binding protein 4 (formin binding protein 21) | formin binding protein 21 |
| 2695 39995_s_at | WWOX | U13395 | WW domain containing oxidoreductase | oxidoreductase |
| 2696 36822_at | WAC | U51334 | WW domain-containing adapter with a coiled-coil region | putative RNA binding protein RBP56 |
| 2697 1307_at | XPA | D14533 | xeroderma pigmentosum, complementation group A | XPAC protein |
| 2698 1873_at | XPC | D21089 | xeroderma pigmentosum, complementation group C | XP-C repair complementing protein (p125) |
| 2699 41756_at | NTPBP | AJ010842 | XPA binding protein 1; putative ATP(GTP)-binding protein | ATP(GTP)-binding protein |
| 2700 38733_at | XRCC5 | M30938 | X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kD) | ATP-dependant DNA helicase II |
| 2701 585_at | XRCC5 | M30938 | X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kD) | ATP-dependant DNA helicase II |
| 2702 2093_s_at | XRCC5 | J04977 | X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kD) | ATP-dependant DNA helicase II |
| 2703 35827_at | KIAA0905 | AB020712 | yeast Sec31p homolog | KIAA0905 protein |
| 2704 40988_at | YME1L1 | AJ132637 | YME1-like 1 (S. cerevisiae) | ATP-dependent metalloprotease YME1L |
| 2705 891_at | YY1 | M77698 | YY1 transcription factor | GLI-Krupple related protein |
| 2706 34887_at | | N92548 | zb29g04.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305046 3', mRNA sequence. | |
| 2707 36308_at | ZIC1 | D76435 | Zic family member 1 (odd-paired homolog, Drosophila) | Zic protein |
| 2708 35681_r_at | ZFX1B | AB011141 | zinc finger homeobox 1b | KIAA0569 protein |

fig. 21

| A | B | C | D | E |
|-----------------|------------|---------------|---|---|
| 2709 34786_at | TSGA | AB018285 | zinc finger protein | KIAA0742 protein |
| 2710 39977_at | ZNF-U69274 | U69274 | zinc finger protein | zinc finger protein |
| 2711 40140_at | ZFP103 | D76444 | zinc finger protein 103 homolog (mouse) | zinc finger protein 103 homolog |
| 2712 36295_at | ZNF134 | U09412 | zinc finger protein 134 (clone pHZ-15) | zinc finger protein ZNF134 |
| 2713 32192_g_at | ZNF144 | D13969 | zinc finger protein 144 (Mel-18) | Mel-18 protein |
| 2714 36928_at | ZNF146 | X70394 | zinc finger protein 146 | zinc finger protein |
| 2715 41532_at | ZNF151 | Y09723 | zinc finger protein 151 (pHZ-67) | Miz-1 protein |
| 2716 32628_at | ZNF161 | D28118 | zinc finger protein 161 | DB1 |
| 2717 41436_at | ZNF198 | AJ224901 | zinc finger protein 198 | ZNF198 protein |
| 2718 40724_at | ZNF200 | Y14443 | zinc finger protein 200 | zinc finger protein |
| 2719 35368_at | ZNF207 | AF046001 | zinc finger protein 207 | zinc finger protein 207 |
| 2720 41542_at | ZNF216 | AF062346 | zinc finger protein 216 | zinc finger protein 216 splice variant 1 |
| 2721 840_at | ZNF220 | U47742 | zinc finger protein 220 | monocytic leukaemia zinc finger protein |
| 2722 39762_at | ZNF262 | AB007885 | zinc finger protein 262 | zinc finger protein 262 |
| 2723 34299_at | ZNF278 | AL096880 | zinc finger protein 278 | hypothetical protein |
| 2724 39005_s_at | ZNF294 | AB018257 | zinc finger protein 294 | KIAA0714 protein |
| 2725 37860_at | ZNF337 | AL049942 | zinc finger protein 337 | hypothetical protein |
| 2726 40448_at | ZFP36 | M92843 | zinc finger protein 36, C3H type, homolog (mouse) | zinc finger transcriptional regulator |
| 2727 38740_at | ZFP36L1 | X79067 | zinc finger protein 36, C3H type-like 1 | butyrate response factor 1 |
| 2728 36046_at | ZNF363 | AL050144 | zinc finger protein 363 | hypothetical protein |
| 2729 32129_at | ZNF364 | AL079314 | zinc finger protein 364 | hypothetical protein, similar to (U06944) |
| 2730 41033_at | ZNF84 | M27878 | zinc finger protein 84 (HPF2) | PRAJA1 [Mus musculus] |
| 2731 40610_at | ZFR | A1743507 | zinc finger RNA binding protein | DNA binding protein |
| 2732 39751_at | ZDHHC3 | AF052182 | zinc finger, DHHC domain containing 3 | |
| 2733 33912_at | ZMPSTE24 | Y13834 | zinc metalloproteinase (STE24 homolog, yeast) | farnesylated-proteins converting enzyme 1 |
| 2734 36521_at | DZIP1 | AB023213 | zinc-finger protein DZIP1 | KIAA0996 protein |
| 2735 35995_at | ZWINT | AF067656 | ZW10 interactor | ZW10 interactor Zwint |
| 2736 706_at | | HG4582-HT4987 | | |
| 2737 960_g_at | | HG2463-HT2559 | | |
| 2738 956_at | | HG1980-HT2023 | | |
| 2739 955_at | | HG1862-HT1897 | | |
| 2740 324_f_at | | HG1515-HT1515 | | |

Fig. 21

| | A | B | C | D | E |
|------|------------|-----------|---------------|---|--|
| 2741 | 327_f_at | | HG1800-HT1823 | | |
| 2742 | 333_s_at | | HG2639-HT2735 | | |
| 2743 | 1840_g_at | | HG1112-HT1112 | | |
| 2744 | 1664_at | | HG3543-HT3739 | | |
| 2745 | 1624_at | | HG2036-HT2090 | | |
| 2746 | 1278_at | | HG162-HT3165 | | |
| 2747 | 1179_at | | HG2855-HT2995 | | |
| 2748 | 1180_g_at | | HG2855-HT2995 | | |
| 2749 | 32243_g_at | | AL036340 | | |
| 2750 | 311_s_at | | HG3044-HT3742 | | |
| 2751 | 297_g_at | | HG4322-HT4592 | | |
| 2752 | 296_at | | HG4322-HT4592 | | |
| 2753 | 1839_at | | HG1112-HT1112 | | |
| 2754 | 723_s_at | | HG1322-HT5143 | | |
| 2755 | 33300_at | dJ283E3.1 | AL031282 | | guanine nucleotide binding protein (G protein), beta polypeptide 1 |
| 2756 | 41249_at | dJ283E3.1 | AL031282 | | guanine nucleotide binding protein (G protein), beta polypeptide 1 |

Fig-21

| A | | B | | C | | D | | E | |
|------------|-----------------|----------|-------------|--|--|---|--|---|--|
| Systematic | Common | Genbank | Description | Product | | | | | |
| 1 | Systematic | Common | Genbank | Description | Product | | | | |
| 2 | AFEX-hum_alu_at | | | ***ALU WARNING: Human Alu-Sq subfamily consensus sequence. | | | | | |
| 3 | 38820_at | 15-Sep | AF051894 | 15 kDa selenoprotein | 15 kDa selenoprotein | | | | |
| 4 | 33247_at | POH1 | U86782 | 26S proteasome-associated pad1 homolog | 26S proteasome-associated pad1 homolog | | | | |
| 5 | 32165_at | SFRS7 | L41887 | 35 kDa protein; Homo sapiens splicing factor, arginine/serine-rich 7 (SFRS7) gene, complete cds. | splicing factor, arginine/serine-rich 7 | | | | |
| 6 | 36851_g_at | N33 | U42360 | 39 kDa protein; Human N33 protein form 2 (N33) gene, exon 11 and complete cds. | N33 protein form 2 | | | | |
| 7 | 39328_at | HMGCR | M11058 | 3-hydroxy-3-methylglutaryl-Coenzyme A reductase | 3-hydroxy-3-methylglutaryl-Coenzyme A reductase | | | | |
| 8 | 41142_at | OXCT | U62961 | 3-oxoacid CoA transferase | succinyl CoA:3-oxoacid CoA transferase precursor | | | | |
| 9 | 34411_at | PAPSS1 | Y10387 | 3'-phosphoadenosine 5'-phosphosulfate synthase 1 | PAPS synthetase | | | | |
| 10 | 738_at | NT5C2 | D38524 | 5'-nucleotidase, cytosolic II | 5'-nucleotidase | | | | |
| 11 | 31794_at | NT5C2 | D38524 | 5'-nucleotidase, cytosolic II | 5'-nucleotidase | | | | |
| 12 | 38811_at | ATIC | D82348 | 5-aminimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase | 5-aminimidazole-4-carboxamide-1-beta-D-ribo-nucl eotide transformylase/inosinase | | | | |
| 13 | 38383_at | MTR | U73338 | 5-methyltetrahydrofolate-homocysteine methyltransferase | methionine synthase | | | | |
| 14 | 39025_at | LOC54543 | AI557912 | 6.2 kd protein | | | | | |

Fig 21

| | A | B | C | D | E |
|----|------------|----------------------|----------------------|--|--|
| 15 | 40446_at | | | 60S Ribosomal Protein L35A LIKE pseudogene match: proteins P04646 P02434 P18077 P05744 P41056 CE04362 match: cDNAs Y16430 X52966 X03475 V01440 X55030 J00995 match: ESTs AA554649 AA747384 AA572868 AA329139 AA745138 AA330809 AA483371 AA507788 AA483213 D55111 N90267 N91909 AA662153 AA720551 AA836920 AA501529 AA526745 AA608598 AA649846 AA654164 match: genomic DNAs Z32550 X05705 X05706 X05704 I23465 I45758 | divalent cation tolerant protein CUTA |
| 16 | 39059_at | cICK0721Q.1 DHCR7 | AL021366 AF034544 | 7-dehydrocholesterol reductase a disintegrin and metalloproteinase domain 10 | delta7-sterol reductase |
| 17 | 40797_at | ADAM10 | AF009615 | a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme) | ADAM10 |
| 18 | 41601_at | ADAM17 | AA142964 | a disintegrin and metalloproteinase domain 9 (meltrin gamma) | metalloproteinase/disintegrin/cysteine-rich protein precursor |
| 19 | 34761_r_at | ADAM9 | U41766 | A kinase (PRKA) anchor protein (gravin) 12 | gravin |
| 20 | 37680_at | AKAP12 | U81607 | A kinase (PRKA) anchor protein 10 | |
| 21 | 36633_at | AKAP10 | AA114830 | A kinase (PRKA) anchor protein 11 | KIAA0629 protein |
| 22 | 34657_at | AKAP11 | AB014529 | A kinase (PRKA) anchor protein 2 | KIAA0920 protein |
| 23 | 35985_at | AKAP2 | AB023137 | | |

Fig 21

| A | B | C | D | E |
|--------------|----------|----------|---|--|
| | | | <p>ABL is the cellular homolog proto-oncogene of Abelson's murine leukemia virus and is associated with the t(9;22) chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia; alternative splicing using alternative first exon 1b; ABL is the cellular homolog proto-oncogene of Abelson's murine leukemia virus and is associated with the t(9;22) chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia; alternative splicing using exon 1a; Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.</p> | <p>proto-oncogene tyrosine-protein kinase accessory proteins BAP31/BAP29</p> |
| 24 1636_g_at | ABL | U07563 | | |
| 25 41724_at | DXS1357E | X81817 | accessory proteins BAP31/BAP29 | |
| 26 41530_at | ACAA2 | D16294 | acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) | mitochondrial 3-oxoacyl-CoA thiolase |
| 27 34668_at | ACATN | D88152 | acetyl-Coenzyme A transporter | acetyl-coenzyme A transporter |
| 28 36553_at | ASMTL | AA669799 | acetylserotonin O-methyltransferase-like | |
| 29 37034_at | ANP32A | U73477 | acidic (leucine-rich) nuclear phosphoprotein 32 family, member A | acidic nuclear phosphoprotein pp32 |
| 30 38479_at | ANP32B | Y07969 | acidic (leucine-rich) nuclear phosphoprotein 32 family, member B | APRIL |
| 31 34397_at | OA48-18 | AF069250 | acid-inducible phosphoprotein | okadaic acid-inducible phosphoprotein |
| 32 39168_at | ALTE | AB018328 | Ac-like transposable element | KIAA0785 protein |
| 33 40077_at | ACO1 | Z11559 | aconitase 1, soluble | iron regulatory factor |
| 34 37578_at | AFAP | D25248 | actin filament associated protein | actin filament associated protein |
| 35 1718_at | ARPC2 | U50523 | actin related protein 2/3 complex, subunit 2 (34 kD) | actin related protein 2/3 complex, subunit 2 (34 kD) |

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| | A | B | C | D | E |
|----|---------------|--------|----------|--|---|
| 36 | 34692_r_at | ARPC4 | AF006087 | actin related protein 2/3 complex, subunit 4 (20 kD) | p20-Arc |
| 37 | 38392_at | ARPC5 | AF006088 | actin related protein 2/3 complex, subunit 5 (16 kD) | p16-Arc |
| 38 | 32755_at | ACTA2 | X13839 | actin, alpha 2, smooth muscle, aorta | alpha 2 actin |
| 39 | AFFX-HSAC07/X | ACTB | X00351 | actin, beta | beta actin |
| 40 | AFFX-HSAC07/X | ACTB | X00351 | actin, beta | beta actin |
| 41 | 32318_s_at | ACTB | X63432 | actin, beta | mutant beta-actin (beta'-actin) |
| 42 | 34160_at | ACTG1 | X04098 | actin, gamma 1 | gamma-actin |
| 43 | 39329_at | ACTN1 | X15804 | actinin, alpha 1 | actinin, alpha 1 |
| 44 | 41753_at | ACTN4 | U48734 | actinin, alpha 4 | alpha actinin |
| 45 | 38642_at | ALCAM | Y10183 | activated leucocyte cell adhesion molecule | MEMD protein |
| 46 | 36171_at | PC4 | AI521453 | activated RNA polymerase II transcription cofactor 4 | |
| 47 | 39764_at | ACVR1 | Z22534 | activin A receptor, type I | ALK-2 |
| 48 | 35162_s_at | ACVR2 | D31770 | activin A receptor, type II | activin type II A receptor precursor |
| 49 | 34394_at | ADNP | AB018327 | activity-dependent neuroprotector | KIAA0784 protein |
| 50 | 40673_at | ACADSB | U12778 | acyl-Coenzyme A dehydrogenase, short/branched chain | acyl-CoA dehydrogenase |
| 51 | 40459_at | ACOX1 | S69189 | acyl-Coenzyme A oxidase 1, palmitoyl | peroxisomal acyl-coenzyme A oxidase |
| 52 | 40745_at | AP1B1 | L13939 | adaptor-related protein complex 1, beta 1 subunit | beta-prime-adaptin |
| 53 | 35275_at | AP1G1 | AL050025 | adaptor-related protein complex 1, gamma 1 subunit | hypothetical protein |
| 54 | 39795_at | AP2M1 | D63475 | adaptor-related protein complex 2, mu 1 subunit | adaptor-related protein complex 2, mu 1 subunit |
| 55 | 39347_at | AP2S1 | X97074 | adaptor-related protein complex 2, sigma 1 subunit | clathrin-associated protein |
| 56 | 32039_at | AP3B1 | U81504 | adaptor-related protein complex 3, beta 1 subunit | beta-3A-adaptin subunit of the AP-3 complex |
| 57 | 36172_s_at | AP3D1 | AF002163 | adaptor-related protein complex 3, delta 1 subunit | delta-adaptin |
| 58 | 38074_at | AP3S1 | U91932 | adaptor-related protein complex 3, sigma 1 subunit | AP-3 complex sigma3A subunit |
| 59 | 33102_at | ADD3 | D67031 | adducin 3 (gamma) | adducin-like protein |

Fig 21

| | A | B | C | D | E |
|----|------------|---------------|----------|---|---|
| 60 | 38014_at | ADAR | X79448 | adenosine deaminase, RNA-specific | adenosine deaminase, RNA-specific, isoform ADAR-a; adenosine deaminase, RNA-specific, isoform ADAR-b; adenosine deaminase, RNA-specific, isoform ADAR-c |
| 61 | 38748_at | ADARB1 | U76421 | adenosine deaminase, RNA-specific (RED1 homolog rat) | dsRNA adenosine deaminase DRADA2b |
| 62 | 168_at | ADK | U50196 | adenosine kinase | adenosine kinase |
| 63 | 33865_at | BS69 | AA127624 | adenovirus 5 E1A binding protein | |
| 64 | 33134_at | ADCY3 | AB011083 | adenylate cyclase 3 | KIAA0511 protein |
| 65 | 40585_at | ADCY7 | D25538 | adenylate cyclase 7 | adenylate cyclase 7 |
| 66 | 33800_at | ADCY9 | AF036927 | adenylate cyclase 9 | adenylate cyclase type IX |
| 67 | 40788_at | AK2 | U84371 | adenylate kinase 2 | adenylate kinase 2A |
| 68 | 36639_at | ADSL | AF067853 | adenylosuccinate lyase | adenylosuccinate lyase |
| 69 | 935_at | CAP | L12168 | adenylyl cyclase-associated protein | adenylyl cyclase-associated protein |
| 70 | 33405_at | CAP2 | N90755 | adenylyl cyclase-associated protein 2 | |
| 71 | 34378_at | ADFP | X97324 | adipose differentiation-related protein | adipophilin |
| 72 | 36861_at | DKFZp56411922 | AL049946 | adican | hypothetical protein |
| 73 | 33987_at | ARF1 | M36340 | ADP-ribosylation factor 1 | ADP-ribosylation factor 1 |
| 74 | 39336_at | ARF3 | M74491 | ADP-ribosylation factor 3 | ADP-ribosylation factor 3 |
| 75 | 36585_at | ARF4 | M36341 | ADP-ribosylation factor 4 | ADP-ribosylation factor 4 |
| 76 | 37537_at | ARFD1 | L04510 | ADP-ribosylation factor domain protein 1, 64kD | nucleotide binding protein |
| 77 | 39905_i_at | ARFGAP1 | AA402332 | ADP-ribosylation factor GTPase activating protein 1 | |
| 78 | 37296_at | ARL1 | L28997 | ADP-ribosylation factor-like 1 | ADP-ribosylation factor-like 1 |
| 79 | 36572_r_at | ARL6IP | D31885 | ADP-ribosylation factor-like 6 interacting protein | |
| 80 | 41146_at | ADPRT | J03473 | ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase) | poly(ADP-ribose)ltransferase |
| 81 | 1287_at | ADPRT | J03473 | ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase) | poly(ADP-ribose)ltransferase |
| 82 | 34777_at | ADM | D14874 | adrenomedullin | adrenomedullin precursor |
| 83 | 32218_at | | AF034176 | AF034176 Human mRNA (Tripodis and Ragoussis) Homo sapiens cDNA clone ntconf contig. | |

Fig 21

| | A | B | C | D | E |
|-----|------------|----------|----------|---|---|
| 84 | 34315_at | AFG3L2 | Y18314 | AFG3 ATPase family gene 3-like 2 (yeast) | paraplegin-like protein |
| 85 | 33454_at | AGRN | AF016903 | agrin | agrin precursor |
| 86 | 37027_at | AHNAK | M80899 | AHNAK nucleoprotein (desmoyokin) | |
| 87 | 36185_at | AARS | D32050 | alanyl-tRNA synthetase | alanyl-tRNA synthetase |
| 88 | 36686_at | ALDH1A3 | U07919 | aldehyde dehydrogenase 1 family, member A3 | aldehyde dehydrogenase 6 |
| 89 | 32747_at | ALDH2 | X05409 | aldehyde dehydrogenase 2 family (mitochondrial) | aldehyde dehydrogenase 2 family (mitochondrial) |
| 90 | 40409_at | ALDH3A2 | U46689 | aldehyde dehydrogenase 3 family, member A2 | aldehyde dehydrogenase |
| 91 | 37331_g_at | ALDH4A1 | U24266 | aldehyde dehydrogenase 4 family, member A1 | pyrroline-5-carboxylate dehydrogenase |
| 92 | 36132_at | ALDH7A1 | S74728 | aldehyde dehydrogenase 7 family, member A1 | antiquitin |
| 93 | 33899_at | ALDH9A1 | U34252 | aldehyde dehydrogenase 9 family, member A1 | gamma-aminobutyraldehyde dehydrogenase |
| 94 | 38780_at | AKR1A1 | J04794 | aldo-keto reductase family 1, member A1 (aldehyde reductase) | aldo-keto reductase family 1, member A1 (aldehyde reductase) |
| 95 | 36589_at | AKR1B1 | X15414 | aldo-keto reductase family 1, member B1 (aldose reductase) | aldo-keto reductase family 1, member B1 (aldose reductase) |
| 96 | 37399_at | AKR1C3 | D17793 | aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II) | aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II) |
| 97 | 32510_at | AKR7A2 | AF026947 | aldo-keto reductase family 7, member A2 (afloxin aldehyde reductase) | afloxin aldehyde reductase AFAR precursor |
| 98 | 39225_at | AGPS | Y09443 | alkylglycerone phosphate synthase | alkyl-dihydroxyacetonephosphate synthase precursor |
| 99 | 36941_at | AF1Q | U16954 | ALL1-fused gene from chromosome 1q | AF1Q protein |
| 100 | 37040_at | G2AN | D42041 | alpha glucosidase II alpha subunit | alpha glucosidase II alpha subunit |
| 101 | 35223_at | KIAA1017 | AB023234 | alpha integrin binding protein 63 | KIAA1017 protein |
| 102 | 39147_g_at | ATRX | U72936 | alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae) | putative DNA dependent ATPase and helicase |

Fig 21

| | A | B | C | D | E |
|-----|------------|----------|----------|--|--|
| 103 | 818_s_at | ATRX | U72936 | alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae) | putative DNA dependent ATPase and helicase |
| 104 | 34327_at | HLTF | Z46606 | alternative translation initiation; H.sapiens HLTF gene for helicase-like transcription factor. | helicase-like transcription factor |
| | | | | aminoacidipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase | hypothetical protein |
| 105 | 35761_at | AASDHPPT | AL050073 | aminopeptidase puromycin sensitive | puromycin sensitive aminopeptidase |
| 106 | 39431_at | NPEPPS | AJ132583 | amino-terminal enhancer of split | |
| 107 | 41338_at | AES | AI951946 | amplified in osteosarcoma | OS-9 precursor |
| 108 | 36996_at | OS-9 | U41635 | amyl-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) | glycogen debranching enzyme isoform 6 |
| 109 | 38253_at | AGL | U84011 | amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) | amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) |
| 110 | 41136_s_at | APP | Y00264 | amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like) | FE65-like protein |
| 111 | 40148_at | APBB2 | U62325 | amyloid beta precursor protein (cytoplasmic tail) binding protein 2 | KIAA0228 protein |
| 112 | 38471_r_at | APPBP2 | D86981 | amyloid beta precursor protein (cytoplasmic tail) binding protein 2 | KIAA0228 protein |
| 113 | 38470_i_at | APPBP2 | D86981 | amyloid beta precursor protein binding protein 1, 59kD | amyloid precursor protein-binding protein 1 |
| 114 | 35364_at | APPBP1 | U50939 | amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3 | KIAA0549 protein |
| 115 | 40064_at | ALS2CR3 | AB011121 | androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease) | androgen receptor |
| 116 | 1577_at | AR | M23263 | angiomotin like 2 | angiomotin like 2 |
| 117 | 38842_at | AMOTL2 | AB023206 | angioipoietin 1 | angioipoietin 1 |
| 118 | 39315_at | ANGPT1 | D13628 | angioipoietin 1 | angioipoietin 1 |
| 119 | 1929_at | ANGPT1 | U83508 | angioipoietin 1 | angioipoietin-1 |

Fig 21

| | A | B | C | D | E |
|-----|------------|-----------------|----------|--|---|
| 120 | 36965_at | ANK3 | U13616 | ankyrin 3, node of Ranvier (ankyrin G) | ankyrin G |
| 121 | 37403_at | ANXA1 | X05908 | annexin A1 | annexin I |
| 122 | 36637_at | ANXA11 | L19605 | annexin A11 | 56K autoantigen |
| 123 | 769_s_at | ANXA2 | D00017 | annexin A2 | lipocortin II |
| 124 | 31684_at | ANXA2P1 | M62896 | annexin A2 pseudogene 1 | |
| 125 | 31444_s_at | ANXA2P3 | M62895 | annexin A2 pseudogene 3 | |
| 126 | 37374_at | ANXA4 | M82809 | annexin A4 | annexin IV (placental anticoagulant protein II) |
| 127 | 37670_at | ANXA7 | J04543 | annexin A7 | annexin VII isoform 1; annexin VII isoform 2 |
| 128 | 41138_at | MIC2 | M16279 | antigen identified by monoclonal antibodies 12E7, F21 and O13 | antigen |
| 129 | 40506_s_at | PABPC4; APP1; A | U75686 | APP-1; Homo sapiens polyadenylate binding protein mRNA, complete cds. | polyadenylate binding protein |
| 130 | 34370_at | ARCN1 | X81198 | archain 1 | archain |
| 131 | 32253_at | RERE | AB007927 | arginine-glutamic acid dipeptide (RE) repeats | KIAA0458 protein |
| 132 | 549_at | RARS | S80343 | arginyl-tRNA synthetase | arginyl-tRNA synthetase |
| 133 | 39164_at | ARIH2 | AF099149 | ariadne homolog 2 (Drosophila) | TRIAD1 type I |
| 134 | 41729_at | ARIH1 | AJ009771 | ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila) | putative RING finger protein |
| 135 | 36057_at | ALEX2 | AB011084 | armadillo repeat protein ALEX2 | KIAA0512 protein |
| 136 | 40052_at | ACTR1A | X82206 | ARP1 actin-related protein 1 homolog A, centractin alpha (yeast) | alpha-centractin |
| 137 | 35734_at | ACTR2 | A1935551 | ARP2 actin-related protein 2 homolog (yeast) | |
| 138 | 35733_at | ACTR2 | AF006082 | ARP2 actin-related protein 2 homolog (yeast) | Arp2 |
| 139 | 35271_at | ACTR3 | AF006083 | ARP3 actin-related protein 3 homolog (yeast) | Arp3 |
| 140 | 40516_at | AHR | L19872 | aryl hydrocarbon receptor | AH-receptor |
| 141 | 36671_at | ASNS | M27396 | asparagine synthetase | asparagine synthetase |
| 142 | 41241_at | NARS | D84273 | asparaginyl-tRNA synthetase | Asparaginyl tRNA Synthetase |
| 143 | 38703_at | DNPEP | AF005050 | aspartyl aminopeptidase | aspartyl aminopeptidase |
| 144 | 34181_at | AGA | X55330 | aspartylglucosaminidase | aspartylglucosaminidase |

Fig 21

| | A | B | C | D | E |
|-----|------------|--------|----------|--|--|
| 145 | 37229_at | ATR | U49844 | ataxia telangiectasia and Rad3 related | FRAP-related protein |
| 146 | 34817_s_at | A2LP | U70671 | ataxin 2 related protein | ataxin-2 related protein |
| 147 | 379_at | APACD | AB006679 | ATP binding protein associated with cell differentiation | ATP binding protein |
| 148 | 40881_at | ACLY | X64330 | ATP citrate lyase | ATP-citrate (pro-S)-lyase |
| 149 | 41228_r_at | ATP5F1 | X60221 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1 | H+-ATP synthase subunit b |
| 150 | 34811_at | ATP5G3 | U09813 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 | mitochondrial ATP synthase subunit 9 precursor |
| 151 | 35760_at | ATP5H | AF087135 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d | F1FO-type ATPase subunit d |
| 152 | 38751_i_at | ATP5I | AA426364 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e | |
| 153 | 36107_at | ATP5J | AA845575 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6 | |
| 154 | 38693_at | ATP5L | AA917672 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g | |
| 155 | 40115_at | ATP5C1 | D16562 | ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1 | ATP synthase gamma-subunit |
| 156 | 39791_at | ATP2A2 | M23114 | ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 | ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 |
| 157 | 39790_at | ATP2A2 | M23115 | ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 | ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 |
| 158 | 38684_at | ATP2C1 | AJ010953 | ATPase, Ca++ transporting, type 2C, member 1 | putative Ca2+-transporting ATPase |
| 159 | 35831_at | ATP9A | AB014511 | ATPase, Class II, type 9A | KIAA0611 protein |
| 160 | 40853_at | ATP10D | A1478147 | ATPase, Class V, type 10D | |
| 161 | 36635_at | ATP11B | AB023173 | ATPase, Class VI, type 11B | KIAA0956 protein |
| 162 | 36523_at | ATP7A | L06133 | ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome) | Cu++-transporting P-type ATPase |
| 163 | 33854_at | ATP6M | AA877795 | ATPase, H+ transporting, lysosomal (vacuolar proton pump) | |

Fig 21

| | A | B | C | D | E |
|-----|------------|----------|----------|---|--|
| 164 | 37395_at | ATP6S14 | D49400 | ATPase, H+ transporting, lysosomal (vacuolar proton pump) 14kD | vacuolar ATPase |
| 165 | 36994_at | ATP6L | M62762 | ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD | vacuolar H+ ATPase proton channel subunit |
| 166 | 36167_at | ATP6F | D89052 | ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kD | proton-ATPase-like protein |
| 167 | 37367_at | ATP6E | X76228 | ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD | vacuolar H+ ATPase E subunit |
| 168 | 37948_at | ATP6C | J05682 | ATPase, H+ transporting, lysosomal (vacuolar proton pump) 42kD | H+ -ATPase C subunit |
| 169 | 33875_at | ATP6H | AI547262 | ATPase, H+ transporting, lysosomal (vacuolar proton pump) 9kD | |
| 170 | 40903_at | ATP6M8-9 | AL049929 | ATPase, H+ transporting, lysosomal (vacuolar proton pump) membrane sector associated protein M8-9 | hypothetical protein |
| 171 | 34889_at | ATP6A1 | AA056747 | ATPase, H+ transporting, lysosomal (vacuolar proton pump), alpha polypeptide, 70kD, isoform 1 | |
| 172 | 40568_at | ATP6B2 | L35249 | ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 2 | vacuolar H+-ATPase 56,000 subunit |
| 173 | 35770_at | ATP6S1 | D16469 | ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1 | ORF |
| 174 | 37669_s_at | ATP1B1 | U16799 | ATPase, Na+/K+ transporting, beta 1 polypeptide | Na,K-ATPase beta subunit |
| 175 | 32563_at | ATP1B3 | U51478 | ATPase, Na+/K+ transporting, beta 3 polypeptide | sodium/potassium-transporting ATPase beta-3 subunit |
| 176 | 35717_at | ABCA8 | AB020629 | ATP-binding cassette, sub-family A (ABC1), member 8 | KIAA0822 protein |
| 177 | 38261_at | ABCC3 | AF085692 | ATP-binding cassette, sub-family C (CFTR/MRP), member 3 | multidrug resistance-associated protein 3B |
| 178 | 35648_at | KIAA0442 | AB007902 | autism-related protein 1 | autism-related protein 1 |
| 179 | 38068_at | AMFR | M63175 | autocrine motility factor receptor | autocrine motility factor receptor |
| 180 | 38433_at | AXL | M76125 | AXL receptor tyrosine kinase | tyrosine kinase receptor |
| 181 | 35268_at | AXOT | AL050171 | axotrophin | hypothetical protein DKFZp586F1122 similar to axotrophin |

Fig 21

| | A | B | C | D | E |
|-----|----------|--------------|----------|--|--|
| 182 | 35350_at | GALNAC4S-6ST | AB011170 | B cell RAG associated protein | KIAA0598 protein |
| 183 | 41562_at | BMI1 | L13689 | B lymphoma Mo-MLV insertion region (mouse) | murine leukemia viral (bmi-1) oncogene homolog |
| 184 | 1728_at | BMI1 | L13689 | B lymphoma Mo-MLV insertion region (mouse) | murine leukemia viral (bmi-1) oncogene homolog |
| 185 | 36578_at | BIRC2 | U37547 | baculoviral IAP repeat-containing 2 | MIHB |
| 186 | 41278_at | BAF53A | AF041474 | BAF53 | BAF53a |
| 187 | 33175_at | BBS4 | AA156237 | Bardet-Biedl syndrome 4 | |
| 188 | 40790_at | BHLHB2 | AB004066 | basic helix-loop-helix domain containing, class B, 2 | 1-Dec |
| 189 | 40108_at | BZAP45 | D13630 | basic leucine-zipper protein BZAP45 | basic leucine-zipper protein BZAP45 |
| 190 | 40202_at | BTEB1 | D31716 | basic transcription element binding protein 1 | GC box binding protein |
| 191 | 35055_at | BTF3 | X53281 | basic transcription factor 3 | general transcription factor |
| 192 | 38364_at | BCE-1 | AF068197 | BCE-1 protein | BCE-1 |
| 193 | 40091_at | BCL6 | U00115 | B-cell CLL/lymphoma 6 (zinc finger protein 51) | zinc-finger protein |
| 194 | 37294_at | BTG1 | X61123 | B-cell translocation gene 1, anti-proliferative | B-cell translocation protein 1 |
| 195 | 32060_at | BNIP2 | U15173 | BCL2/adenovirus E1B 19kD interacting protein 2 | BCL2/adenovirus E1B 19kD-interacting protein 2 |
| 196 | 38010_at | BNIP3 | AF002697 | BCL2/adenovirus E1B 19kD interacting protein 3 | E1B 19K/Bcl-2-binding protein Nip3 |
| 197 | 39436_at | BNIP3L | AF079221 | BCL2/adenovirus E1B 19kD interacting protein 3-like | BCL2/adenovirus E1B 19kDa-interacting protein 3a |
| 198 | 34798_at | BAG1 | Z35491 | BCL2-associated athanogene | glucocorticoid receptor-associated protein RAP46 |
| 199 | 35291_at | BAG2 | AL050287 | BCL2-associated athanogene 2 | hypothetical protein |
| 200 | 36463_at | BAG5 | AB020680 | BCL2-associated athanogene 5 | KIAA0873 protein |
| 201 | 38050_at | BTF | D79986 | Bcl-2-associated transcription factor | KIAA0184 gene product |
| 202 | 38101_at | BDG-29 | AB011151 | BDG-29 protein | KIAA0579 protein |
| 203 | 39378_at | BECN1 | U17999 | beclin 1 (coiled-coil, myosin-like BCL2 interacting protein) | |
| 204 | 39160_at | PDHB | D90086 | beta subunit; Human pyruvate dehydrogenase (EC 1.2.4.1) beta subunit gene, exons 1-10. | pyruvate dehydrogenase (lipoamide) beta |

Fig 21

| | A | B | C | D | E |
|-----|------------|--------|----------|---|---|
| 205 | 34644_at | B2M | AB021288 | beta-2-microglobulin | beta 2-microglobulin |
| 206 | 40601_at | BBP | AI057115 | beta-amyloid binding protein precursor | |
| | | | | beta-hexosaminidase alpha chain; Human | |
| 207 | 39340_at | HEXA | M16424 | beta-hexosaminidase alpha chain (HEXA) gene, exon 14. | hexosaminidase A preproprotein |
| 208 | 38126_at | BGN | J04599 | biglycan | biglycan preproprotein |
| 209 | 33198_at | BART1 | AA206524 | binder of Arl Two | |
| | | | | biotin-amide amidohydrolase; Homo sapiens biotinidase (BTD) gene, exons 2, 3, and 4 and complete cds. | |
| 210 | 37274_at | Btd | AF018631 | biphenyl hydrolase-like (serine hydrolase; breast epithelial mucin-associated antigen) | biotinidase |
| | | | | bladder cancer associated protein | biphenyl hydrolase-related protein |
| 211 | 40912_s_at | BPHL | X81372 | bladder cancer associated protein | bladder cancer associated protein |
| 212 | 35267_g_at | BLCAP | AL049288 | bladder cancer associated protein | bladder cancer associated protein |
| 213 | 35266_at | BLCAP | AL049288 | bleomycin hydrolase | bleomycin hydrolase |
| 214 | 37700_at | BLMH | X92106 | bone morphogenetic protein receptor, type IA | ALK-3 |
| 215 | 39565_at | BMPR1A | Z22535 | BRAF35/HDAC2 complex (80 kDa) | |
| 216 | 39551_at | BHC80 | N98667 | brain abundant, membrane attached signal protein 1 | neuronal tissue-enriched acidic protein |
| 217 | 32607_at | BASP1 | AF039656 | brain abundant, membrane attached signal protein 1 | |
| 218 | 32606_at | BASP1 | AA135683 | brain acyl-CoA hydrolase | acyl-CoA thioester hydrolase |
| 219 | 37945_at | BACH | U91316 | brain cell membrane protein 1 | brain cell membrane protein 1 |
| 220 | 37958_at | BCMP1 | AL049257 | brain-derived neurotrophic factor | brain-derived neurotrophic factor |
| 221 | 40023_at | BDNF | X60201 | branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) | branched chain alpha-ketoacid dehydrogenase E1 beta subunit |
| 222 | 41683_i_at | BCKDHB | U50708 | breast cancer anti-estrogen resistance 3 | breast cancer antiestrogen resistance 3 protein |
| 223 | 36812_at | BCAR3 | U92715 | breifeldin A-inhibited guanine nucleotide-exchange protein 1 | |
| 224 | 38306_at | BIG1 | AA477576 | bromodomain containing 3 | bromodomain containing protein 3 |
| 225 | 37947_at | BRD3 | D26362 | BTB and CNC homology 1, basic leucine zipper transcription factor 1 | BTB and CNC homology 1, basic leucine zipper transcription factor 1 |
| 226 | 31895_at | BACH1 | AB002803 | | |

Fig 21

| | A | B | C | D | E |
|-----|------------|----------|----------|---|--|
| 227 | 36634_at | BTG2 | U72649 | BTG family, member 2 | BTG2 |
| 228 | 37218_at | BTG3 | D64110 | BTG family, member 3 | ANA |
| 229 | 41547_at | BUB3 | AF047472 | BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast) | spleen mitotic checkpoint BUB3 |
| 230 | 34783_s_at | BUB3 | AF047473 | BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast) | testis mitotic checkpoint BUB3 |
| 231 | 32781_f_at | BPAG1 | AA058762 | bullous pemphigoid antigen 1 (230/240kD) | |
| 232 | 32780_at | BPAG1 | AB018271 | bullous pemphigoid antigen 1 (230/240kD) | KIAA0728 protein |
| 233 | 32629_f_at | BTN3A1 | U90552 | butyrophilin, subfamily 3, member A1 | butyrophilin |
| 234 | 39357_at | C2F | U72514 | C2f protein | C2f |
| 235 | 40709_at | LOC58502 | W27601 | C2H2 (Krueppel-type) zinc finger protein | |
| 236 | 37031_at | C9orf10 | D80005 | C9orf10 protein | C9orf10 protein |
| 237 | 33856_at | CXX1 | Y13374 | CAAX box 1 | putative prenylated protein |
| 238 | 36976_at | CDH11 | D21255 | cadherin 11, type 2, OB-cadherin (osteoblast) | OB-cadherin-2 |
| 239 | 2087_s_at | CDH11 | D21254 | cadherin 11, type 2, OB-cadherin (osteoblast) | OB-cadherin-1 |
| 240 | 2053_at | CDH2 | M34064 | cadherin 2, type 1, N-cadherin (neuronal) | cadherin 2, type 1 preproprotein |
| 241 | 31670_s_at | CAMK2G | U81554 | calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma | CaM kinase II isoform |
| 242 | 38716_at | CAMKK2 | AB018330 | calcium/calmodulin-dependent protein kinase kinase 2, beta | KIAA0787 protein |
| 243 | 31854_at | CASK | AF035582 | calcium/calmodulin-dependent serine protein kinase (MAGUK family) | CASK |
| 244 | 41738_at | CALD1 | M64110 | caldesmon 1 | caldesmon |
| 245 | 41739_s_at | CALD1 | M83216 | caldesmon 1 | caldesmon |
| 246 | 41288_at | CALM1 | AL036744 | calmodulin 1 (phosphorylase kinase, delta) | |
| 247 | 911_s_at | CALM2 | M19311 | calmodulin 2 (phosphorylase kinase, delta) | calmodulin 2 (phosphorylase kinase, delta) |
| 248 | 40125_at | CANX | L10284 | calnexin | calnexin |
| 249 | 37001_at | CAPN2 | M23254 | calpain 2, (m/l) large subunit | neutral protease large subunit |
| 250 | 36138_at | CAPNS1 | X04106 | calpain, small subunit 1 | calpain, small subunit 1 |

Fig 21

| | A | B | C | D | E |
|-----|------------|---------|----------|---|--|
| 251 | 41257_at | CAST | D16217 | calpastatin | calpastatin |
| 252 | 33385_g_at | CAST | U31346 | calpastatin | calpastatin |
| 253 | 40953_at | CNN3 | S80562 | calponin 3, acidic | acidic calponin |
| 254 | 37345_at | CALU | AF013759 | calumenin | calumein |
| 255 | 37535_at | CREB1 | M27691 | cAMP responsive element binding protein 1 | cAMP responsive element binding protein 1, isoform A; cAMP responsive element binding protein 1, isoform B |
| 256 | 40849_s_at | CREB3 | U88528 | cAMP responsive element binding protein 3 (luman) | transcription factor LZIP |
| 257 | 39438_at | CREBL2 | AF039081 | cAMP responsive element binding protein-like 2 | Cre binding protein-like 2 |
| 258 | 32065_at | CREM | S68134 | cAMP responsive element modulator | cyclic AMP-responsive element modulator |
| 259 | 32067_at | CREM | S68271 | cAMP responsive element modulator | cyclic AMP-responsive element modulator |
| 260 | 32066_g_at | CREM | S68134 | cAMP responsive element modulator | cyclic AMP-responsive element modulator |
| 261 | 40910_at | CAPZA1 | U56637 | capping protein (actin filament) muscle Z-line, alpha 1 | beta isoform |
| 262 | 36641_at | CAPZA2 | U03851 | capping protein (actin filament) muscle Z-line, alpha 2 | capping protein alpha subunit isoform 1 |
| 263 | 37012_at | CAPZB | U03271 | capping protein (actin filament) muscle Z-line, beta | capping protein alpha |
| 264 | 32094_at | CHST3 | AB017915 | carbohydrate (chondroitin 6) sulfotransferase 3 | F-actin capping protein beta subunit |
| 265 | 41447_at | CHSY1 | AB023207 | carbohydrate (chondroitin) synthase 1 | chondroitin 6-sulfotransferase |
| 266 | 41395_at | CHST1 | AB003791 | carbohydrate (keratan sulfate Gal-6) sulfotransferase 1 | KIAA0990 protein |
| 267 | 37960_at | CHST2 | AB014679 | carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 | keratan sulfate Gal-6-sulfotransferase |
| 268 | 36454_at | CA12 | AF037335 | carbonic anhydrase XII | N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST) |
| 269 | 34876_at | CPD | U65090 | carboxypeptidase D | carbonic anhydrase precursor |
| 270 | 36606_at | CPE | X51405 | carboxypeptidase E | carboxypeptidase D |
| 271 | 35632_at | CBLB | U26710 | Cas-Br-M (murine) ectropic retroviral transforming sequence b | carboxypeptidase E precursor |
| 272 | 40184_at | CSNK1A1 | L37042 | casein kinase 1, alpha 1 | cbl-b |
| 273 | 36949_at | CSNK1D | U29171 | casein kinase 1, delta | casein kinase I-alpha |

fig 21

| | A | B | C | D | E |
|-----|------------|---------|----------|---|---|
| 274 | 38019_at | CSNK1E | L37043 | casein kinase 1, epsilon | casein kinase I-epsilon |
| 275 | 1211_s_at | CRADD | U84388 | CASP2 and RIPK1 domain containing adaptor with death domain | death domain containing protein CRADD |
| 276 | 1867_at | CFLAR | AF005775 | CASP8 and FADD-like apoptosis regulator | caspase-like apoptosis regulatory protein 2 |
| 277 | 195_s_at | CASP4 | U28014 | caspase 4, apoptosis-related cysteine protease | cysteine protease |
| 278 | 33774_at | CASP8 | X98172 | caspase 8, apoptosis-related cysteine protease | MACH-alpha-1 |
| 279 | 41156_g_at | CTNNA1 | U03100 | catenin (cadherin-associated protein), alpha 1 (102kD) | alpha2(E)-catenin |
| 280 | 41155_at | CTNNA1 | U03100 | catenin (cadherin-associated protein), alpha 1 (102kD) | alpha2(E)-catenin |
| 281 | 2085_s_at | CTNNA1 | D14705 | catenin (cadherin-associated protein), alpha 1 (102kD) | 'human alpha-catenin' |
| 282 | 2069_s_at | CTNNA1 | L23805 | catenin (cadherin-associated protein), alpha 1 (102kD) | alpha1(E)-catenin |
| 283 | 35331_at | CTNNAL1 | U97067 | catenin (cadherin-associated protein), alpha-like 1 | alpha-catenin-like protein |
| 284 | 40777_at | CTNNB1 | X87838 | catenin (cadherin-associated protein), beta 1 (88kD) | beta-catenin |
| 285 | 40444_s_at | CTNND1 | AB002382 | catenin (cadherin-associated protein), delta 1 | |
| 286 | 38466_at | CTSK | X82153 | cathepsin K (pseudosynthesis) | Cathepsin O |
| 287 | 37391_at | CTSL | X12451 | cathepsin L | pro-(cathepsin L) |
| 288 | 36915_at | CTSO | AI810485 | cathepsin O | |
| 289 | 36119_at | CAV1 | AF070648 | caveolin 1, caveolae protein, 22kD | |
| 290 | 339_at | CAV2 | AF035752 | caveolin 2 | caveolin-2 |
| 291 | 33113_at | CITED2 | U65093 | Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 | msg-related gene 1 |
| 292 | 1052_s_at | CEBPD | M83667 | CCAAT/enhancer binding protein (C/EBP), delta | NF-IL6-beta protein |
| 293 | 39219_at | CEBPG | U20240 | CCAAT/enhancer binding protein (C/EBP), gamma | C/EBP gamma |

Fig 21

| | A | B | C | D | E |
|-----|------------|---------|----------|--|--|
| 294 | 33861_at | CNOT2 | AI123426 | CCR4-NOT transcription complex, subunit 2 | |
| 295 | 32820_at | CNOT4 | U71267 | CCR4-NOT transcription complex, subunit 4 | |
| 296 | 34819_at | CD164 | D14043 | CD164 antigen, sialomucin | potential transcriptional repressor NOT4Hp |
| 297 | 34699_at | CD2AP | AL050105 | CD2-associated protein | MGC-24 precursor |
| | | | | | hypothetical protein |
| 298 | 33823_at | CD36L2 | D12676 | CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal integral membrane protein II) | 85kDa human lysosomal sialoglycoprotein |
| 299 | 2036_s_at | CD44 | M59040 | CD44 antigen (homing function and Indian blood group system) | cell adhesion molecule |
| 300 | 35282_r_at | CD81 | M33680 | CD81 antigen (target of antiproliferative antibody 1) | CD81 antigen |
| 301 | 39389_at | CD9 | M38690 | CD9 antigen (p24) | CD9 antigen |
| 302 | 32175_at | CDC10 | S72008 | CDC10 cell division cycle 10 homolog (S. cerevisiae) | cell division cycle 10 |
| 303 | 40404_s_at | CDC16 | U18291 | CDC16 cell division cycle 16 homolog (S. cerevisiae) | CDC16Hs |
| 304 | 31877_at | CDC23 | AF053977 | CDC23 (cell division cycle 23, yeast, homolog) | cell division cycle protein 23 |
| 305 | 40690_at | CKS2 | X54942 | CDC28 protein kinase 2 | Cks1 protein homologue |
| 306 | 33362_at | CEP3 | AF094521 | Cdc42 effector protein 3 | MSE55-related protein |
| 307 | 32833_at | CLK1 | M59287 | CDC-like kinase 1 | |
| 308 | 41535_at | CDK2AP1 | AF006484 | CDK2-associated protein 1 | putative oral tumor suppressor protein |
| 309 | 41343_at | CDS2 | Y16521 | CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 2 | CDS2 protein |
| 310 | 33397_at | CDIPT | AL050383 | CDP-diacylglycerol--inositol 3-phosphatidyltransferase | |
| 311 | 40591_at | CDC27 | S78234 | (phosphatidylinositol synthase) cell division cycle 27 | H-NUC |
| 312 | 450_g_at | CGR19 | U66469 | cell growth regulatory with ring finger domain | cell growth regulator CGR19 |
| 313 | 36514_at | CGR19 | U66469 | cell growth regulatory with ring finger domain | cell growth regulator CGR19 |

Fig 21

| | A | B | C | D | E |
|-----|------------|----------|----------|--|--|
| 314 | 35311_at | CREG | AF084523 | cellular repressor of E1A-stimulated genes | cellular repressor of E1A-stimulated genes |
| 315 | 41333_at | CENTB2 | D26069 | centaurin, beta 2 | centaurin, beta 2 |
| 316 | 34676_at | CENTG2 | AB029022 | centaurin, gamma 2 | KIAA1099 protein |
| 317 | 38410_at | CETN2 | X72964 | centrin, EF-hand protein, 2 | caltractin |
| 318 | 35232_f_at | CETN3 | AI056696 | centrin, EF-hand protein, 3 (CDC31 homolog, yeast) | |
| 319 | 31894_at | CENPC1 | M95724 | centromere protein C 1 | centromere autoantigen C |
| 320 | 33805_at | CAP350 | AB007949 | centrosome-associated protein 350 | KIAA0480 protein |
| 321 | 36190_at | CDR2 | M63256 | cerebellar degeneration-related protein (62kD) | major Yo paraneoplastic antigen |
| 322 | 32262_at | CGI-01 | AL049669 | CGI-01 protein | hypothetical protein |
| 323 | 40931_at | LOC50999 | AL080084 | CGI-100 protein | |
| 324 | 38500_at | LOC51014 | AB002450 | CGI-109 protein | |
| 325 | 34359_at | LOC51020 | AA524058 | CGI-130 protein | |
| 326 | 38667_at | LOC51031 | AA189161 | CGI-150 protein | |
| 327 | 41824_at | LOC51096 | AI140114 | CGI-48 protein | |
| 328 | 34862_at | LOC51097 | AA005018 | CGI-49 protein | |
| 329 | 37199_at | LOC51626 | AI760932 | CGI-60 protein | |
| 330 | 41411_at | LOC51103 | AI566877 | CGI-65 protein | |
| 331 | 39814_s_at | LOC51635 | AI052724 | CGI-86 protein | |
| 332 | 35759_at | CCT2 | AF026166 | chaperonin containing TCP1, subunit 2 (beta) | chaperonin-containing TCP-1 beta subunit homolog |
| 333 | 40774_at | CCT3 | X74801 | chaperonin containing TCP1, subunit 3 (gamma) | gamma subunit of CCT chaperonin |
| 334 | 32594_at | CCT4 | AF026291 | chaperonin containing TCP1, subunit 4 (delta) | chaperonin containing t-complex polypeptide 1, delta subunit |
| 335 | 38416_at | CCT6A | L27706 | chaperonin containing TCP1, subunit 6A (zeta 1) | chaperonin-like protein |
| 336 | 38720_at | CCT7 | AF026292 | chaperonin containing TCP1, subunit 7 (eta) | chaperonin containing t-complex polypeptide 1, eta subunit |
| 337 | 39767_at | CCT8 | D13627 | chaperonin containing TCP1, subunit 8 (theta) | chaperonin containing TCP1, subunit 8 (theta) |
| 338 | 41000_at | CHES1 | U68723 | checkpoint suppressor 1 | checkpoint suppressor 1 |
| 339 | 37855_at | CTBS | M95767 | chitinase, di-N-acetyl- | di-N-acetylchitinase |

Fig 21

| | A | B | C | D | E |
|-----|------------|----------|----------|---|---|
| 340 | 38732_at | CLNS1A | X91788 | chloride channel, nucleotide-sensitive, 1A | Ich protein |
| 341 | 33891_at | CLIC4 | AL080061 | chloride intracellular channel 4 | |
| 342 | 32363_at | CH25H | AF059214 | cholesterol 25-hydroxylase | cholesterol 25-hydroxylase |
| 343 | 38112_g_at | CSPG2 | X15998 | chondroitin sulfate proteoglycan 2 (versican) | chondroitin sulfate proteoglycan 2 (versican) |
| 344 | 38111_at | CSPG2 | X15998 | chondroitin sulfate proteoglycan 2 (versican) | chondroitin sulfate proteoglycan 2 (versican) |
| 345 | 34763_at | CSPG6 | AF020043 | chondroitin sulfate proteoglycan 6 (bamacan) | chromosome-associated polypeptide |
| 346 | 37304_at | CBX1 | U35451 | chromobox homolog 1 (HP1 beta homolog Drosophila) | heterochromatin protein p25 |
| 347 | 38085_at | CBX3 | A1740522 | chromobox homolog 3 (HP1 gamma homolog, Drosophila) | |
| 348 | 38084_at | CBX3 | AA648295 | chromobox homolog 3 (HP1 gamma homolog, Drosophila) | |
| 349 | 36137_at | CHD4 | X86691 | chromodomain helicase DNA binding protein 4 | Mi-2 protein |
| 350 | 32111_at | CDYL | AL050164 | chromodomain protein, Y chromosome-like | hypothetical protein |
| 351 | 39550_at | C1orf17 | AB011156 | chromosome 1 open reading frame 17 | KIAA0584 protein |
| 352 | 39033_at | C1orf8 | Z78368 | chromosome 1 open reading frame 8 | |
| 353 | 32217_at | C12orf22 | AF052105 | chromosome 12 open reading frame 22 | TGF-beta induced apoptosis protein 12 |
| 354 | 40979_at | C14orf3 | AJ243310 | chromosome 14 open reading frame 3 | C14orf3 protein |
| 355 | 40045_g_at | C18orf1 | AF009425 | chromosome 18 open reading frame 1 | clone 22 |
| 356 | 36860_at | C19orf7 | AB028987 | chromosome 19 open reading frame 7 | KIAA1064 protein |
| 357 | 34287_at | C21orf80 | AB023175 | chromosome 21 open reading frame 80 | KIAA0958 protein |
| 358 | 33406_at | C22orf2 | AL050345 | chromosome 22 open reading frame 2 | hypothetical protein |
| 359 | 33778_at | C22orf4 | AL096779 | chromosome 22 open reading frame 4 | hypothetical protein |
| 360 | 41758_at | C22orf5 | AL096879 | chromosome 22 open reading frame 5 | hypothetical protein |
| 361 | 38690_at | C3orf4 | AL080097 | chromosome 3 open reading frame 4 | hypothetical protein |
| 362 | 36013_at | C4orf1 | AF006621 | chromosome 4 open reading frame 1 | embryonic lung protein |
| 363 | 36955_at | C5orf8 | U10362 | chromosome 5 open reading frame 8 | GP36b glycoprotein |
| 364 | 41375_at | C6orf28 | AJ245416 | chromosome 6 open reading frame 28 | G7b protein |
| 365 | 41454_at | C6orf34 | W27949 | chromosome 6 open reading frame 34 | |
| 366 | 36139_at | C6orf5 | AL050289 | chromosome 6 open reading frame 5 | hypothetical protein |

Fig 21

| | A | B | C | D | E |
|-----|------------|-----------|----------|--|--|
| 367 | 35193_at | CHC1L | AF060219 | chromosome condensation 1-like | RCC1-like G exchanging factor RLG |
| 368 | 34292_at | CXorf12 | X92475 | chromosome X open reading frame 12 | chromosome X open reading frame 12 |
| 369 | 41314_at | CS | AF047042 | citrate synthase | citrate synthase |
| 370 | 41159_at | CLTC | D21260 | clathrin, heavy polypeptide (Hc) | clathrin heavy chain |
| 371 | 38657_s_at | CLTA | M20471 | clathrin, light polypeptide (Lca) | clathrin, light polypeptide A, isoform a; |
| 372 | 35743_at | CPSF4 | U79569 | cleavage and polyadenylation specific factor 4, 30kD subunit | clathrin, light polypeptide A, isoform b |
| 373 | 32723_at | CSTF1 | L02547 | cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kD | no arches |
| 374 | 41183_at | CSTF3 | U15782 | cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD | cleavage stimulation factor |
| 375 | 38711_at | CLASP2 | AB014527 | CLIP-associating protein 2 | cleavage stimulation factor 77kDa subunit |
| 376 | 36017_at | LOC57213 | AF055016 | CLLL6 protein | KIAA0627 protein |
| 377 | 36780_at | CLU | M25915 | clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J) | CLLL6 protein |
| 378 | 35180_at | LOC113251 | AL050205 | c-Mpl binding protein | clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J) |
| 379 | 40811_at | COASTER | AB011148 | coactivator for steroid receptors | apolipoprotein J |
| 380 | 38052_at | F13A1 | M14539 | coagulation factor XIII, A1 polypeptide | KIAA0576 protein |
| 381 | 36972_at | RNP24 | X92098 | coated vesicle membrane protein | coagulation factor XIII A1 subunit precursor |
| 382 | 34326_at | COPB | X82103 | coatamer protein complex, subunit beta | transmembrane protein |
| 383 | 36677_at | COPB2 | X70476 | coatamer protein complex, subunit beta 2 (beta prime) | beta-Coat protein |
| 384 | 35205_at | COBRA1 | AL050280 | colactor of BRCA1 | subunit of coatamer complex |
| 385 | 36648_at | CRSP9 | AF031383 | colactor required for Sp1 transcriptional activation, subunit 9 (33kD) | hypothetical protein |
| 386 | 33659_at | CFL1 | X95404 | cofilin 1 (non-muscle) | hMed7 |
| 387 | 40879_at | BICD2 | AB014599 | coiled-coil protein BICD2 | cofilin |
| 388 | 39854_at | CIRBP | D78134 | cold inducible RNA binding protein | KIAA0699 protein |
| 389 | 39839_at | CSDA | M24069 | cold shock domain protein A | CIRP |
| 390 | 32307_s_at | COL1A2 | V00503 | collagen, type I, alpha 2 | cold shock domain protein A |
| 391 | 32306_g_at | COL1A2 | J03464 | collagen, type I, alpha 2 | alpha 2 type I collagen preproprotein |
| 392 | 32305_at | COL1A2 | J03464 | collagen, type I, alpha 2 | alpha 2 type I collagen preproprotein |

Fig 21

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| | A | B | C | D | E |
|-----|------------|------------|----------|--|---|
| 393 | 32488_at | | | collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) | prepro-alpha-1 type 3 collagen |
| 394 | 36659_at | COL3A1 | X14420 | | alpha (2) chain |
| 395 | 38420_at | COL4A2 | X05610 | collagen, type IV, alpha 2 | procollagen alpha 2(V) |
| 396 | 38722_at | COL5A2 | Y14690 | collagen, type V, alpha 2 | alpha-1 collagen VI (AA 574-1009) |
| 397 | 38077_at | COL6A1 | X15880 | collagen, type VI, alpha 1 | collagen type VI, alpha 3 chain |
| 398 | 37459_at | COL6A3 | X52022 | collagen, type VI, alpha 3 | alpha 1(VIII) collagen |
| | | COL8A1 | X57527 | collagen, type VIII, alpha 1 | alpha 1 type XI collagen, isoform A |
| | | | | | preproprotein; alpha 1 type XI collagen, isoform B preproprotein; alpha 1 type XI collagen, isoform C preproprotein |
| 399 | 37892_at | COL11A1 | J04177 | collagen, type XI, alpha 1 | alpha-1 type XVI collagen |
| 400 | 35168_f_at | COL16A1 | M92642 | collagen, type XVI, alpha 1 | complement component 1, q subcomponent |
| 401 | 37668_at | C1QBP | M69039 | complement component 1, q subcomponent binding protein | binding protein precursor |
| 402 | 39409_at | C1R | M14058 | complement component 1, r subcomponent | complement component 1, r subcomponent |
| 403 | 40496_at | C1S | J04080 | complement component 1, s subcomponent | complement component 1, s subcomponent |
| 404 | 36638_at | CTGF | X78947 | connective tissue growth factor | connective tissue growth factor |
| 405 | 41202_s_at | OS4 | AF000152 | conserved gene amplified in osteosarcoma | OS-4 protein |
| 406 | 33770_at | CHUK | AF009225 | conserved helix-loop-helix ubiquitous kinase | IKB kinase alpha subunit |
| 407 | 1789_at | COPS5 | U65928 | COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis) | Jun activation domain binding protein |
| 408 | 32539_at | COP9 | U51205 | COP9 homolog | COP9 signalosome subunit 1 CSN1 |
| 409 | 40138_at | MOV34-34KD | U70735 | COP9 subunit 6 (MOV34 homolog, 34 kD) | 34 kDa Mov34 homolog |
| 410 | 40452_at | CPNE1 | U83246 | copine I | copine I |
| 411 | 39706_at | CPNE3 | AB014536 | copine III | KIAA0636 protein |
| 412 | 37999_at | CPO | D16611 | coproporphyrinogen oxidase (coproporphyrin, harderoporphyria) | coproporphyrinogen oxidase |
| 413 | 37026_at | COPEB | AF001461 | core promoter element binding protein | Kruppel-like zinc finger protein Z19 |
| 414 | 41175_at | CBFB | L20298 | core-binding factor, beta subunit | transcription factor |
| 415 | 32803_at | CN1L | AF104398 | cornichon-like | cornichon |

Fig 21

| | A | B | C | D | E |
|-----|------------|--------------|----------|---|--|
| 416 | 34723_at | COX11 | U79270 | COX11 homolog, cytochrome c oxidase assembly protein (yeast) | COX11 homolog |
| 417 | 37907_at | F8A; DXS522E | M34677 | CpG island protein; Human nested gene protein gene, complete cds. | coagulation factor VIII-associated protein |
| 418 | 38664_at | CFDP1 | AB009285 | craniofacial development protein 1 | craniofacial development protein 1 |
| 419 | 33831_at | CREBBP | U47741 | CREB binding protein (Rubinstein-Taybi syndrome) | CREB-binding protein |
| 420 | 36948_at | CRI1 | AL109701 | CREBBP/EP300 inhibitory protein 1 | C15orf3 |
| 421 | 38148_at | CRY1 | D83702 | cryptochrome 1 (photolyase-like) | photolyase |
| 422 | 37902_at | CRY2 | L13278 | crystallin, zeta (quinone reductase) | zeta-crystallin |
| 423 | 40167_s_at | LOC55884 | AF038187 | CS box-containing WD protein | |
| 424 | 38804_at | CSE1L | AF053641 | CSE1 chromosome segregation 1-like (yeast) | cellular apoptosis susceptibility protein |
| 425 | 1768_s_at | CSK | X59932 | c-src tyrosine kinase | c-src-kinase |
| 426 | 41309_g_at | CTBP1 | U37408 | C-terminal binding protein 1 | phosphoprotein CtBP |
| 427 | 40780_at | CTBP2 | AF016507 | C-terminal binding protein 2 | C-terminal binding protein 2 |
| 428 | 39723_at | CUL1 | AF062536 | cullin 1 | cullin 1 |
| 429 | 40141_at | CUL4B | AB014595 | cullin 4B | KIAA0695 protein |
| 430 | 31823_at | CUTL1 | M74099 | cut-like 1, CCAAT displacement protein (Drosophila) | cut-like 1, CCAAT displacement protein |
| 431 | 36872_at | ARPP-19 | AL120559 | cyclic AMP phosphoprotein, 19 kD | |
| 432 | 41808_at | DMTF1 | AF052102 | cyclin D binding myb-like transcription factor 1 | cyclin D binding myb-like transcription factor 1 |
| 433 | 38418_at | CCND1 | X59798 | cyclin D1 (PRAD1; parathyroid adenomatosis 1) | cyclin |
| 434 | 2020_at | CCND1 | M73554 | cyclin D1 (PRAD1; parathyroid adenomatosis 1) | bcl-1 |
| 435 | 36650_at | CCND2 | D13639 | cyclin D2 | cyclin D2 |
| 436 | 40225_at | GAK | D88435 | cyclin G associated kinase | HsGAK |
| 437 | 37723_at | CCNG2 | U47414 | cyclin G2 | cyclin G2 |
| 438 | 1913_at | CCNG2 | U47414 | cyclin G2 | cyclin G2 |
| 439 | 1924_at | CCNH | U11791 | cyclin H | cyclin H |
| 440 | 1836_at | CCNI | D50310 | cyclin I | cyclin I |
| 441 | 1792_g_at | CDK2 | M68520 | cyclin-dependent kinase 2 | cdc2-related protein kinase |

Fig 21

| | A | B | C | D | E |
|-----|------------|---------|----------|--|---|
| 442 | 33317_at | CDK7 | L20320 | cyclin-dependent kinase 7 (MO15 homolog, <i>Xenopus laevis</i> , cdk-activating kinase) | protein serine/threonine kinase |
| 443 | 1969_s_at | CDK7 | X77743 | cyclin-dependent kinase 7 (MO15 homolog, <i>Xenopus laevis</i> , cdk-activating kinase) | CDK activating kinase |
| 444 | 35140_at | CDK8 | R59697 | cyclin-dependent kinase 8 | |
| 445 | 2031_s_at | CDKN1A | U03106 | cyclin-dependent kinase inhibitor 1A (p21, Cip1) | cyclin-dependent kinase inhibitor 1A |
| 446 | 33847_s_at | CDKN1B | A1304854 | cyclin-dependent kinase inhibitor 1B (p27, Kip1) | |
| 447 | 36053_at | CDKN2C | AF041248 | cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4) | cyclin-dependent kinase inhibitor |
| 448 | 38700_at | CSRP1 | M33146 | cysteine and glycine-rich protein 1 | cysteine and glycine-rich protein 1 |
| 449 | 41401_at | CSRP2 | U57646 | cysteine and glycine-rich protein 2 | cysteine and glycine-rich protein 2 |
| 450 | 40936_at | CRIM1 | A1651806 | cysteine-rich motor neuron 1 | |
| 451 | 38772_at | CYR61 | Y11307 | cysteine-rich, angiogenic inducer, 61 | CYR61 protein |
| 452 | 40408_at | CARS | L06845 | cysteinyl-tRNA synthetase | cysteinyl-tRNA synthetase |
| 453 | 39317_at | CMAH | D86324 | cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminic acid hydroxylase) | CMP-N-acetylneuraminic acid hydroxylase |
| 454 | 34340_at | CYB5-M | AA173896 | cytochrome b5 outer mitochondrial membrane precursor | |
| 455 | 35818_at | HCS | D00265 | cytochrome c | cytochrome c |
| 456 | 39921_at | COX5B | A1526089 | cytochrome c oxidase subunit Vb | |
| 457 | 41206_r_at | COX6A1 | A1540925 | cytochrome c oxidase subunit VIa | |
| 458 | 36165_at | COX6C | W51774 | polypeptide 1 | |
| 459 | 39031_at | COX7A1 | AA152406 | cytochrome c oxidase subunit VIc | |
| 460 | 41760_at | COX7A2 | AA978033 | cytochrome c oxidase subunit VIIa | |
| 461 | 34330_at | COX7A2L | AB007618 | polypeptide 2 (liver) | |
| 462 | 34381_at | COX7C | A1708889 | cytochrome c oxidase subunit VIIa | COX7RP |
| | | | | polypeptide 2 like | |
| | | | | cytochrome c oxidase subunit VIIc | |

Fig 21

| | A | B | C | D | E |
|-----|------------|----------|----------|---|--|
| 463 | 38080_at | COX8 | A1525665 | cytochrome c oxidase subunit VIII | |
| 464 | 35819_at | CYC1 | X06994 | cytochrome c-1 | cytochrome c-1 |
| 465 | 33389_at | CYP51 | U23942 | cytochrome P450, 51 (lanosterol 14-alpha-demethylase) | lanosterol 14-demethylase cytochrome P450 |
| 466 | 859_at | CYP1B1 | U03688 | cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) | cytochrome P450 |
| 467 | 40071_at | CYP1B1 | U03688 | cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) | cytochrome P450 |
| 468 | 37509_at | CRLF3 | AF046059 | cytokine receptor-like factor 3 | cytokine receptor related protein 4 |
| 469 | 37306_at | KIAA0068 | D38549 | cytoplasmic FMRP interacting protein 1 | |
| 470 | 1706_at | A-RAF-1 | U01337 | cytoplasmic; Human Ser/Thr protein kinase (A-RAF-1) gene, complete cds. | Ser/Thr protein kinase |
| 471 | 34338_at | CKAP1 | D49738 | cytoskeleton-associated protein 1 | cytoskeleton associated protein |
| 472 | 32529_at | CKAP4 | X69910 | cytoskeleton-associated protein 4 | P63 protein |
| 473 | 40282_s_at | DF | M84526 | D component of complement (adipsin) | adipsin/complement factor D |
| 474 | 40877_s_at | MN7 | AF041080 | D15F37 (pseudogene) | |
| 475 | 1243_at | DDB2 | U18300 | damage-specific DNA binding protein 2 (48kD) | DDBb p48 |
| 476 | 36616_at | DAZAP2 | D31767 | DAZ associated protein 2 | DAZ associated protein 2 |
| 477 | 37663_at | DDX1 | X70649 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 | member of DEAD box protein family |
| 478 | 35306_at | DDX15 | AB001636 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 15 | ATP-dependent RNA helicase #46 |
| 479 | 40490_at | DDX21 | U41387 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 21 | Gu protein |
| 480 | 39744_at | DDX3 | AF000982 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3 | dead box, X isoform |
| 481 | 34647_at | DDX5 | X52104 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kD) | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 |
| 482 | 36153_at | DDX9 | L13848 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase II; leukophysin) | RNA helicase A |
| 483 | 41872_at | DFNA5 | AF073308 | deafness, autosomal dominant 5 | nonsyndromic hearing impairment protein |

Fig 21

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| | A | B | C | D | E |
|-----|------------|-----------|----------|--|---|
| 484 | 1356_at | DAP3 | U18321 | death associated protein 3 | ionizing radiation resistance conferring protein |
| 485 | 39114_at | DEPP | AB022718 | decidual protein induced by progesterone | DEPP |
| 486 | 37638_at | DOCK1 | D50857 | dedicator of cyto-kinesis 1 | DOCK180 protein |
| 487 | 38413_at | DAD1 | D15057 | defender against cell death 1 | DAD-1 |
| 488 | 32824_at | CLN2 | AF039704 | deficient in late-infantile neuronal ceroid lipofuscinosis; Homo sapiens lysosomal pepstatin insensitive protease (CLN2) gene, complete cds. | lysosomal pepstatin insensitive protease |
| 489 | 33337_at | DEGS | AF002668 | degenerative spermatocyte homolog, lipid desaturase (Drosophila) | MLD |
| 490 | 38992_at | DEK | X64229 | DEK oncogene (DNA binding) | putative oncogene |
| 491 | 37951_at | DLC1 | AF035119 | deleted in liver cancer 1 | deleted in liver cancer-1 |
| 492 | 33791_at | DLEU1 | Y15227 | deleted in lymphocytic leukemia, 1 | deleted in lymphocytic leukemia, 1 |
| 493 | 38744_at | DSS1 | IN95406 | Deleted in split-hand/split-foot 1 region | |
| 494 | 36629_at | DSIP1 | AI635895 | delta sleep inducing peptide, immunoreactor | |
| 495 | 35814_at | GA17 | AF064603 | dendritic cell protein | GA17 protein |
| 496 | 38385_at | DSTN | S65738 | desmin (actin depolymerizing factor) | actin depolymerizing factor |
| 497 | 39410_at | DDEF2 | AB007860 | development and differentiation enhancing factor 2 | development- and differentiation-enhancing factor 2 |
| 498 | 39044_s_at | DGKD | D73409 | diacylglycerol kinase, delta (130kD) | diacylglycerol kinase delta |
| 499 | 38003_s_at | DGKZ | U94905 | diacylglycerol kinase, zeta (104kD) | diacylglycerol kinase zeta |
| 500 | 33920_at | DIAPH1 | AF051782 | diaphanous homolog 1 (Drosophila) | diaphanous 1 |
| 501 | 37692_at | DBI | AI557240 | diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein) | |
| 502 | 39041_at | DLAT | Y00978 | dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) | PDC-E2 precursor (AA -54 to 561) |
| 503 | 40607_at | DPYSL2 | U97105 | dihydropyrimidinase-like 2 | N2A3 |
| 504 | 36149_at | DPYSL3 | D78014 | dihydropyrimidinase-like 3 | dihydropyrimidinase related protein-3 |
| 505 | 39503_s_at | DPYSL4 | AB006713 | dihydropyrimidinase-like 4 | dihydropyrimidinase related protein 4 |
| 506 | 38220_at | DPYD | U20938 | dihydropyrimidine dehydrogenase | dihydropyrimidine dehydrogenase |
| 507 | 40485_at | HSA249128 | AA176780 | DIPB protein | |

Fig 21

| | A | B | C | D | E |
|----------------|---|------------|----------|---|---|
| 508 479_at | | DAB2 | U53446 | disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) | DOC-2 |
| 509 36643_at | | DDR1 | L20817 | discoidin domain receptor family, member 1 | tyrosine protein kinase |
| 510 40575_at | | DLG5 | AB011155 | discs, large (Drosophila) homolog 5 | KIAA0583 protein |
| 511 33753_at | | DAAM1 | AB014566 | dishevelled associated activator of morphogenesis 1 | KIAA0666 protein |
| 512 33150_at | | SAS10 | AI126004 | disrupter of silencing 10 | |
| 513 40916_at | | dJ635G19.1 | AL035494 | dJ635G19.1 (LAMR1 (Laminin Receptor 1 (67kD) (RPSA, 40S Ribosomal Protein SA, P40)) pseudogene); match: cDNAs: Em:X15005 Em:J03799 Em:X61156 Em:M64923 Em:X06406 Em:AF140348 Em:J02870 Em:L16589 Em:Z22749 Em:D25224 Em:M14199 Em:M27798; match: ESTs: Em:AA642 | dJ635G19.2.1 (novel protein (isoform 1)) |
| 514 38456_s_at | | dJ734P14.1 | AL049650 | dJ734P14.1 (KRAB box and C2H2 Zinc finger domain protein pseudogene) match: cDNAs: Em:M27878 Em:M29580 Em:U27186 Em:D31763 Em:AB007872 Em:U09366 Em:U09413 Em:X17617 Em:AF011573 Em:AF020591 Em:X78925 match: proteins: Sw:P52736 Sw:Q06730 Sw:P51523 Tr:Q14585 Sw:P15620 Sw:Q02386 Sw:P51786 Sw:Q99676 Tr:O60792 Sw:Q03923 Sw:O75820 Tr:Q61116 Tr:Q64247 | dJ734P14.2.1 (snRNP (small nuclear ribonucleoprotein particle) protein B) |

Fig 2.1

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| | A | B | C | D | E |
|-----|------------|------------|----------|---|--|
| 515 | 38455_at | dJ734P14.1 | AL049650 | dJ734P14.1 (KRAB box and C2H2 Zinc finger domain protein pseudogene) match: cDNAs: Em:M27878 Em:M29580 Em:U27186 Em:D31763 Em:AB007872 Em:U09366 Em:U09413 Em:X17617 Em:AF011573 Em:AF020591 Em:X78925 match: proteins: Sw:P52736 Sw:Q06730 Sw:P51523 Tr:Q14585 Sw:P15620 Sw:Q02386 Sw:P51786 Sw:Q99676 Tr:O60792 Sw:Q03923 Sw:O75820 Tr:Q61116 Tr:Q64247 | dJ734P14.2.1 (snRNP (small nuclear ribonucleoprotein particle) protein B) |
| 516 | 35809_g_at | dJ862K6.4 | AL031681 | dJ862K6.4 (pseudogene similar to part of NBP (Nucleotide Binding Protein)) match: proteins: Sw:P53384 Sw:P52920 Sw:P21590 Sw:Q57731 Sw:P40558 | dJ862K6.2.2 (splicing factor, arginine/serine-rich 6 (SRP55-2)(isoform 2)) |
| 517 | 35808_at | dJ862K6.4 | AL031681 | dJ862K6.4 (pseudogene similar to part of NBP (Nucleotide Binding Protein)) match: proteins: Sw:P53384 Sw:P52920 Sw:P21590 Sw:Q57731 Sw:P40558 | dJ862K6.2.2 (splicing factor, arginine/serine-rich 6 (SRP55-2)(isoform 2)) |
| 518 | 32433_at | dJ90L6.1 | Z97353 | dJ90L6.1 (RPL15 (60S Ribosomal Protein L15) pseudogene); match: proteins: Sw:O74895 Sw:P51417 Sw:P39030 Sw:O17445 Sw:P54780 Sw:O23515 Sw:O65050 Wp:CE12148 Sw:P30736 Sw:P41051 Sw:P54060 Sw:O65082 Sw:P52818 Sw:P79324 Sw:O82712 Sw:O13418 Sw:O82528 Sw:P05748; Human DNA sequence from clone RP1-90L6 on chromosome 22q11.21-11.23 Contains an RPL15 (60S Ribosomal Protein L15) pseudogene, ESTs, STSs and GSSs, complete sequence. | |

Fig 21

| | A | B | C | D | E |
|-----|------------|---------------|----------|--|--|
| 519 | 34183_at | DKFZP434C171 | AL080169 | DKFZP434C171 protein | hypothetical protein |
| 520 | 40801_at | DKFZP434C212 | AA643063 | DKFZP434C212 protein | |
| 521 | 38400_at | DKFZP434D1335 | AI920820 | DKFZP434D1335 protein | |
| 522 | 33392_at | DKFZP434J154 | AL080155 | DKFZP434J154 protein | hypothetical protein |
| 523 | 39411_at | DKFZP434J214 | AL080156 | DKFZP434J214 protein | hypothetical protein |
| 524 | 40564_at | DKFZP564A043 | N42007 | DKFZP564A043 protein | |
| 525 | 37000_at | DKFZP564B167 | AL035304 | DKFZP564B167 protein | hypothetical protein |
| 526 | 33433_at | DKFZP564F0522 | AL049943 | DKFZP564F0522 protein | hypothetical protein |
| 527 | 41437_at | DKFZP564F1123 | AL080118 | DKFZP564F1123 protein | hypothetical protein |
| 528 | 39442_at | DKFZP564G0222 | AL080115 | DKFZP564G0222 protein | hypothetical protein |
| 529 | 40437_at | DKFZP564G2022 | AL049944 | DKFZP564G2022 protein | hypothetical protein |
| 530 | 36456_at | DKFZP564I052 | AL080063 | DKFZP564I052 protein | hypothetical protein |
| 531 | 38033_at | DKFZP564M1416 | AL049934 | DKFZP564M1416 protein | hypothetical protein |
| 532 | 36078_at | DKFZP564O0423 | AL080120 | DKFZP564O0423 protein | hypothetical protein |
| 533 | 38256_s_at | DKFZP564O092 | W21827 | DKFZP564O092 protein | |
| 534 | 39034_at | DKFZP564O123 | AL080122 | DKFZP564O123 protein | hypothetical protein |
| 535 | 41662_at | DKFZP566B183 | AL050272 | DKFZP566B183 protein | hypothetical protein |
| 536 | 32807_at | DKFZP566C134 | AF004292 | DKFZP566C134 protein | |
| 537 | 38687_at | DKFZP566D193 | AL050051 | DKFZP566D193 protein | hypothetical protein |
| 538 | 33776_at | DKFZP566K023 | AL050062 | DKFZP566K023 protein | hypothetical protein |
| 539 | 41335_at | DC8 | AL050084 | DKFZP566O1646 protein | hypothetical protein |
| 540 | 36961_at | DKFZP586A011 | AL050286 | DKFZP586A011 protein | hypothetical protein |
| 541 | 38717_at | DKFZP586A0522 | AL050159 | DKFZP586A0522 protein | hypothetical protein |
| 542 | 40831_at | DKFZP586B0923 | AL050190 | DKFZP586B0923 protein | hypothetical protein |
| 543 | 34821_at | DKFZP586D0623 | AL050197 | DKFZP586D0623 protein | hypothetical protein |
| 544 | 39986_at | DKFZP586D0919 | AL050100 | DKFZP586D0919 protein | hypothetical protein |
| 545 | 34269_at | DKFZP586F1019 | AL050102 | DKFZP586F1019 protein | hypothetical protein |
| 546 | 35736_at | DKFZP586F1918 | AL050091 | DKFZP586F1918 protein | hypothetical protein |
| 547 | 40832_s_at | DKFZP586G011 | AL050126 | DKFZP586G011 protein | hypothetical protein |
| 548 | 36007_at | DKFZP586L151 | AL050137 | DKFZP586L151 protein | hypothetical protein |
| 549 | 34833_at | DKFZP586O0120 | AL050157 | DKFZP586O0120 protein | hypothetical protein |
| 550 | 37333_at | DNMT1 | X63692 | DNA (cytosine-5-)-methyltransferase 1 | DNA (cytosine-5-)-methyltransferase |
| 551 | 40891_f_at | DXS9879E | X92896 | DNA segment on chromosome X (unique) 9879 expressed sequence | ITBA2' protein |
| 552 | 34215_at | DXYS155E | L03426 | DNA segment on chromosome X and Y (unique) 155 expressed sequence | DNA segment on chromosome X and Y (unique) 155 expressed sequence |

Fig 21

| | A | B | C | D | E |
|-----|------------|---------|----------|---|--|
| 553 | 1252_at | D5S346 | M73547 | DNA segment, single copy probe LNS-CAV/LNS-CAII (deleted in polyposis) | polyposis locus-encoded protein |
| 554 | 37162_at | D10S170 | S72869 | DNA segment, single copy, probe pH4 (transforming sequence, thyroid-1, | DNA segment, single copy, probe pH4 (transforming sequence, thyroid-1, |
| 555 | 39118_at | DNAJA1 | L08069 | DnaJ (Hsp40) homolog, subfamily A, member 1 | DNAJ homologue-2 |
| 556 | 276_at | DNAJA1 | L08069 | DnaJ (Hsp40) homolog, subfamily A, member 1 | DNAJ homologue-2 |
| 557 | 41233_at | DNAJB6 | AB014888 | DnaJ (Hsp40) homolog, subfamily B, member 6 | MRJ |
| 558 | 35799_at | DNAJB9 | AL080081 | DnaJ (Hsp40) homolog, subfamily B, member 9 | hypothetical protein |
| 559 | 36166_at | DNAJC8 | AF083190 | DnaJ (Hsp40) homolog, subfamily C, member 8 | SPF31 |
| 560 | 816_g_at | DOK1 | U70987 | docking protein 1, 62kD (downstream of tyrosine kinase 1) | GAP binding protein p62dok |
| 561 | 34433_at | DOK1 | AF035299 | docking protein 1, 62kD (downstream of tyrosine kinase 1) | docking protein 1 |
| 562 | 34879_at | DPM1 | AF007875 | dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit | dolichol monophosphate mannosyltransferase |
| 563 | 38957_at | DCAMKL1 | AB002367 | doublecortin and CaM kinase-like 1 | doublecortin and CaM kinase-like 1 |
| 564 | 32168_s_at | DSCR1 | U85267 | Down syndrome critical region gene 1 | Down syndrome critical region protein 1 |
| 565 | 36088_at | DSCR2 | AJ006291 | Down syndrome critical region gene 2 | leucine rich protein |
| 566 | 35166_at | DSCR3 | D87343 | Down syndrome critical region gene 3 | DCRA |
| 567 | 32621_at | DR1 | M97388 | down-regulator of transcription 1, TBP-binding (negative cofactor 2) | TATA binding protein-associated phosphoprotein |
| 568 | 37981_at | DBN1 | D17530 | drebrin 1 | drebrin E |
| 569 | 40920_at | cdc14B | AF023158 | dual specific protein; Homo sapiens tyrosine phosphatase (cdc14B) mRNA, complete cds. | tyrosine phosphatase |
| 570 | 39727_at | DUSP11 | AF023917 | dual specificity phosphatase 11 (RNA/RNP complex 1-interacting) | PIR1 |
| 571 | 38272_at | DUSP14 | AF038844 | dual specificity phosphatase 14 | MKP-1 like protein tyrosine phosphatase |
| 572 | 41225_at | DUSP3 | AL049417 | dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related) | |

Fig 21

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| | A | B | C | D | E |
|-----|------------|----------|----------|---|--|
| 573 | 41193_at | DUSP6 | AB013382 | dual specificity phosphatase 6 | DUSP6 |
| 574 | 36946_at | DYRK1A | D86550 | dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A | serine/threonine protein kinase |
| 575 | 1512_at | DYRK1A | D86550 | dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A | serine/threonine protein kinase |
| 576 | 760_at | DYRK2 | Y09216 | dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 | dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 isoform 1 |
| 577 | 39931_at | DYRK3 | Y12735 | dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 | Dyrk3 protein |
| 578 | 38368_at | DUT | U31930 | dUTP pyrophosphatase | deoxyuridine nucleotidohydrolase |
| 579 | 38475_at | DCTN2 | U50733 | dynactin 2 (p50) | dynamitin |
| 580 | 34891_at | PIN | A1540958 | dynein, cytoplasmic, light polypeptide | |
| 581 | 34829_at | DKC1 | U59151 | dyskeratosis congenita 1, dyskerin | Cbl5p homolog |
| 582 | 32234_at | DYT1 | AF007871 | dystonia 1, torsion (autosomal dominant; torsin A) | torsinA |
| 583 | 36989_at | DAG1 | L19711 | dystroglycan 1 (dystrophin-associated glycoprotein 1) | dystroglycan |
| 584 | 40488_at | DMD | M18533 | dystrophin (muscular dystrophy, Duchenne and Becker types) | dystrophin |
| 585 | 40106_at | E1B-AP5 | AJ007509 | E1B-55kDa-associated protein 5 | E1B-55kDa-associated protein |
| 586 | 33354_at | SMURF2 | AA630312 | E3 ubiquitin ligase SMURF2 | |
| 587 | 40375_at | EGR3 | X63741 | early growth response 3 | transcription factor |
| 588 | 36135_at | EBNA1BP2 | U86602 | EBNA1 binding protein 2 | nucleolar protein p40 |
| 589 | 37730_at | p100 | U22055 | EBNA-2 co-activator (100kD) | 100 kDa coactivator |
| 590 | 33254_at | EVI5 | AF008915 | ectopic viral integration site 5 | EVI-5 homolog |
| 591 | 39542_at | ENC1 | AF059611 | ectodermal-neural cortex (with BTB-like domain) | nuclear matrix protein NRP/B |
| 592 | 41124_r_at | ENPP2 | L35594 | ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin) | autotaxin |
| 593 | 41123_s_at | ENPP2 | L35594 | ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin) | autotaxin |
| 594 | 32551_at | EFEMP1 | U03877 | EGF-containing fibulin-like extracellular matrix protein 1 | extracellular protein |

Fig 21

| | A | B | C | D | E |
|-----|-----------|------------|----------|--|---|
| 595 | 36488_at | EGFL5 | AB011542 | EGF-like-domain, multiple 5 | MEGF9 |
| 596 | 40509_at | ETFA | J04058 | electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II) | electron transfer flavoprotein, alpha polypeptide |
| 597 | 36881_at | ETFB | X71129 | electron-transfer-flavoprotein, beta polypeptide | electron transfer flavoprotein beta subunit |
| 598 | 1288_s_at | EEF1A | J04617 | elongation factor EF-1-alpha; Human | eukaryotic translation elongation factor 1 |
| 599 | 31853_at | EED | AF080227 | complete cds. | alpha 1 |
| | | | | embryonic ectoderm development | embryonic ectoderm development protein |
| 600 | 39861_at | EMS1 | M98343 | ems1 sequence (mammary tumor and squamous cell carcinoma-associated (p80/85 src substrate) | amplixin |
| | | | | end of last exon based on GENSCAN prediction presumably this gene and dJ477H23.2 are part of the same gene | |
| 601 | 41478_at | dJ477H23.1 | AL033538 | match: ESTs: Em:AA354647 | dJ477H23.1 (novel protein) |
| 602 | 37408_at | ENDO180 | AB014609 | endocytic receptor (macrophage mannose receptor family) | KIAA0709 protein |
| 603 | 37914_at | ENDOFIN | AB002303 | endosome-associated FYVE-domain protein | endosome-associated FYVE-domain protein |
| 604 | 39010_at | ENSA | A1658639 | endosulfine alpha | |
| | | | | endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2 | lysophosphatidic acid receptor homolog |
| 605 | 40387_at | EDG2 | U80811 | | |
| 606 | 40874_at | EDF1 | AJ005259 | endothelial differentiation-related factor 1 | endothelial differentiation-related factor 1 |
| 607 | 39079_at | ERH | D85758 | enhancer of rudimentary homolog (Drosophila) | human protein homologous to DROER protein |
| 608 | 2035_s_at | ENO1 | M55914 | enolase 1, (alpha) | c-myc binding protein |
| 609 | 34335_at | EFNB2 | A1765533 | ephrin-B2 | |
| 610 | 37731_at | EPS15 | Z29064 | epidermal growth factor receptor pathway substrate 15 | epidermal growth factor receptor pathway substrate 15 |
| 611 | 1467_at | EPS8 | U12535 | epidermal growth factor receptor pathway substrate 8 | epidermal growth factor receptor kinase substrate |
| 612 | 37762_at | EMP1 | Y07909 | epithelial membrane protein 1 | progression associated protein |
| 613 | 39631_at | EMP2 | U52100 | epithelial membrane protein 2 | XMP |

Fig 21

| | A | B | C | D | E |
|-----|------------|------------|----------|--|---------------|
| 614 | 35816_at | cystatin B | U46692 | EPM1 disease gene; cysteine protease inhibitor; Human cystatin B gene, complete cds. | cystatin B |
| 615 | 32585_at | EPB41L2 | AF027299 | erythrocyte membrane protein band 4.1-like 2 | protein 4.1-G |
| 616 | 38375_at | ESD | AF112219 | esterase D/formylglutathione hydrolase | esterase D |
| 617 | 38283_at | EBAG9 | AB007619 | estrogen receptor binding site associated, antigen, 9 | EBAG9 |
| 618 | 37161_at | | W28948 | ESTs | |
| 619 | 40885_s_at | | N30151 | ESTs | |
| 620 | 33328_at | C1S | W28612 | ESTs | |
| 621 | 33453_at | ATP6S1 | AI400326 | ESTs | |
| 622 | 31801_at | | AI808712 | ESTs | |
| 623 | 41598_at | | AA890010 | ESTs | |
| 624 | 32744_at | RPS21 | AI526078 | ESTs, Highly similar to RS21_HUMAN 40S RIBOSOMAL PROTEIN S21 [H.sapiens] | |
| 625 | 39750_at | | W61005 | ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens] | |
| 626 | 34906_g_at | | AA977136 | ESTs, Moderately similar to GLK5_HUMAN GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 5 PRECURSOR [H.sapiens] | |
| 627 | 35787_at | | AI986201 | ESTs, Moderately similar to T46365 hypothetical protein DKFZp434A1518.1 [H.sapiens] | |
| 628 | 41463_at | | AL042729 | ESTs, Weakly similar to 0903209A peptide PD, basic Pro rich [H.sapiens] | |
| 629 | 41273_at | | AL046940 | ESTs, Weakly similar to N-WASP [H.sapiens] | |
| 630 | 38097_at | PIG8 | AF010313 | etoposide-induced mRNA | Pig8 |
| 631 | 40888_f_at | EEF1A1 | W28170 | eukaryotic translation elongation factor 1 alpha 1 | |

fig 21

| | A | B | C | D | E |
|-----|------------|--------|----------|--|---|
| 632 | 35175_f_at | EEF1A2 | X70940 | eukaryotic translation elongation factor 1 alpha 2 | elongation factor 1 alpha-2 |
| 633 | 35748_at | EEF1B2 | X60489 | eukaryotic translation elongation factor 1 beta 2 | elongation factor-1-beta |
| 634 | 41256_at | EEF1D | Z21507 | eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) | human elongation factor-1-delta |
| 635 | 1676_s_at | EEF1G | M55409 | eukaryotic translation elongation factor 1 gamma | pancreatic tumor-related protein |
| 636 | 36587_at | EEF2 | Z11692 | eukaryotic translation elongation factor 2 | human elongation factor 2 |
| 637 | 663_at | EIF1A | L18960 | eukaryotic translation initiation factor 1A | protein synthesis factor |
| 638 | 34278_at | EIF1A | L18960 | eukaryotic translation initiation factor 1A | protein synthesis factor |
| 639 | 1154_at | EIF2S1 | J02645 | eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kD) | eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kD) |
| 640 | 40515_at | EIF2B2 | AF035280 | eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) | eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) |
| 641 | 1644_at | EIF3S2 | U36764 | eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD) | TGF-beta receptor interacting protein 1 |
| 642 | 35327_at | EIF3S3 | U54559 | eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD) | translation initiation factor eIF3 p40 subunit |
| 643 | 32576_at | EIF3S5 | U94855 | eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD) | translation initiation factor 3 47 kDa subunit |
| 644 | 38681_at | EIF3S6 | U62962 | eukaryotic translation initiation factor 3, subunit 6 (48kD) | murine mammary tumor integration site 6 (oncogene homolog) |
| 645 | 35298_at | EIF3S7 | U54558 | eukaryotic translation initiation factor 3, subunit 7 (zeta, 66/67kD) | translation initiation factor eIF3 p66 subunit |
| 646 | 35323_at | EIF3S9 | U78525 | eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD) | eukaryotic translation initiation factor |
| 647 | 41785_at | EIF4G2 | U73824 | eukaryotic translation initiation factor 4 gamma, 2 | p97 |
| 648 | 33907_at | EIF4G3 | AF012072 | eukaryotic translation initiation factor 4 gamma, 3 | eIF4GII |

Fig 21

| | A | B | C | D | E |
|-----|------------|----------|----------|--|---|
| 649 | 1420_s_at | EIF4A2 | D30655 | eukaryotic translation initiation factor 4A, isoform 2 | eukaryotic initiation factor 4AII |
| 650 | 37752_at | EIF4E | M15353 | eukaryotic translation initiation factor 4E | cap-binding protein |
| 651 | 35263_at | EIF4EBP2 | N73769 | eukaryotic translation initiation factor 4E binding protein 2 | |
| 652 | 167_at | EIF5 | U49436 | eukaryotic translation initiation factor 5 | translation initiation factor 5 |
| 653 | 37318_at | ETF1 | X81625 | eukaryotic translation termination factor 1 | C11 protein |
| | | | | excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing) | excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing) |
| 654 | 1885_at | ERCC3 | M31899 | excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome)) | |
| 655 | 2063_at | ERCC5 | L20046 | | excision repair protein |
| 656 | 33734_at | HSD11B1 | AL022398 | exons 1-4 beyond this clone; match: proteins P28845 P50172 P51975 Q29608 | dJ434O14.1 (Hydroxysteroid (11-beta) Dehydrogenase 1 (EC 1.1.1.146)) |
| 657 | 222_at | EXT1 | S79639 | exostoses (multiple) 1 | exostoses (multiple) 1 |
| 658 | 36526_at | EXTL2 | AF000416 | exostoses (multiple)-like 2 | EXT-like protein 2 |
| 659 | 38809_s_at | EXTL3 | AB011091 | exostoses (multiple)-like 3 | KIAA0519 protein |
| 660 | 37729_at | XPO1 | Y08614 | exportin 1 (CRM1 homolog, yeast) | exportin 1 |
| 661 | 38753_at | XPOT | AF039022 | exportin, tRNA (nuclear export receptor for tRNAs) | exportin t |
| 662 | 39673_i_at | ECM2 | AB011792 | extracellular matrix protein 2, female organ and adipocyte specific | extracellular matrix protein |
| 663 | 39674_r_at | ECM2 | AB011792 | extracellular matrix protein 2, female organ and adipocyte specific | extracellular matrix protein |
| 664 | 35226_at | EYA2 | U71207 | eyes absent homolog 2 (Drosophila) | Eab1 |
| 665 | 38318_at | FAM8A1 | AL050128 | family with sequence similarity 8, member A1 | |
| 666 | 31879_at | FUBP3 | U69127 | far upstream element (FUSE) binding protein 3 | FUSE binding protein 3 |

Fig 21

| | A | B | C | D | E |
|-----|-----------|---------|---------------|--|---|
| 667 | 37325_at | FDPS | D14697 | farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) | farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) |
| 668 | 34848_at | FDFT1 | X69141 | farnesyl-diphosphate farnesyltransferase 1 | farnesyl-diphosphate farnesyltransferase |
| 669 | 1499_at | FNTA | L10413 | farnesyltransferase, CAAX box, alpha | farnesyl-protein transferase alpha-subunit |
| 670 | 38755_at | FADD | X84709 | Fas (TNFRSF6)-associated via death domain | mediator of receptor induced toxicity |
| 671 | 37743_at | FEZ1 | U60060 | fasciculation and elongation protein zeta 1 (zyglin I) | FEZ1 |
| 672 | 38651_at | FEZ2 | U60061 | fasciculation and elongation protein zeta 2 (zyglin II) | FEZ2 |
| 673 | 40454_at | FAT | X87241 | FAT tumor suppressor homolog 1 (Drosophila) | homologue of Drosophila Fat protein |
| 674 | 40082_at | FACL2 | D10040 | fatty-acid-Coenzyme A ligase, long-chain 2 | long-chain acyl-CoA synthetase |
| 675 | 33880_at | FACL3 | D89053 | fatty-acid-Coenzyme A ligase, long-chain 3 | Acyl-CoA synthetase 3 |
| 676 | 33881_at | FACL3 | AA977580 | fatty-acid-Coenzyme A ligase, long-chain 3 | |
| 677 | 33360_at | FBXL11 | AB023221 | F-box and leucine-rich repeat protein 11 | KIAA1004 protein |
| 678 | 37205_at | FBXL7 | AB020647 | F-box and leucine-rich repeat protein 7 | KIAA0840 protein |
| 679 | 32854_at | FBXW1B | AB014596 | F-box and WD-40 domain protein 1B | KIAA0696 protein |
| 680 | 32169_at | FBXO21 | AB020682 | F-box only protein 21 | KIAA0875 protein |
| 681 | 35337_at | FBXO7 | AL050254 | F-box only protein 7 | hypothetical protein |
| 682 | 33817_at | D10S102 | S63912 | FBFNP; heterogeneous ribonucleoprotein homolog; This sequence comes from Fig. 3; D10S102=FBFNP [human, fetal brain, mRNA, 3043 nt] | FBFNP |
| 683 | 1877_g_at | nifH | HG1103-HT1103 | Fe protein | dinitrogenase reductase |
| 684 | 34678_at | FER1L3 | AL096713 | fer-1-like 3, myoferlin (C. elegans) | hypothetical protein |
| 685 | 32148_at | FARP1 | AI701049 | FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) | |

Fig 21

| | A | B | C | D | E |
|-----|------------|-------|----------|--|--|
| 686 | 33943_at | FTH1 | L20941 | ferritin, heavy polypeptide 1 | ferritin heavy chain |
| 687 | 41091_at | FALZ | U05237 | fetal Alzheimer antigen | fetal Alzheimer antigen |
| 688 | 32535_at | FBN1 | X63556 | fibrillin 1 (Marfan syndrome) | fibrillin |
| 689 | 39945_at | FAP | U09278 | fibroblast activation protein, alpha | fibroblast activation protein |
| 690 | 1380_at | FGF7 | M60828 | fibroblast growth factor 7 (keratinocyte growth factor) | keratinocyte growth factor |
| 691 | 2057_g_at | FGFR1 | M34641 | fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome) | fibroblast growth factor receptor 1, isoform 1 precursor; fibroblast growth factor receptor 1, isoform 2 precursor; fibroblast growth factor receptor 1, isoform 3 precursor; fibroblast growth factor receptor 1, isoform 4 precursor; fibroblast growth factor receptor 1, isoform 5 precursor; fibroblast growth factor receptor 1, isoform 6 precursor; fibroblast growth factor receptor 1, isoform 7 precursor; fibroblast growth factor receptor 1, isoform 8 precursor; fibroblast growth factor receptor 1, isoform 9 precursor |
| 692 | 31720_s_at | FN1 | M10905 | | fibronectin 1, isoform 1 preproprotein; |
| 693 | 31719_at | FN1 | X02761 | | fibronectin 1, isoform 2 preproprotein |
| 694 | 34853_at | FLRT2 | AB007865 | | fibronectin precursor |
| 695 | 38026_at | FBLN1 | U01244 | fibronectin leucine rich transmembrane protein 2 | protein 2 |
| 696 | 39038_at | FBLN5 | AF093118 | fibulin 1 | fibulin-1D |
| 697 | 38078_at | FLNB | AF042166 | fibulin 5 | UP50 |
| 698 | 38761_s_at | FKBP9 | AA487755 | filamin B, beta (actin binding protein 278) | beta-filamin |
| 699 | 40665_at | FMO3 | M83772 | FK506 binding protein 9 (63 kD) | flavoprotein |
| 700 | 35254_at | FLN29 | AB007447 | flavin containing monooxygenase 3 | Fln29 |
| 701 | 38356_at | FST | M19481 | FLN29 gene product | follistatin isoform FST317 precursor; |
| | | | | follistatin precursor; Human follistatin gene, exon 6. | follistatin isoform FST344 precursor |

Fig 21

| | A | B | C | D | E |
|-----|------------|-----------|----------|---|--|
| 702 | 41027_at | FKHL7 | AF078096 | forkhead (Drosophila)-like 7; FREAC3; Homo sapiens forkhead/winged helix-like transcription factor 7 (FKHL7) gene, complete cds. | forkhead/winged helix-like transcription factor 7 |
| 703 | 36319_at | FOXF2 | U13220 | forkhead box F2 | forkhead protein FREAC-2 |
| 704 | 40570_at | FOXO1A | AF032885 | forkhead box O1A (rhabdomyosarcoma) | forkhead protein |
| 705 | 34740_at | FOXO3A | AF032886 | forkhead box O3A | forkhead protein |
| 706 | 32542_at | FHL1 | AF063002 | four and a half LIM domains 1 | LIM protein SLIMMER |
| 707 | 38422_s_at | FHL2 | U29332 | four and a half LIM domains 2 | heart protein |
| 708 | 41649_at | FHX | AF038177 | FOXJ2 forkhead factor | |
| 709 | 34997_r_at | FZD5 | U43318 | frizzled homolog 5 (Drosophila) | transmembrane receptor |
| 710 | 34472_at | FZD6 | AB012911 | frizzled homolog 6 (Drosophila) | Frizzled-6 |
| 711 | 33222_at | FZD7 | AB017365 | frizzled homolog 7 (Drosophila) | frizzled-7 |
| 712 | 38923_at | FRG1 | L76159 | FSDH region gene 1 | FSDH region gene 1 |
| 713 | 38139_at | FPGT | AF017445 | fructose-1-phosphate guanylyltransferase | GDP-L-fucose pyrophosphorylase |
| 714 | 41814_at | FUCA1 | M29877 | fructosidase, alpha-L-1, tissue | fructosidase, alpha-L-1, tissue |
| 715 | 40022_at | FCMD | AB008226 | Fukuyama type congenital muscular dystrophy (fukutin) | fukutin |
| 716 | 32546_at | FH | U59309 | fumarate hydratase | fumarate precursor |
| 717 | 36145_at | SIAHBP1 | U51586 | fuse-binding protein-interacting repressor | siah binding protein 1 |
| 718 | 40480_s_at | FYN | M14333 | FYN oncogene related to SRC, FGR, YES | FYN oncogene related to SRC, FGR, YES |
| 719 | 2039_s_at | FYN | M14333 | FYN oncogene related to SRC, FGR, YES | FYN oncogene related to SRC, FGR, YES |
| 720 | 34288_at | RDC1 | U67784 | G protein-coupled receptor | orphan G protein-coupled receptor |
| 721 | 37308_at | GPR107 | AI88084 | G protein-coupled receptor 107 | |
| 722 | 37298_at | GABARAP | AF044671 | GABA(A) receptor-associated protein | MM46 |
| 723 | 35785_at | GABARAPL1 | W28281 | GABA(A) receptor-associated protein like 1 | |
| 724 | 35767_at | GABARAPL2 | AI565760 | GABA(A) receptor-associated protein-like 2 | |
| 725 | 37825_at | GALK2 | M84443 | galactokinase 2 | galactokinase |
| 726 | 37742_at | GLB1 | M34423 | galactosidase, beta 1 | galactosidase, beta 1 |

Fig 21

| | A | B | C | D | E |
|-----|------------|----------|----------|---|--|
| 727 | 37263_at | GGH | U55206 | gamma-glutamyl hydrolase (conjugase, poly/polyglutamyl hydrolase) | human gamma-glutamyl hydrolase |
| 728 | 32531_at | GJA1 | X52947 | gap junction protein, alpha 1, 43kD (connexin 43) | connexin 43 |
| 729 | 36603_at | GCN1L1 | D86973 | GCN1 general control of amino-acid synthesis 1-like 1 (yeast) | |
| 730 | 35307_at | GDI2 | Y13286 | GDP dissociation inhibitor 2 | GDP dissociation inhibitor beta |
| 731 | 39386_at | KIAA0110 | D14811 | gene predicted from cDNA with a complete coding sequence | gene predicted from cDNA with a complete coding sequence |
| 732 | 32180_s_at | RES4-22 | AB000461 | gene with multiple splice variants near HD locus on 4p16.3 | gene with multiple splice variants near HD locus on 4p16.3 |
| 733 | 466_at | GTF2I | U77948 | general transcription factor II, i | Bruton's tyrosine kinase-associated protein-135 |
| 734 | 35450_s_at | GTF2I | AF015553 | general transcription factor II, i | TFII-I protein |
| 735 | 37010_at | GTF2A2 | AI203737 | general transcription factor IIA, 2 (12kD subunit) | |
| 736 | 869_at | GTF2A2 | U14193 | general transcription factor IIA, 2 (12kD subunit) | transcription factor IIA small 12 kDa subunit |
| 737 | 37882_at | GTF2E1 | X63468 | general transcription factor IIE, polypeptide 1 (alpha subunit, 56kD) | TFIIE-alpha |
| 738 | 37295_at | GTF2E2 | X63469 | general transcription factor IIE, polypeptide 2 (beta subunit, 34kD) | TFIIE-beta |
| 739 | 38782_at | GTF2H1 | M95809 | general transcription factor IIH, polypeptide 1 (62kD subunit) | basic transcription factor 62kD subunit |
| 740 | 40754_at | GTF2H3 | Z30093 | general transcription factor IIH, polypeptide 3 (34kD subunit) | basic transcription factor 2, 35 kD subunit |
| 741 | 36188_at | GTF3A | D32257 | general transcription factor IIIA | Xenopus transcription factor IIIA homologue |
| 742 | 35296_at | GGPS1 | AB019036 | geranylgeranyl diphosphate synthase 1 | geranylgeranyl pyrophosphate synthase |
| 743 | 763_at | GMFB | AB001106 | glia maturation factor, beta | glia maturation factor |
| 744 | 39793_at | GBAS | AF029786 | glioblastoma amplified sequence | GBAS |
| | | | | glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) | |
| 745 | 32643_at | GBE1 | L07956 | | 1,4-alpha-glucan branching enzyme |
| 746 | 34332_at | GNPI | D31766 | glucosamine-6-phosphate isomerase | glucosamine-6-phosphate isomerase |

Fig 21

| | A | B | C | D | E |
|-----|--------------|----------|----------|--|---|
| 747 | 38218_at | GCNT1 | M97347 | glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylglucosaminyltransferase) | beta-1,6-N-acetylglucosaminyltransferase |
| 748 | 39122_at | GPI | K03515 | glucose phosphate isomerase | neuroleukin |
| 749 | 38986_at | GRP58 | Z49835 | glucose regulated protein, 58kD | protein disulfide isomerase |
| 750 | 38042_at | G6PD | X03674 | glucose-6-phosphate dehydrogenase | glucose-6-phosphate dehydrogenase |
| 751 | 33308_at | GUSB | M15182 | glucuronidase, beta | glucuronidase, beta |
| 752 | 37341_at | GLUD1 | M20867 | glutamate dehydrogenase 1 | glutamate dehydrogenase 1 |
| 753 | 35485_at | GRM4 | X80818 | glutamate receptor, metabotropic 4 | metabotropic glutamate receptor type 4 |
| 754 | 40522_at | GLUL | X59834 | glutamate-ammonia ligase (glutamine synthase) | glutamate--ammonia ligase |
| 755 | 31850_at | GCLC | M90656 | glutamate-cysteine ligase, catalytic subunit | gamma-glutamylcysteine synthetase |
| 756 | 33163_r_at | GCLM | L35546 | glutamate-cysteine ligase, modifier subunit | gamma-glutamylcysteine synthetase light subunit |
| 757 | 35343_at | GOT1 | M37400 | glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1) | aspartate aminotransferase 1 |
| 758 | 40764_at | GOT2 | M22632 | glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) | aspartate aminotransferase 2 precursor |
| 759 | 34719_at | GLS | AB020645 | glutaminase | KIAA0838 protein |
| 760 | 32626_at | GFPT1 | M90516 | glutamine-fructose-6-phosphate transaminase 1 | glutamine:fructose-6-phosphate amidotransferase |
| 761 | 39640_at | GFPT2 | AB016789 | glutamine-fructose-6-phosphate transaminase 2 | Glutamine:fructose-6-phosphate amidotransferase |
| 762 | 35300_at | EPRS | X54326 | glutamyl-prolyl-tRNA synthetase | glutamyl-tRNA synthetase |
| 763 | 34311_at | GLRX | X76648 | glutaredoxin (thioltransferase) | glutaredoxin |
| 764 | 37033_s_at | GPX1 | X13710 | glutathione peroxidase 1 | |
| 765 | 40508_at | GSTA4 | AF025887 | glutathione S-transferase A4 | glutathione S-transferase A4-4 |
| 766 | 38386_r_at | GSS | U34683 | glutathione synthetase | glutathione synthetase |
| 767 | 824_at | GSTT1p28 | U90313 | glutathione-S-transferase like; glutathione transferase omega | glutathione-S-transferase homolog |
| 768 | AFFX-HUMGAP1 | GAPD | M33197 | glyceraldehyde-3-phosphate dehydrogenase | glyceraldehyde-3-phosphate dehydrogenase |
| 769 | 35905_s_at | GAPD | U34995 | glyceraldehyde-3-phosphate dehydrogenase | |

Fig 21

| | A | B | C | D | E |
|-----|--------------|--------|----------|---|---|
| 770 | AFEX-HUMGAP1 | GAPD | M33197 | glyceraldehyde-3-phosphate dehydrogenase | glyceraldehyde-3-phosphate dehydrogenase |
| 771 | 39392_at | GNPAT | AJ002190 | glyceronephosphate O-acyltransferase | dihydroxyacetone phosphate acyltransferase |
| 772 | 37357_at | GCSH | D00723 | glycine cleavage system protein H (aminomethyl carrier) | glycine cleavage system protein H (aminomethyl carrier) |
| 773 | 39665_at | GLRB | U33267 | glycine receptor, beta | glycine receptor beta subunit |
| 774 | 40645_at | GSK3B | L33801 | glycogen synthase kinase 3 beta | protein kinase |
| 775 | 40876_at | GYG | U31525 | glycogenin | glycogenin |
| 776 | 35334_at | GYG2 | U94362 | glycogenin 2 | glycogenin-2 alpha |
| 777 | 38379_at | GPNMB | X76534 | glycoprotein (transmembrane) nmb | glycoprotein (transmembrane) nmb |
| 778 | 37251_s_at | GPM6B | AF016004 | glycoprotein M6B | |
| 779 | 33126_at | AD-017 | L13435 | glycosyltransferase AD-017 | |
| 780 | 36582_g_at | GARS | U09510 | glycyl-tRNA synthetase | glycyl-tRNA synthetase |
| 781 | 36581_at | GARS | U09510 | glycyl-tRNA synthetase | glycyl-tRNA synthetase |
| 782 | 38201_at | GLO1 | D13315 | glyoxalase I | lactoyl glutathione lyase |
| 783 | 40133_s_at | GRHPR | W28944 | glyoxylate reductase/hydroxypyruvate reductase | |
| 784 | 37449_i_at | GNAS | X04409 | | guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform alpha-s-2; neuroendocrine secretory protein 55; guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform XL-alpha-s; guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform alpha-s-1 |
| 785 | 37448_s_at | GNAS | X56009 | GNAS complex locus GNAS complex locus | alpha subunit of GsGTP binding protein |

Fig 21

| | A | B | C | D | E |
|-----|------------|-----------|----------|---|---|
| 786 | 37450_r_at | GNAS | X0409 | GNAS complex locus | guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform alpha-s-2; neuroendocrine secretory protein 55; guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform XL-alpha-s; guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform |
| 787 | 37959_at | GGA3 | D63876 | golgi associated, gamma adaptin ear containing, ARF binding protein 3 | ADP-ribosylation factor binding protein 3, isoform short; ADP-ribosylation factor binding protein 3, isoform long |
| 788 | 32713_at | GOLGA1 | U51587 | golgi autoantigen, golgin subfamily a, 1 | Golgi complex autoantigen golgin-97 |
| 789 | 32150_at | GOLGA4 | X82834 | golgi autoantigen, golgin subfamily a, 4 | 256 kD golgin |
| 790 | 36827_at | GOLPH1 | AF020762 | golgi phosphoprotein 1 | unknown protein |
| 791 | 38620_at | GOSR2 | AA905543 | golgi SNAP receptor complex member 2 | putative 13 S Golgi transport complex 90kD subunit brain-specific isoform KIAA0855 protein |
| 792 | 34737_at | GOLTC1 | AF058718 | golgi transport complex 1 (90 kD subunit) | |
| 793 | 41767_r_at | KIAA0855 | AB020662 | golgin-67 | |
| 794 | 36950_at | HSGP25L2G | X90872 | gp25L2 protein | |
| 795 | 36035_at | GPAA1 | AB002135 | GPAA1P anchor attachment protein 1 homolog (yeast) | glycosylphosphatidylinositol anchor attachment 1 (GPAA1) |
| 796 | 32595_at | GRSF1 | U07231 | G-rich RNA sequence binding factor 1 | G-rich sequence factor-1 |
| 797 | 39822_s_at | GADD45B | AF078077 | growth arrest and DNA-damage-inducible, beta | growth arrest and DNA-damage-inducible protein GADD45beta |
| 798 | 39821_s_at | GADD45B | N95168 | growth arrest and DNA-damage-inducible, beta | |
| 799 | 661_at | GAS1 | L13698 | growth arrest-specific 1 | growth arrest-specific 1 |
| 800 | 41839_at | GAS1 | L13698 | growth arrest-specific 1 | growth arrest-specific 1 |
| 801 | 37658_at | GAS6 | L13720 | growth arrest-specific 6 | growth-arrest-specific protein |
| 802 | 1598_g_at | GAS6 | L13720 | growth arrest-specific 6 | growth-arrest-specific protein |
| 803 | 37615_at | GRB10 | D86962 | growth factor receptor-bound protein 10 | growth factor receptor-bound protein 10 |
| 804 | 41752_at | GHITM | W28190 | growth hormone inducible transmembrane protein | |

Fig 21

| | A | B | C | D | E |
|-----|------------|--------------------|----------|---|---|
| 805 | 160030_at | GHR | X06562 | growth hormone receptor | growth hormone receptor |
| 806 | 40113_at | GS3955 | D87119 | GS3955 protein | GS3955 |
| 807 | 37279_at | GEM | U10550 | GTP binding protein overexpressed in skeletal muscle | Gem |
| 808 | 33809_at | GNAI1 | AL049933 | guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1 | hypothetical protein |
| 809 | 37307_at | GNAI2 | X04828 | guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2 | guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2 |
| 810 | 34608_at | GNB2L1 | M24194 | guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 | MHC B complex protein 12.3 |
| 811 | 35272_at | GNB5 | AI541042 | guanine nucleotide binding protein (G protein), gamma 5 | |
| 812 | 37735_at | GNB10 | U31383 | guanine nucleotide binding protein 10 | G protein gamma-10 subunit |
| 813 | 35735_at | GBP1 | M55542 | guanylate binding protein 1, interferon-inducible, 67kD | guanylate binding protein isoform I |
| 814 | 905_at | GUK1 | L76200 | guanylate kinase 1 | guanylate kinase |
| 815 | 32249_at | HFL1 | M65292 | H factor (complement)-like 1 | factor H homologue |
| 816 | 32250_at | HF1 | X07523 | H factor 1 (complement) | complement factor H |
| 817 | 420_at | ACTH-R | X65633 | H.sapiens ACTH-R gene for adrenocorticotrophic hormone receptor. | candidate adrenocorticotrophic hormone receptor |
| 818 | 31673_s_at | cell adhesion regu | X65784 | H.sapiens CAR gene. | cell matrix adhesion regulator |
| 819 | 37003_at | CD63; MLA1; ME4 | X62654 | H.sapiens gene for Me491/CD63 antigen. | ME491 /CD63 antigen |
| 820 | 38076_at | P1 gene for c subu | X69907 | H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form). | ATP synthase, H+ transporting, mitochondrial FO complex, subunit c (subunit 9), isoform 1 |
| 821 | 35125_at | hrp S6 | X67309 | H.sapiens gene for ribosomal protein S6. | ribosomal protein S6 |
| 822 | 34646_at | rpS7 | Z25749 | H.sapiens gene for ribosomal protein S7. | ribosomal protein S7 |
| 823 | 31510_s_at | hH3.3B | Z48950 | H.sapiens hH3.3B gene for histone H3.3. | histone H3.3 |

Fig 21

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| | A | B | C | D | E |
|-----|------------|------------|----------|---|---|
| 824 | 33820_g_at | ldhB | X13794 | H.sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (and joined CDS). | lactate dehydrogenase B |
| 825 | 33819_at | ldhB | X13794 | H.sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (and joined CDS). | lactate dehydrogenase B |
| 826 | 34787_at | ORF1 | X93209 | H.sapiens mRNA for NRD1 convertase. | NRD1 convertase |
| 827 | 36012_at | PIBF1 | Y09631 | H.sapiens mRNA for PIBF1 protein, complete. | PIBF1 protein |
| 828 | 31526_f_at | tre | X63547 | H.sapiens mRNA for tre oncogene (clone 213). | oncogene |
| 829 | 40471_at | PxF | Y09048 | H.sapiens PxF gene. | PxF protein |
| 830 | 37038_at | PXMP1 | X83467 | H.sapiens PXMP1 gene, exon 1 (and joined CDS). | 70kD peroxisomal integral membrane protein |
| 831 | 31583_at | rpS8 | X67247 | H.sapiens rpS8 gene for ribosomal protein S8. | ribosomal protein S8 |
| 832 | 1685_at | SPHAR | X82554 | H.sapiens SPHAR gene for cyclin-related protein. | S-phase response (cyclin-related) |
| 833 | 38127_at | syndecan-1 | Z48199 | H.sapiens syndecan-1 gene (exons 2-5). | syndecan 1 |
| 834 | 37310_at | uPA | X02419 | H.sapiens uPA gene. | urokinase-plasminogen activator |
| 835 | 34308_at | H2AFL | U90551 | H2A histone family, member L | histone 2A-like protein |
| 836 | 39337_at | H2AFZ | M37583 | H2A histone family, member Z | H2A histone family, member Z |
| 837 | 33458_r_at | H2BFL | A168098 | H2B histone family, member L | |
| 838 | 40818_at | LOC51580 | D14041 | H2B histone family, member L | |
| 839 | 254_at | H3F3A | M11353 | H3 histone, family 3A | H-2K binding factor-2 |
| 840 | 39969_at | H4FG | AA255502 | H4 histone family, member G | H3 histone, family 3A |
| 841 | 32591_at | HCDI | A1494623 | HCDI protein | |
| 842 | 35215_at | HDCMA18P | AL049996 | HDCMA18P protein | hypothetical protein |
| 843 | 39353_at | HSPE1 | A1912041 | heat shock 10kD protein 1 (chaperonin 10) | |
| 844 | 37720_at | HSPD1 | M22382 | heat shock 60kD protein 1 (chaperonin) | mitochondrial matrix protein |
| 845 | 36614_at | HSPA5 | X87949 | heat shock 70kD protein 5 (glucose-regulated protein, 78kD) | heat shock 70kD protein 5 (glucose-regulated protein, 78kD) |
| 846 | 41510_s_at | HSPA9B | L15189 | heat shock 70kD protein 9B (mortalin-2) | MTHSP75 |

Fig 21

| | A | B | C | D | E |
|-----|------------|----------|----------|---|--|
| 847 | 32316_s_at | HSPCA | X15183 | heat shock 90kD protein 1, alpha | heat shock 90kD protein 1, alpha |
| 848 | 33984_at | HSPCB | M16660 | heat shock 90kD protein 1, beta | heat shock 90kD protein 1, beta |
| 849 | 31906_at | HSBP1 | AF068754 | heat shock factor binding protein 1 | heat shock factor binding protein 1 HSBP1 |
| 850 | 1468_at | TRAP1 | U12595 | heat shock protein 75 | tumor necrosis factor type 1 receptor associated protein |
| 851 | 38054_at | HBXIP | AF029890 | hepatitis B virus x interacting protein | hepatitis B virus X interacting protein |
| 852 | 38779_r_at | HDGF | D16431 | hepatoma-derived growth factor (high-mobility group protein 1-like) | hepatoma-derived GF |
| 853 | 35644_at | HEPH | AB014598 | hephaestin | KIAA0698 protein |
| 854 | 38094_at | HNRPA0 | M65028 | heterogeneous nuclear ribonucleoprotein A/B | hnRNP type A/B protein |
| 855 | 37334_at | HNRPA0 | U23803 | heterogeneous nuclear ribonucleoprotein A0 | heterogeneous ribonucleoprotein A0 |
| 856 | 34987_s_at | HNRPA1 | X79536 | heterogeneous nuclear ribonucleoprotein A1 | hnRNPcore protein A1 |
| 857 | 36654_s_at | HNRPA2B1 | M29065 | heterogeneous nuclear ribonucleoprotein A2/B1 | heterogeneous nuclear ribonucleoprotein A2/B1, isoform A2; heterogeneous nuclear ribonucleoprotein A2/B1, isoform B1 |
| 858 | 33666_at | HNRPC | M16342 | heterogeneous nuclear ribonucleoprotein C (C1/C2) | heterogeneous nuclear ribonucleoprotein C, isoform b; heterogeneous nuclear ribonucleoprotein C, isoform a |
| 859 | 38016_at | HNRPD | M94630 | heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kD) | DNA-binding protein |
| 860 | 33845_at | HNRPH1 | W28483 | heterogeneous nuclear ribonucleoprotein H1 (H) | |
| 861 | 41132_r_at | HNRPH2 | U01923 | heterogeneous nuclear ribonucleoprotein H2 (H') | heterogeneous nuclear ribonucleoprotein H2 |
| 862 | 41283_at | HNRPH3 | AF052131 | heterogeneous nuclear ribonucleoprotein H3 (2H9) | heterogeneous nuclear ribonucleoprotein H3, isoform a; heterogeneous nuclear ribonucleoprotein H3, isoform b |
| 863 | 40836_s_at | HNRPH3 | W26677 | heterogeneous nuclear ribonucleoprotein H3 (2H9) | |

Fig 21

| | A | B | C | D | E |
|-----|----------|---------|----------|--|---|
| 864 | 39415_at | HNRPK | X72727 | heterogeneous nuclear ribonucleoprotein K | transformation upregulated nuclear protein |
| 865 | 35201_at | HNRPL | X16135 | heterogeneous nuclear ribonucleoprotein L | heterogeneous nuclear ribonucleoprotein L |
| 866 | 37717_at | HNRPM | L03532 | heterogeneous nuclear ribonucleoprotein M | M4 protein |
| 867 | 39792_at | HNRPR | AF000364 | heterogeneous nuclear ribonucleoprotein R | heterogeneous nuclear ribonucleoprotein R |
| 868 | 38654_at | HNRPU | X65488 | heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) | hnRNP U protein |
| 869 | 32818_at | HXB | X78565 | hexabrachion (tenascin C, cytotactin) | human tenascin-C |
| 870 | 39827_at | RTP801 | AA522530 | HIF-1 responsive RTP801 | |
| 871 | 31504_at | HDLBP | M64098 | high density lipoprotein binding protein (vigilin) | high density lipoprotein binding protein |
| 872 | 32220_at | HMG1 | D63874 | high-mobility group (nonhistone chromosomal) protein 1 | HMG-1 |
| 873 | 306_s_at | HMG14 | J02621 | high-mobility group (nonhistone chromosomal) protein 14 | high-mobility group (nonhistone chromosomal) protein 14 |
| 874 | 35738_at | HMG17L3 | AI347088 | high-mobility group (nonhistone chromosomal) protein 17-like 3 | |
| 875 | 38065_at | HMG2 | X62534 | high-mobility group (nonhistone chromosomal) protein 2 | high-mobility group (nonhistone chromosomal) protein 2 |
| 876 | 38843_at | HMG2L1 | AL079310 | high-mobility group protein 2-like 1 | hypothetical protein |
| 877 | 35693_at | HPCAL1 | AF070616 | hippocalcin-like 1 | BDP-1 protein |
| 878 | 1009_at | HINT1 | U51004 | histidine triad nucleotide binding protein 1 | protein kinase C inhibitor |
| 879 | 34231_at | HBOA | AF074606 | histone acetyltransferase | histone acetyltransferase |
| 880 | 41855_at | HAT1 | AF030424 | histone acetyltransferase 1 | histone acetyltransferase 1 |
| 881 | 38771_at | HDAC1 | D50405 | histone deacetylase 1 | RPD3 protein |
| 882 | 34368_at | HDAC2 | U31814 | histone deacetylase 2 | transcriptional regulator homolog RPD3 |
| 883 | 38271_at | HDAC4 | AB006626 | histone deacetylase 4 | KIAA0288 protein |
| 884 | 39046_at | H2AV | AL049324 | histone H2A.F/Z variant | |
| 885 | 39092_at | H2AV | AW007731 | histone H2A.F/Z variant | |
| 886 | 38824_at | HTATIP2 | AF039103 | HIV-1 Tat interactive protein 2, 30 kD | Tat-interacting protein TIP30 |
| 887 | 40220_at | HIS1 | AB021179 | HMBA-inducible | HEXIM1 protein |

Fig 21

| | A | B | C | D | E |
|-----|------------|------------|----------|--|---|
| 888 | 39809_at | HBP1 | AF019214 | HMG-box containing protein 1 | HMG box containing protein 1 |
| 889 | 33828_at | BAF57 | AF035262 | HMG-domain containing protein which is the 57 kd subunit within SWI/SNF-related BAF complexes; contains a proline-rich N-terminus, a kinesin-like coiled-coil region, and a highly acidic c-terminus; Homo sapiens BAF57 (BAF57) gene, complete cds. | BAF57 |
| 890 | 39348_at | HRMT1L1 | X99209 | HMT1 hnRNP methyltransferase-like 1 (S. cerevisiae) | arginine methyltransferase |
| 891 | 32825_at | HRMT1L2 | Y10805 | HMT1 hnRNP methyltransferase-like 2 (S. cerevisiae) | arginine methyltransferase |
| 892 | 31463_s_at | dJ256G22.1 | AL022097 | HNRNP Core Protein A1 LIKE pseudogene; match: proteins P04256 Q28521 P49312 P09651 P51991 P51992 P51968 P17130 P22626 | |
| 893 | 38943_at | HCCS | U36787 | holocytochrome c synthase (cytochrome c heme-lyase) | holocytochrome c-type synthetase |
| 894 | 39610_at | HOXB2 | X16665 | homeo box B2 | homeo box B2 |
| 895 | 40674_s_at | HOXC6 | S82986 | homeo box C6 | homeo box C6 |
| 896 | 38233_at | HOMER-3 | AF093265 | Homer, neuronal immediate early gene, 3 | homer-3 |
| 897 | 34401_at | UQCRRF51 | L32977 | Homo sapiens (clone f17252) ubiquinol cytochrome c reductase Rieske iron-sulphur protein (UQCRRF51) gene, exon 2. | Rieske Fe-S protein |
| 898 | 36624_at | IMPDH2 | L33842 | Homo sapiens (clone FFE-7) type II inosine monophosphate dehydrogenase (IMPDH2) gene, exons 1-13, complete cds. | inosine monophosphate dehydrogenase type II |
| 899 | 37599_at | AOX1 | AF017060 | Homo sapiens aldehyde oxidase (AOX1) gene, exon 35 and complete cds. | aldehyde oxidase |
| 900 | 39740_g_at | NACA | AF054187 | Homo sapiens alpha NAC mRNA, complete cds. | alpha NAC |

Fig 21

| | A | B | C | D | E |
|-----|------------|--------|----------|---|----------------|
| 901 | 39739_at | NACA | AF054187 | Homo sapiens alpha NAC mRNA, complete cds. | alpha NAC |
| 902 | 41154_r_at | CTNNA1 | AF102803 | Homo sapiens alphaE-catenin (CTNNA1) gene, exon 18 and complete cds. | alphaE-catenin |
| 903 | 41153_f_at | CTNNA1 | AF102803 | Homo sapiens alphaE-catenin (CTNNA1) gene, exon 18 and complete cds. | alphaE-catenin |
| 904 | 39324_at | | AL050078 | Homo sapiens cDNA FLJ10784 fis, clone NT2RP4000448, highly similar to Homo sapiens mRNA; cDNA DKFZp566G0746 | |
| 905 | 35310_at | | D45288 | Homo sapiens cDNA FLJ13267 fis, clone OVARC1000964 | |
| 906 | 35754_at | | L40391 | Homo sapiens cDNA FLJ13553 fis, clone PLACE1007454 | |
| 907 | 33325_at | | W26667 | Homo sapiens cDNA FLJ14821 fis, clone OVARC1000556, highly similar to RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.-) | |
| 908 | 38102_at | | W28575 | Homo sapiens cDNA FLJ25016 fis, clone CBL01574 | |
| 909 | 41253_s_at | | A1983043 | Homo sapiens cDNA FLJ30436 fis, clone BRACE2009037 | |
| 910 | 39162_at | | AA156987 | Homo sapiens cDNA FLJ30544 fis, clone BRAWH2001412 | |
| 911 | 41807_at | | AL040137 | Homo sapiens cDNA FLJ31959 fis, clone NT2RP7007422 | |
| 912 | 38643_at | | W87466 | Homo sapiens cDNA FLJ33151 fis, clone UTERU2000263 | |
| 913 | 34246_at | | AA418437 | Homo sapiens cDNA: FLJ21175 fis, clone CAS11071 | |
| 914 | 40813_at | | A1768188 | Homo sapiens cDNA: FLJ21243 fis, clone COL01164 | |

Fig 21

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| | A | B | C | D | E |
|-----|------------|-----------------|----------|---|--|
| | | | | Homo sapiens cDNA: FLJ21449 fis, clone COL04483, highly similar to AF010235 | |
| 915 | 40923_at | | AA290994 | Homo sapiens mRNA from chromosome 5q31-33 region | |
| 916 | 38993_r_at | | W27522 | Homo sapiens cDNA: FLJ21904 fis, clone HEP03585 | |
| | | | | Homo sapiens cDNA: FLJ21927 fis, clone HEP04178, highly similar to HSU0909 | |
| 917 | 38093_at | | U90909 | Human clone 23722 mRNA sequence | |
| 918 | 34840_at | | AI700633 | Homo sapiens cDNA: FLJ22642 fis, clone HSI06970 | |
| | | | | Homo sapiens cDNA: FLJ23324 fis, clone HEP12482, highly similar to HUMMYOHC Human nonmuscle myosin heavy chain-B (MYH10) mRNA | smooth muscle myosin heavy chain isoform SMemb |
| 919 | 32838_at | smooth muscle m | S67247 | Homo sapiens cervical cancer suppressor-1 mRNA, complete cds | |
| 920 | 33737_f_at | | AI871359 | Homo sapiens clone 23570 mRNA sequence | |
| 921 | 41663_at | | AF038202 | Homo sapiens clone 23700 mRNA sequence | |
| 922 | 36815_at | | AF038185 | Homo sapiens clone 23718 mRNA sequence | |
| 923 | 41841_at | | AF052138 | Homo sapiens clone 23903 mRNA sequence | |
| 924 | 37794_at | | AF035281 | Homo sapiens clone 23938 mRNA sequence | |
| 925 | 38764_at | | AF007142 | Homo sapiens clone 24416 mRNA sequence | |
| 926 | 35342_at | | AF052159 | Homo sapiens clone 24630 mRNA sequence | |
| 927 | 31867_at | | AF052174 | Homo sapiens clone 24674 mRNA sequence | |
| 928 | 36758_at | | AF070578 | Homo sapiens clone 24790 mRNA sequence | |
| 929 | 41864_at | | AF052181 | | |

Fig 21

| | A | B | C | D | E |
|-----|------------|------------------|----------|--|---|
| 930 | 38070_at | | AL080234 | Homo sapiens clone FBD3 Cri-du-chat critical region mRNA | |
| 931 | 34773_at | TBCA | AF038952 | Homo sapiens cofactor A protein mRNA, complete cds. | cofactor A protein |
| 932 | 39027_at | COX4 | AF017115 | Homo sapiens cytochrome c oxidase subunit IV precursor (COX4) gene, nuclear gene encoding mitochondrial protein, complete cds. | cytochrome c oxidase subunit IV precursor |
| 933 | 40878_f_at | D15F37 | AF041081 | Homo sapiens D15F37 pseudogene, S4 allele, mRNA sequence. | |
| 934 | 631_g_at | DCTD | L39874 | Homo sapiens deoxycytidylate deaminase gene, complete cds. | deoxycytidylate deaminase |
| 935 | 630_at | DCTD | L39874 | Homo sapiens deoxycytidylate deaminase gene, complete cds. | deoxycytidylate deaminase |
| 936 | 33936_at | GALC | D86181 | Homo sapiens DNA for galactocerebrosidase, exon 17 and complete cds. | galactocerebrosidase |
| 937 | 40134_at | ATP5J2; ATP5JL | AF047436 | Homo sapiens F1Fo-ATPase synthase f subunit mRNA, complete cds. | F1Fo-ATPase synthase f subunit |
| 938 | 36103_at | SCYA3; LD78ALP | D90144 | Homo sapiens gene for LD78 alpha precursor, complete cds. | LD78 alpha precursor |
| 939 | 40725_at | GOSR1; P28; GS2 | AF047438 | Homo sapiens GOS28/P28 protein mRNA, complete cds. | GOS28/P28 protein |
| 940 | 38708_at | RAN; TC4; ARA24 | AF054183 | Homo sapiens GTP binding protein mRNA, complete cds. | GTP binding protein |
| 941 | 35790_at | VPS26; HB58; HB | AF054179 | Homo sapiens H beta 58 homolog mRNA, complete cds. | H beta 58 homolog |
| 942 | 36576_at | H2AFY; H2A.y; H2 | AF054174 | Homo sapiens histone macroH2A1.2 mRNA, complete cds. | histone macroH2A1.2 |
| 943 | 35303_at | INSIG1 | U96876 | Homo sapiens insulin induced protein 1 (INSIG1) gene, complete cds. | insulin induced protein 1 |
| 944 | 1038_s_at | interferon-gamma | U19247 | Homo sapiens interferon-gamma receptor alpha chain gene, exon 7 and complete cds. | interferon-gamma receptor alpha chain |

Fig 21

| | A | B | C | D | E |
|-----|------------|---------------------------|----------|--|--|
| 945 | 895_at | MIF | L19686 | Homo sapiens macrophage migration inhibitory factor (MIF) gene, complete cds. | macrophage migration inhibitory factor |
| 946 | 38967_at | C14orf2; MP68; P1AF054175 | | Homo sapiens mitochondrial proteolipid 68MP homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds. | mitochondrial proteolipid 68MP homolog |
| 947 | 31881_at | | Y14155 | Homo sapiens mRNA for Hmob33 protein, 3' untranslated region | |
| 948 | 34677_f_at | tl132 | AJ012755 | Homo sapiens mRNA for TL132 | TL132 protein |
| 949 | 38786_at | | AL079279 | Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 248114 | |
| 950 | 33418_at | | AL096752 | Homo sapiens mRNA; cDNA DKFZp434A012 (from clone DKFZp434A012) | |
| 951 | 38630_at | | AL080192 | Homo sapiens mRNA; cDNA DKFZp434B102 (from clone DKFZp434B102) | |
| 952 | 41529_g_at | | W72239 | Homo sapiens mRNA; cDNA DKFZp434M162 (from clone DKFZp434M162) | |
| 953 | 36451_at | | A1743299 | Homo sapiens mRNA; cDNA DKFZp434M245 (from clone DKFZp434M245) | |
| 954 | 36821_at | DKFZp564A026 | AL050367 | Homo sapiens mRNA; cDNA DKFZp564A026 (from clone DKFZp564A026) | hypothetical protein |
| 955 | 37366_at | | AL049969 | Homo sapiens mRNA; cDNA DKFZp564A072 (from clone DKFZp564A072) | |
| 956 | 39506_at | | AA933984 | Homo sapiens mRNA; cDNA DKFZp564B222 (from clone DKFZp564B222) | |
| 957 | 39748_at | | AL050021 | Homo sapiens mRNA; cDNA DKFZp564D016 (from clone DKFZp564D016) | |

Fig 21

| | A | B | C | D | E |
|-----|------------|---|----------|--|---|
| 958 | 38357_at | | AL049321 | Homo sapiens mRNA; cDNA DKFZp564D156 (from clone DKFZp564D156) | |
| 959 | 33716_at | | N95443 | Homo sapiens mRNA; cDNA DKFZp564E122 (from clone DKFZp564E122) | |
| 960 | 35301_at | | AL049941 | Homo sapiens mRNA; cDNA DKFZp564E2222 (from clone DKFZp564E2222) | |
| 961 | 35842_at | | AL049265 | Homo sapiens mRNA; cDNA DKFZp564F053 (from clone DKFZp564F053) | |
| 962 | 40552_s_at | | AL049987 | Homo sapiens mRNA; cDNA DKFZp564F112 (from clone DKFZp564F112) | |
| 963 | 39170_at | | AL049957 | Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323) | |
| 964 | 34303_at | | AL049949 | Homo sapiens mRNA; cDNA DKFZp564L0822 (from clone DKFZp564L0822) | |
| 965 | 36509_at | | AL049998 | Homo sapiens mRNA; cDNA DKFZp564L222 (from clone DKFZp564L222) | |
| 966 | 40353_at | | AL049962 | Homo sapiens mRNA; cDNA DKFZp564P0823 (from clone DKFZp564P0823) | |
| 967 | 35290_at | | AL050081 | Homo sapiens mRNA; cDNA DKFZp566J2146 (from clone DKFZp566J2146) | |
| 968 | 38079_at | | AL049367 | Homo sapiens mRNA; cDNA DKFZp586B0918 (from clone DKFZp586B0918) | |
| 969 | 32195_at | | AL049450 | Homo sapiens mRNA; cDNA DKFZp586B1922 (from clone DKFZp586B1922) | |

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| | A | B | C | D | E |
|-----|------------|-------|----------|--|---|
| 970 | 39379_at | | AL049397 | Homo sapiens mRNA; cDNA DKFZp586C1019 (from clone DKFZp586C1019) | |
| 971 | 37575_at | | AL050192 | Homo sapiens mRNA; cDNA DKFZp586C1723 (from clone DKFZp586C1723) | |
| 972 | 34283_at | | AL050125 | Homo sapiens mRNA; cDNA DKFZp586F071 (from clone DKFZp586F071) | |
| 973 | 39600_at | | AL080110 | Homo sapiens mRNA; cDNA DKFZp586G1922 (from clone DKFZp586G1922) | |
| 974 | 34752_at | | AL080111 | Homo sapiens mRNA; cDNA DKFZp586G2222 (from clone DKFZp586G2222) | |
| 975 | 39103_s_at | | H98552 | Homo sapiens mRNA; cDNA DKFZp586I0523 (from clone DKFZp586I0523) | |
| 976 | 36092_at | | AL080213 | Homo sapiens mRNA; cDNA DKFZp586I1823 (from clone DKFZp586I1823) | |
| 977 | 35187_at | | AL080216 | Homo sapiens mRNA; cDNA DKFZp586K1123 (from clone DKFZp586K1123) | |
| 978 | 35363_at | DDX17 | AL080113 | Homo sapiens mRNA; cDNA DKFZp586K2322 (from clone DKFZp586K2322) | |
| 979 | 41013_at | | AL080114 | Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp586M2022) | |
| 980 | 41690_at | | AL049471 | Homo sapiens mRNA; cDNA DKFZp586N012 (from clone DKFZp586N012) | |
| 981 | 40349_at | | AL049442 | Homo sapiens mRNA; cDNA DKFZp586N1720 (from clone DKFZp586N1720) | |

Fig 21

| | A | B | C | D | E |
|-----|------------|------------------------|----------|---|--|
| 982 | 32672_at | | | Homo sapiens mRNA; cDNA DKFZp586N1918 (from clone DKFZp586N1918) | |
| 983 | 36668_at | DIA1 | AL049387 | Homo sapiens NADH-cytochrome b5 reductase (b5R) gene, exon 9. | NADH-cytochrome b5 reductase |
| 984 | 38542_at | | M28713 | Homo sapiens nucleophosmin phosphoprotein (NPM) gene, 3' flanking sequence. | |
| 985 | 40587_s_at | EEF1E1; P18 | U89322 | Homo sapiens p18 protein mRNA, complete cds. | |
| 986 | 41448_at | HOXA4 | AF054186 | Homo sapiens PAC clone RP1-170O19 from 7p15-p21, complete sequence. | p18 protein even-skipped homeo box 1 (homolog of Drosophila) |
| 987 | 36159_s_at | PrP | AC004080 | Homo sapiens prion protein (PrP) gene, complete cds. | prion protein |
| 988 | 32756_at | ECH1 | U29185 | Homo sapiens putative dienoyl-CoA isomerase (ECH1) gene, exons 7-10, and complete cds. | |
| 989 | 35824_at | RP58 | AF030249 | Homo sapiens RP58 gene, complete CDS. | putative dienoyl-CoA isomerase |
| 990 | 39169_at | SEC61G | AJ223321 | Homo sapiens Sec61 gamma mRNA, complete cds. | RP58 protein |
| 991 | 41222_at | STAT6 | AF054184 | Homo sapiens signal transducer and activator of transcription 6 (STAT6) gene, exons 15 through 23 and complete cds. | Sec61 gamma |
| 992 | 38817_at | SPAG7; ACRP; FAF047437 | AF067575 | Homo sapiens sperm acrosomal protein mRNA, complete cds. | signal transducer and activator of transcription 6 |
| 993 | 36033_at | | | Homo sapiens splicing factor, arginine/serine-rich 12 (SFRS12) mRNA, complete cds. | sperm acrosomal protein |
| 994 | 31481_s_at | TMSB10 | AL049309 | Homo sapiens thymosin beta-10 gene, 3' end. | |
| 995 | 1693_s_at | TIMP | M92383 | Homo sapiens TIMP gene for tissue inhibitor of metalloproteinases, partial cds. | thymosin beta-10 |
| | | | D11139 | | tissue inhibitor of metalloproteinases |

Fig 21

| A | B | C | D | E |
|-----------------|------------------|----------|---|------------------------------------|
| 996 37311_at | TALDO1; TAL-H; | AF010400 | Homo sapiens transaldolase-related protein gene, exons 3-8 and complete cds. | transaldolase-related protein |
| 997 32229_at | EIF4EL3; 4EHP; 4 | AF038957 | Homo sapiens translation initiation factor 4e mRNA, complete cds. | translation initiation factor 4e |
| 998 1323_at | UBB | X04803 | Homo sapiens ubiquitin gene. | ubiquitin |
| 999 32153_s_at | UBB | U49869 | Homo sapiens ubiquitin gene. | ubiquitin |
| 1000 38372_at | | U66042 | Homo sapiens unknown mRNA | |
| 1001 38814_at | ATP6V1G1; ATP6 | AF038954 | Homo sapiens vacuolar H(+)-ATPase subunit mRNA, complete cds. | vacuolar H(+)-ATPase subunit |
| 1002 41597_s_at | SEC22L1; SEC22 | AF047442 | Homo sapiens vesicle trafficking protein sec22b mRNA, complete cds. | vesicle trafficking protein sec22b |
| 1003 34957_at | X5L | Y18504 | Homo sapiens X5L gene. | XAP-5-like protein |
| 1004 38662_at | | AL047596 | Homo sapiens, clone IMAGE:3028427, mRNA, partial cds | |
| 1005 38312_at | | AL050002 | Homo sapiens, clone IMAGE:3140802, mRNA | |
| 1006 33388_at | | AL080223 | Homo sapiens, clone IMAGE:3855224, mRNA, partial cds | |
| 1007 38676_at | | AA059408 | Homo sapiens, clone IMAGE:4132509, mRNA | |
| 1008 40238_at | | AI674208 | Homo sapiens, clone IMAGE:4150198, mRNA, partial cds | |
| 1009 32119_at | | AL049423 | Homo sapiens, clone IMAGE:4182947, mRNA | |
| 1010 38650_at | IGFBP5 | L27560 | Homo sapiens, clone IMAGE:4183312, mRNA, partial cds | |
| 1011 1396_at | IGFBP5 | L27560 | Homo sapiens, clone IMAGE:4183312, mRNA, partial cds | |
| 1012 40432_at | | AA522891 | Homo sapiens, clone IMAGE:4391536, mRNA | |
| 1013 36130_f_at | MT1E | R92331 | Homo sapiens, Similar to RNA helicase-related protein, clone MGC:9246 IMAGE:3892441, mRNA, complete cds | |

Fig 21

| | A | B | C | D | E |
|------|------------|--------------|----------|--|--|
| 1014 | 41246_at | | | Homo sapiens. Similar to serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2, clone MGC:23129 IMAGE:4578406, mRNA, complete cds | |
| 1015 | 41533_at | | | Homo sapiens, similar to unknown, clone MGC:39325 IMAGE:5440447, mRNA, complete cds | |
| 1016 | 39733_at | HERPUD1 | AF055001 | homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1 | homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1 |
| 1017 | 525_g_at | hPMS1 | U13695 | homolog of yeast mutL gene; Human homolog of yeast mutL (hPMS1) gene, complete cds. | |
| 1018 | 32545_r_at | RSU-1 | L12535 | homologous to mouse Rsu-1; putative; Human RSU-1/RSP-1 mRNA, complete cds. | postmeiotic segregation 1 |
| 1019 | 32544_s_at | RSU-1 | L12535 | homologous to mouse Rsu-1; putative; Human RSU-1/RSP-1 mRNA, complete cds. | ras suppressor protein 1 |
| 1020 | 39800_s_at | HAX1 | U68566 | Hs1 binding protein | ras suppressor protein 1 |
| 1021 | 38104_at | DECRI; NADPH | U78302 | Human 2,4-dienoyl-CoA reductase gene, exon 10 and complete cds. | HAX-1 |
| 1022 | 37708_r_at | ADH5 | M81118 | Human alcohol dehydrogenase chi polypeptide (ADH5) gene exons 8-9, complete cds. | 2,4-dienoyl-CoA reductase |
| 1023 | 37707_i_at | ADH5 | M81118 | Human alcohol dehydrogenase chi polypeptide (ADH5) gene exons 8-9, complete cds. | alcohol dehydrogenase |
| 1024 | 39333_at | COL4A1 | M26576 | Human alpha-1 collagen type IV gene, exon 52. | alcohol dehydrogenase |
| 1025 | 38417_at | AMPD2 | M91029 | Human AMP deaminase (AMPD2) mRNA. | alpha-1 type IV collagen |
| 1026 | 37747_at | ANX5 | U05770 | Human annexin V (ANX5) gene, exon 13. | AMP deaminase isoform L splicing variant |
| | | | | | annexin V |

Fig 21

| | A | B | C | D | E |
|------|------------|-------------------|----------|--|--|
| 1027 | 41143_at | CALM1 | U12022 | Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds. | calmodulin |
| 1028 | 239_at | CTSD | M63138 | Human cathepsin D (catD) gene, exons 7, 8, and 9. | cathepsin D |
| 1029 | 1916_s_at | c-fos | V01512 | Human cellular oncogene c-fos (complete sequence). | v-fos FBJ murine osteosarcoma viral oncogene homolog |
| 1030 | 1915_s_at | c-fos | V01512 | Human cellular oncogene c-fos (complete sequence). | v-fos FBJ murine osteosarcoma viral oncogene homolog |
| 1031 | 32583_at | JUN | J04111 | Human c-jun proto oncogene (JUN), complete cds, clone hCJ-1. | v-jun avian sarcoma virus 17 oncogene homolog |
| 1032 | 1895_at | JUN | J04111 | Human c-jun proto oncogene (JUN), complete cds, clone hCJ-1. | v-jun avian sarcoma virus 17 oncogene homolog |
| 1033 | 41604_at | | U79297 | Human clone 23589 mRNA sequence | |
| 1034 | 32185_at | | U00946 | Human clone A9A2BRB5 (CAC)n/(GTG)n repeat-containing mRNA | |
| 1035 | 33667_at | PPIA | X52851 | Human cyclophilin gene for cyclophilin (EC 5.2.1.8). | peptidyl/prolyl isomerase |
| 1036 | 38459_g_at | CYB5 | L39945 | Human cytochrome b5 (CYB5) gene, exon 6 and complete cds. | cytochrome b5 |
| 1037 | 38458_at | CYB5 | L39945 | Human cytochrome b5 (CYB5) gene, exon 6 and complete cds. | cytochrome b5 |
| 1038 | 36163_at | DLD; E3; LAD; DLU | L13761 | Human dihydrolipoamide dehydrogenase gene, exon 14. | dihydrolipoamide dehydrogenase |
| 1039 | 1424_s_at | YWHAH; YWHA1 | D78577 | Human DNA for 14-3-3 protein eta chain, exon2 and complete cds. | 14-3-3 protein eta chain |
| 1040 | 31797_at | dJ73H22.1 | AL035699 | Human DNA sequence from clone 73H22 on chromosome 6q23, complete sequence. | dJ73H22.1 (TBP-like protein) |
| 1041 | 40193_at | ENO2 | X51956 | Human ENO2 gene for neuron specific (gamma) enolase. | human gamma enolase |
| 1042 | 38326_at | GOS2 | M69199 | Human GOS2 protein gene, complete cds. | GOS2 protein |
| 1043 | 40567_at | TUBA3; FLJ25113 | X01703 | Human gene for alpha-tubulin (b alpha 1). | alpha-tubulin |

Fig 21

| | A | B | C | D | E |
|------|------------|------------------|--------|--|---|
| 1044 | 39775_at | SERPING1; C1IN | X54486 | Human gene for C1-inhibitor. | C1 inhibitor |
| 1045 | 40862_i_at | CKB; CKBB | X15334 | Human gene for creatine kinase B (EC 2.7.3.2). | creatine kinase B |
| 1046 | 37641_at | IFI44; p44; MTAP | D28915 | Human gene for hepatitis C-associated microtubular aggregate protein p44, exon 9 and complete cds. | hepatitis C-associated microtubular aggregate protein p44 |
| 1047 | 40211_at | HNRPA1; HNRNP | X12671 | Human gene for heterogeneous nuclear ribonucleoprotein (hnRNP) core protein A1. | hnmp a1 protein |
| 1048 | 408_at | MGSA | X54489 | Human gene for melanoma growth stimulatory activity (MGSA). | melanoma growth stimulatory activity preprotein |
| 1049 | 36203_at | ODC1 | X16277 | Human gene for ornithine decarboxylase ODC (EC 4.1.1.17). | ornithine decarboxylase (ODC) |
| 1050 | 36873_at | VLDLR | D16532 | Human gene for very low density lipoprotein receptor, exon 19. | very low density lipoprotein receptor |
| 1051 | 34759_at | | U68494 | Human hbc647 mRNA sequence | |
| 1052 | 32805_at | AKR1C1; DD1; D | U05861 | Human hepatic dihydrodiol dehydrogenase gene, exon 9. | hepatic dihydrodiol dehydrogenase |
| 1053 | 41231_f_at | HMG17; MGC562 | X13546 | Human HMG-17 gene for non-histone chromosomal protein HMG-17. | put. HMG-17 protein |
| 1054 | 38294_at | HOXD4; HOX4; H | X17360 | Human HOX 5.1 gene for HOX 5.1 protein. | hox 5.1 protein |
| 1055 | 40637_at | HSP73 HSC70 HS | Y00371 | Human hsc70 gene for 71 kd heat shock cognate protein. | 71 Kd heat shock cognate protein |
| 1056 | 232_at | LAMB2 | M55210 | Human laminin B2 chain gene, exon 28. | laminin B2 chain |
| 1057 | 40767_at | TFPI | M59499 | Human lipoprotein-associated coagulation inhibitor (LACI) gene, exon 9 and complete cds. | lipoprotein-associated coagulation inhibitor |
| 1058 | 38637_at | LOX | L16895 | Human lysyl oxidase (LOX) gene, exon 7. | lysyl oxidase |
| 1059 | 37532_at | MCAD | M91432 | Human medium-chain acyl-CoA dehydrogenase (MCAD) gene, exon 12. | medium-chain acyl-CoA dehydrogenase |
| 1060 | 870_f_at | MT3; GIF; GIFB | M93311 | Human metallothionein-III gene, complete cds. | metallothionein-III |

Fig 21

| | A | B | C | D | E |
|------|------------|-----------------|--------|---|--|
| 1061 | 40890_at | MTX | U46920 | Human metaxin (MTX) gene, complete cds. | metaxin |
| 1062 | 32145_at | ADD1 | X58141 | Human mRNA for erythrocyte adducin alpha subunit. | erythrocyte alpha adducin |
| 1063 | 37381_g_at | TF2B | X59268 | Human mRNA for general transcription factor IIB. | IIB protein |
| 1064 | 33683_at | TI-227H | D50525 | Human mRNA for TI-227H. | |
| 1065 | 41747_s_at | MEF2A | U49020 | Human myocyte-specific enhancer factor 2A (MEF2A) gene, last coding exon, and complete cds. | myocyte-specific enhancer factor 2A, C9 form; myocyte-specific enhancer factor 2A, C4 form |
| 1066 | 38066_at | NQO1 | M81600 | Human NAD(P)H:quinone oxidoreductase gene, exon 6. | NAD(P)H:quinone oxidoreductase |
| 1067 | 39729_at | NKEFB | L19185 | Human natural killer cell enhancing factor (NKEFB) mRNA, complete cds. | enhancer protein |
| 1068 | 33994_g_at | MLC | M22919 | Human nonmuscle/smooth muscle alkali myosin light chain gene, complete cds. | non-muscle myosin light chain; smooth muscle myosin light chain |
| 1069 | 32841_at | ZNF9; DM2; CNB1 | U19765 | Human nucleic acid binding protein gene, complete cds. | nucleic acid binding protein |
| 1070 | 32590_at | NCL | M60858 | Human nucleolin gene, complete cds. | nucleolin |
| 1071 | 1782_s_at | Op18 | M31303 | Human oncoprotein 18 (Op18) gene, complete cds. | oncoprotein 18 |
| 1072 | 216_at | PTGDS | M98539 | Human prostaglandin D2 synthase gene, exon 7. | prostaglandin D2 synthase (21kD, brain) |
| 1073 | 237_s_at | PPP2CA | M60483 | Human protein phosphatase 2A catalytic subunit-alpha gene, complete cds. | protein phosphatase-2A catalytic subunit-alpha |
| 1074 | 812_at | PPP1R2 | U68111 | Human protein phosphatase inhibitor 2 (PPP1R2) gene, exon 6 and complete cds. | protein phosphatase inhibitor 2 |
| 1075 | 33180_at | PPP1R2 | U68111 | Human protein phosphatase inhibitor 2 (PPP1R2) gene, exon 6 and complete cds. | protein phosphatase inhibitor 2 |
| 1076 | 35356_at | | W21884 | Human putative ribosomal protein S1 mRNA | |

Fig 21

| | A | B | C | D | E |
|------|------------|----------------|----------|---|--|
| 1077 | 491_at | PTPRG | U46116 | Human receptor tyrosine phosphatase gamma (PTPRG) gene, exon 30 and complete cds. | receptor tyrosine phosphatase gamma |
| 1078 | 492_g_at | PTPRG | U46116 | Human receptor tyrosine phosphatase gamma (PTPRG) gene, exon 30 and complete cds. | receptor tyrosine phosphatase gamma |
| 1079 | 36611_at | ACP1 | U25849 | Human red cell-type low molecular weight acid phosphatase (ACP1) gene, exon 6 and 7, complete cds. | red cell-type low molecular weight acid phosphatase |
| 1080 | 174_s_at | SH3P18 | U61167 | Human SH3 domain-containing protein SH3P18 mRNA, complete cds. | SH3 domain-containing protein SH3P18 |
| 1081 | 241_g_at | SRM | M64231 | Human spermidine synthase gene, complete cds. | spermidine synthase |
| 1082 | 36688_at | SCP-X/SCP-2 | U11313 | Human sterol carrier protein-X/sterol carrier protein-2 (SCP-X/SCP-2) gene, exon 16, and complete cds. | sterol carrier protein-X/sterol carrier protein-2 |
| 1083 | 32587_at | ZFP36L2; BRF2; | U07802 | Human Tis11d gene, complete cds. | Tis11d |
| 1084 | 31680_at | TOP1P2 | M55630 | Human topoisomerase I pseudogene 2. | |
| 1085 | 36446_s_at | HMG1L2 | L24521 | Human transformation-related protein mRNA, 3' end | transformation-related protein |
| 1086 | 39351_at | CD59 | M84349 | Human transmembrane protein (CD59) gene, exon 4. | CD59 protein |
| 1087 | 38727_at | THE1 | M23161 | Human transposon-like element mRNA | |
| 1088 | 41433_at | VCAM1 | M73255 | Human vascular cell adhesion molecule-1 (VCAM1) gene, complete CDS. | vascular cell adhesion molecule-1 |
| 1089 | 40121_at | HIP2 | U58522 | Huntingtin interacting protein 2 | huntingtin interacting protein |
| 1090 | 35973_at | HYPH | AB023163 | Huntingtin interacting protein H | KIAA0946 protein |
| 1091 | 40196_at | HYA22 | D88153 | HYA22 protein | HYA22 |
| 1092 | 36952_at | HADHA | D16480 | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit | enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase alpha-subunit of trifunctional protein |

Fig 21

| | A | B | C | D | E |
|---------------|---------|----------|---|---|---|
| | | | | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit | 3-ketoacyl-CoA thiolase beta-subunit of trifunctional protein |
| 1093 39741_at | HADHB | D16481 | | hydroxysteroid (17-beta) dehydrogenase 4 | 17beta-hydroxysteroid dehydrogenase |
| 1094 36626_at | HSD17B4 | X87176 | | Hypothetical protein of unknown function; Hypothetical 52 kDa protein; Hypothetical protein exhibits similarity to motifs found in (U79010) delta 6 desaturase, a hypothetical cytochrome b5 containing fusion protein, and hypothetical proteins encoded by (Z81122) T13F2.1 [Caenorhabditis elegans] and (Z70271) W08D2.4 [Caenorhabditis elegans]; DNA structure-specific endonuclease FEN1; FLAP ENDONUCLEASE-1; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN; Hypothetical human Best's macular dystrophy related protein; Simulated translation extends ORF of previously reported partial coding sequence for Best's macular dystrophy related protein (AF038536); Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence. | |
| 1095 41583_at | FEN1 | AC004770 | | | BC269730_1; BC269730_2; FEN1_HUMAN; BC269730_4 |

Fig 21

| A | B | C | D | E |
|----------------|----------|----------|--|--|
| | | | <p>Hypothetical protein of unknown function; Hypothetical 52 kDa protein; Hypothetical protein exhibits similarity to motifs found in (U79010) delta 6 desaturase, a hypothetical cytochrome b5 containing fusion protein, and hypothetical proteins encoded by (Z81122) T13F2.1 [Caenorhabditis elegans] and (Z70271) W08D2.4 [Caenorhabditis elegans]; DNA structure-specific endonuclease FEN1; FLAP ENDONUCLEASE-1; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN; Hypothetical human Best's macular dystrophy related protein; Simulated translation extends ORF of previously reported partial coding sequence for Best's macular dystrophy related protein (AF038536); Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.</p> | <p>BC269730_1; BC269730_2; FEN1_HUMAN; BC269730_4 hypothetical protein CG018 hypothetical protein AF038182</p> |
| 1096 34224_at | FEN1 | AC004770 | | |
| 1097 1527_s_at | CG018 | U50527 | hypothetical gene CG018 | hypothetical protein CG018 |
| 1098 33466_at | LOC90355 | AF038182 | hypothetical gene supported by AF038182; BC009203 | hypothetical protein AF038182 |

Fig 21

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| A | B | C | D | E |
|-----------------|----------|----------|--|---|
| | | | <p>Hypothetical human protein (partial CDS); CDS constructed from combination of BLASTX, EST matches and Xgrail predictions. N-terminus of protein likely encoded in flanking cosmid R29942. Predicted protein exhibits weak similarity to hypothetical protein PIDle1226191 (AL021106) from <i>Drosophila melanogaster</i>; Hypothetical human protein most similar to Rat ionotropic glutamate receptor (L34938); CDS constructed primarily from XGRail predictions and BLASTX similarity to (L34938) ionotropic glutamate receptor [<i>Rattus norvegicus</i>] and gil2160125 (U29873) NMDAR-L [<i>Rattus norvegicus</i>]. Also exhibits similarity to PIDle258718 (Z78413) T01C3.10 [<i>Caenorhabditis elegans</i>]. C-terminus of hypothetical protein is ill-defined at this point; definition will require identification and characterization of appropriate cDNAs; Hypothetical 59.8 kDa human protein; CDS constructed from EST matches and Xgrail predictions. C-terminus of predicted protein not fully confirmed by EST or cDNA coverage. Hypothetical protein exhibits no significant database similarities when queried against R32184_1; R32184_2; R32184_3</p> | |
| 1099 35983_at | MGC2436 | AC004528 | | |
| 1100 38440_s_at | FLJ20811 | AA015605 | hypothetical protein | hypothetical protein, similar to (AC007017) putative RNA helicase A [<i>Arabidopsis thaliana</i>] |
| 1101 39140_at | LOC54505 | AL079292 | hypothetical protein | |
| 1102 37819_at | LOC54104 | AF007130 | hypothetical protein | |
| 1103 39517_at | LOC56007 | AF035313 | hypothetical protein 23851 | |
| 1104 41561_s_at | LOC55977 | AI651368 | hypothetical protein 24636 | |

Fig 21

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| A | B | C | D | E |
|-----------------|---------------|----------|---|-------------------------------|
| 1105 41128_at | LOC92703 | AF070537 | hypothetical protein BC013073 | |
| 1106 39972_at | LOC115207 | AF052169 | hypothetical protein BC013764 | |
| 1107 34864_at | CGI-57 | AF070638 | hypothetical protein CGI-57 | hypothetical protein CGI-57 |
| 1108 39960_at | CL640 | AF091086 | hypothetical protein CL640 | hypothetical protein CL640 |
| 1109 38837_at | DJ971N18.2 | W26226 | hypothetical protein DJ971N18.2 | |
| 1110 35142_at | DKFZP564D172 | AF070617 | hypothetical protein DKFZP564D172 | |
| 1111 34830_at | DKFZP564K0822 | W25986 | hypothetical protein DKFZP564K0822 | |
| 1112 31852_at | DKFZP564O043 | AL050390 | hypothetical protein DKFZP564O043 | |
| 1113 33895_at | DKFZP586F1318 | AL050373 | hypothetical protein DKFZP586F1318 | hypothetical protein |
| 1114 39692_at | DKFZP586F2423 | AL080209 | hypothetical protein DKFZP586F2423 | |
| 1115 35682_at | FLB6421 | AI133727 | hypothetical protein FLB6421 | |
| 1116 36647_at | FLJ10326 | AA526812 | hypothetical protein FLJ10326 | |
| 1117 34804_at | FLJ10618 | AL049246 | hypothetical protein FLJ10618 | |
| 1118 36840_at | FLJ10737 | AF052158 | hypothetical protein FLJ10737 | |
| 1119 35283_at | FLJ10738 | H05692 | hypothetical protein FLJ10738 | |
| 1120 37610_at | FLJ10803 | AI765280 | hypothetical protein FLJ10803 | |
| 1121 33173_g_at | FLJ10849 | T75292 | hypothetical protein FLJ10849 | |
| 1122 39923_at | FLJ10971 | AI935420 | hypothetical protein FLJ10971 | |
| 1123 38105_at | FLJ11021 | W26521 | hypothetical protein FLJ11021 similar to splicing factor, arginine/serine-rich 4 | |
| 1124 33394_at | FLJ11126 | AA034074 | hypothetical protein FLJ11126 | |
| 1125 35709_at | FLJ11149 | AF038172 | hypothetical protein FLJ11149 | |
| 1126 38141_at | FLJ11193 | AF038176 | hypothetical protein FLJ11193 | |
| 1127 40859_at | FLJ11806 | AI561196 | hypothetical protein FLJ11806 | |
| 1128 41177_at | FLJ12443 | AW024285 | hypothetical protein FLJ12443 | |
| 1129 41434_at | FLJ12552 | AF070557 | hypothetical protein FLJ12552 | hypothetical protein FLJ12552 |
| 1130 36580_at | FLJ13910 | AL050139 | hypothetical protein FLJ13910 | hypothetical protein FLJ13910 |
| 1131 32222_at | FLJ14639 | AA152202 | hypothetical protein FLJ14639 | |
| 1132 38710_at | FLJ20113 | AL096714 | hypothetical protein FLJ20113 | |
| 1133 38652_at | FLJ20154 | AF070644 | hypothetical protein FLJ20154 | |
| 1134 40868_at | FLJ20274 | AA442799 | hypothetical protein FLJ20274 | |
| 1135 34739_at | FLJ20275 | W26023 | hypothetical protein FLJ20275 | |
| 1136 34857_at | FLJ20986 | Z24724 | hypothetical protein FLJ20986 | |
| 1137 32251_at | FLJ21174 | AA149307 | hypothetical protein FLJ21174 | |
| 1138 40615_at | FLJ21439 | AA780049 | hypothetical protein FLJ21439 | |
| 1139 33915_at | FLJ23027 | W22655 | hypothetical protein FLJ23027 | |

Fig 21

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| A | B | C | D | E |
|----------------|-----------|----------|---|---|
| 1140 35198_at | LOC57146 | AF070596 | hypothetical protein from clone 24796 | hypothetical protein from clone 24796 |
| 1141 38483_at | HSA011916 | AJ011916 | hypothetical protein HSA011916 | hypothetical protein |
| 1142 41236_at | HSU79252 | U79252 | hypothetical protein HSU79252 | hypothetical protein HSU79252 |
| 1143 38443_at | MGC14433 | U79291 | hypothetical protein MGC14433 | |
| 1144 39811_at | MGC2749 | AA402538 | hypothetical protein MGC2749 | |
| 1145 32051_at | MGC2840 | AJ224875 | hypothetical protein MGC2840 similar to a putative glucosyltransferase | glucosyltransferase |
| 1146 35219_at | MGC3047 | AL050202 | hypothetical protein MGC3047 | |
| 1147 41696_at | MGC3077 | AI620381 | hypothetical protein MGC3077 | |
| 1148 41147_at | MGC4276 | AF038186 | hypothetical protein MGC4276 similar to CG8198 | hypothetical protein MGC4276 similar to CG8198 |
| 1149 37242_at | MGC5149 | U79260 | hypothetical protein MGC5149 | |
| 1150 36975_at | MGC8721 | W26659 | hypothetical protein MGC8721 | |
| 1151 35677_at | MGC9084 | AL035369 | hypothetical protein MGC9084 | hypothetical protein |
| 1152 32504_at | MY014 | AW024812 | hypothetical protein MY014 | |
| 1153 38106_at | YR-29 | AJ012409 | hypothetical protein YR-29 | hypothetical protein |
| 1154 37640_at | HPRT1 | M31642 | hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome) | hypoxanthine phosphoribosyltransferase 1 |
| 1155 1039_s_at | HIF1A | U22431 | hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor) | hypoxia-inducible factor 1 alpha |
| 1156 39781_at | IGFBP4 | U20982 | IGF binding protein-4; Human insulin-like growth factor binding protein-4 (IGFBP4) | |
| 1157 38046_at | IK | AJ005579 | gene, promoter and complete cds. | insulin-like growth factor binding protein-4 |
| 1158 218_at | IK | S74221 | IK cytokine, down-regulator of HLA II | Prer. protein |
| 1159 37690_at | ILVBL | U61263 | IK cytokine, down-regulator of HLA II | IK factor |
| 1160 36097_at | ETR101 | M62831 | ilvB (bacterial acetolactate synthase)-like immediate early protein | acetolactate synthase homolog |
| 1161 1237_at | IER3 | S81914 | immediate early response 3 | immediate early protein |
| 1162 34391_at | IGBP1 | Y08915 | immunoglobulin (CD79A) binding protein 1 | immediate early response 3, isoform short; immediate early response 3, isoform long |

Fig 21

| A | B | C | D | E |
|------------------|----------|----------|--|--|
| 1163 38636_at | ISLR | AB003184 | immunoglobulin superfamily containing leucine-rich repeat | ISLR |
| 1164 40695_at | IMPDH1 | | IMP (inosine monophosphate) | IMP (inosine monophosphate) |
| 1165 36875_at | IBTK | J05272 | dehydrogenase 1 | dehydrogenase 1 |
| 1166 36617_at | ID1 | AL050018 | inhibitor of Bruton's tyrosine kinase | hypothetical protein |
| 1167 41215_s_at | ID2 | X77956 | inhibitor of DNA binding 1, dominant negative helix-loop-helix protein | inhibitor of DNA binding 1, dominant negative helix-loop-helix protein |
| | | D13891 | inhibitor of DNA binding 2, dominant negative helix-loop-helix protein | Id-2H |
| | | | inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein | |
| 1168 34344_at | IKBKAP | AF044195 | inner membrane protein, mitochondrial (mitofilin) | IkappaB kinase complex associated protein |
| 1169 37659_at | IMMT | L42572 | | transmembrane protein |
| 1170 755_at | ITPR1 | D26070 | inositol 1,4,5-triphosphate receptor, type 1 | human type 1 inositol 1,4,5-trisphosphate receptor |
| 1171 32778_at | ITPR1 | D26070 | inositol 1,4,5-triphosphate receptor, type 1 | human type 1 inositol 1,4,5-trisphosphate receptor |
| 1172 36154_at | IHPK1 | D87452 | inositol hexaphosphate kinase 1 | KIAA0263 protein |
| 1173 32697_at | IMPA1 | AF042729 | inositol(myo)-1(or 4)-monophosphatase 1 | lithium-sensitive myo-inositol monophosphatase A1 |
| 1174 36496_at | IMPA2 | AF014398 | inositol(myo)-1(or 4)-monophosphatase 2 | myo-inositol monophosphatase 2 |
| 1175 35833_at | LOC51141 | AL080184 | insulin induced protein 2 | |
| 1176 41049_at | IRS1 | S62539 | insulin receptor substrate 1 | insulin receptor substrate-1 |
| 1177 851_s_at | IRS1 | S62539 | insulin receptor substrate 1 | insulin receptor substrate-1 |
| 1178 38737_at | IGF1 | X57025 | insulin-like growth factor 1 (somatomedin C) | insulin-like growth factor I |
| 1179 1501_at | IGF1 | X57025 | insulin-like growth factor 1 (somatomedin C) | insulin-like growth factor I |
| 1180 160027_s_at | IGF2R | Y00285 | insulin-like growth factor 2 receptor | insulin-like growth factor 2 receptor |
| 1181 40422_at | IGFBP2 | X16302 | insulin-like growth factor binding protein 2 (36kD) | insulin-like growth factor binding protein 2 (36kD) |
| 1182 1737_s_at | IGFBP4 | M62403 | insulin-like growth factor binding protein 4 | insulin-like growth factor binding protein 4 |

Fig 21

| A | B | C | D | E |
|-----------------|------------------|----------|---|--|
| 1183 2062_at | IGFBP7 | L19182 | insulin-like growth factor binding protein 7 | |
| 1184 37991_at | ITM1 | L38961 | integral membrane protein 1 | integral membrane protein 1 |
| 1185 37326_at | A4 | U93305 | integral membrane protein; swiss-prot accession: O04901; may play role in cell differentiation in intestinal epithelium | LIM domain only 6 |
| 1186 41163_at | P24B | AL109672 | integral type I protein | p24B protein |
| 1187 32808_at | ITGB1; CD29; FN1 | X07979 | integrin beta 1 subunit precursor; Human mRNA for integrin beta 1 subunit. | integrin beta 1 isoform 1A precursor; integrin beta 1 isoform 1B precursor; integrin beta 1 isoform 1C-1 precursor; integrin beta 1 isoform 1D precursor; integrin beta 1 isoform 1C-2 precursor |
| 1188 1195_s_at | ICAP-1A | AF012024 | integrin cytoplasmic domain-associated protein 1 | integrin cytoplasmic domain associated protein |
| 1189 120_at | ITGA1 | X68742 | integrin, alpha 1 | |
| 1190 37484_at | ITGA1 | X68742 | integrin, alpha 1 | |
| 1191 36892_at | ITGA7 | AF032108 | integrin, alpha 7 | integrin alpha-7 |
| 1192 39071_at | ITGAV | M14648 | integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) | integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) |
| 1193 39754_at | ITGB5 | X53002 | integrin, beta 5 | |
| 1194 2058_s_at | ITGB5 | M35011 | integrin, beta 5 | integrin, beta 5 |
| 1195 40681_at | ITGBL1 | AB008375 | integrin, beta-like 1 (with EGF-like repeat domains) | osteoblast specific cysteine-rich protein |
| 1196 35365_at | ILK | U40282 | integrin-linked kinase | integrin-linked kinase |
| 1197 41743_i_at | OPTN; NRP; FIP2 | AF061034 | interacts with adenovirus E3-14.7KDa, a TNF-alpha cytolysis antagonist; leucine zipper protein; alternatively translated; long form; interacts with adenovirus E3-14.7KDa, a TNF-alpha cytolysis antagonist; leucine zipper protein; alternatively translated; short form; Homo sapiens FIP2 alternatively translated mRNA, complete cds. | FIP2 |

Fig 21

| A | B | C | D | E |
|-----------------|-----------------|----------|---|---|
| 1198 41742_s_at | OPTN; NRP; FIP2 | AF061034 | interacts with adenovirus E3-14.7KDa, a TNF-alpha cytolysis antagonist; leucine zipper protein; alternatively translated; long form; interacts with adenovirus E3-14.7KDa, a TNF-alpha cytolysis antagonist; leucine zipper protein; alternatively translated; short form; Homo sapiens FIP2 alternatively translated mRNA, complete cds. | FIP2 |
| 1199 676_g_at | IFITM1 | J04164 | interferon induced transmembrane protein 1 (9-27) | interferon induced transmembrane protein 1 (9-27) |
| 1200 675_at | IFITM1 | J04164 | interferon induced transmembrane protein 1 (9-27) | interferon induced transmembrane protein 1 (9-27) |
| 1201 41745_at | IFITM3 | X57352 | interferon induced transmembrane protein 3 (1-8U) | interferon induced transmembrane protein 3 (1-8U) |
| 1202 1456_s_at | IFI16 | M63838 | interferon, gamma-inducible protein 16 | interferon-gamma induced protein |
| 1203 925_at | IFI30 | J03909 | interferon, gamma-inducible protein 30 | interferon, gamma-inducible protein 30 |
| 1204 39728_at | IFI30 | J03909 | interferon, gamma-inducible protein 30 | interferon, gamma-inducible protein 30 |
| 1205 32814_at | IFIT1 | M24594 | interferon-induced protein with tetratricopeptide repeats 1 | interferon-induced protein with tetratricopeptide repeats 1 |
| 1206 37679_at | IFRD1 | Y10313 | interferon-related developmental regulator 1 | PC4 protein |
| 1207 1368_at | IL1R1 | M27492 | interleukin 1 receptor, type I | interleukin 1 receptor, type I |
| 1208 33228_g_at | IL10RB | A1984234 | interleukin 10 receptor, beta | |
| 1209 33227_at | IL10RB | A1984234 | interleukin 10 receptor, beta | |
| 1210 38969_at | IL27 | A1828168 | interleukin 27 | |
| 1211 38299_at | IL6 | X04430 | interleukin 6 (interferon, beta 2) | interleukin 6 (interferon, beta 2) |
| 1212 35372_r_at | IL8 | M17017 | interleukin 8 | interleukin 8 |
| 1213 36189_at | ILF2 | U10323 | interleukin enhancer binding factor 2, 45kD | NF-45 protein |
| 1214 36030_at | DKFZP586I2223 | AL080214 | intermediate filament-like MGC:2625 | hypothetical protein |
| 1215 35776_at | ITSN1 | AF064243 | intersectin 1 (SH3 domain protein) | intersectin short form |
| 1216 41431_at | ICK | AB023153 | intestinal cell kinase | KIAA09336 protein |
| 1217 1825_at | IQGAP1 | L33075 | IQ motif containing GTPase activating protein 1 | ras GTPase-activating-like protein |

Fig 21

| A | B | C | D | E |
|-----------------|------------|----------|---|---|
| 1218 39023_at | IDH1 | AF020038 | isocitrate dehydrogenase 1 (NADP+), soluble | NADP-dependent isocitrate dehydrogenase |
| 1219 40112_at | IDH3B | AA522698 | isocitrate dehydrogenase 3 (NAD+) beta | |
| 1220 40111_g_at | IDH3B | U49283 | isocitrate dehydrogenase 3 (NAD+) beta | NAD+-specific isocitrate dehydrogenase |
| 1221 40478_at | KIAA1162 | AL021396 | isoform 1 match: protein: Tr:Q9UJA1 | beta precursor |
| 1222 32695_at | dJ196E23.1 | Z97632 | isoform 2 match: protein Q99991 | hypothetical protein |
| 1223 40827_at | IARS | U04953 | isoleucine-tRNA synthetase | bombesin-like receptor 3 |
| 1224 36985_at | IDH1 | X17025 | isopentenyl-diphosphate delta isomerase | isoleucyl-tRNA synthetase |
| 1225 41775_at | ICMT | AF064084 | isoprenylcysteine carboxyl methyltransferase | isopentenyl-diphosphate delta isomerase |
| 1226 34877_at | JAK1 | AL039831 | Janus kinase 1 (a protein tyrosine kinase) | prenylcysteine carboxyl methyltransferase |
| 1227 34318_at | JM4 | AJ005896 | JM4 protein | JM4 protein |
| 1228 40957_at | JJAZ1 | D63881 | joined to JAZF1 | joined to JAZF1 |
| 1229 41250_at | JTV1 | U24169 | JTV1 gene | JTV-1 |
| 1230 41483_s_at | JUND | X56681 | jun D proto-oncogene | junD protein |
| 1231 1612_s_at | JUND | X56681 | jun D proto-oncogene | junD protein |
| 1232 40464_g_at | KPNB2 | U70322 | karyopherin (importin) beta 2 | transportin |
| 1233 39028_at | KPNB3 | Y08890 | karyopherin (importin) beta 3 | Ran_GTP binding protein 5 |
| 1234 35725_at | KPNA3 | D89618 | karyopherin alpha 3 (importin alpha 4) | karyopherin alhph 3 |
| 1235 32487_s_at | KPNA4 | AB002533 | karyopherin alpha 4 (importin alpha 3) | Qip1 |
| 1236 32708_g_at | KATNA1 | AI191768 | katanin p60 (ATPase-containing) subunit A 1 | |
| 1237 37386_i_at | KDELR1 | X55885 | KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1 | KDEL receptor |
| 1238 39080_at | KDELR2 | M88458 | KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2 | KDEL receptor 2 |
| 1239 33402_at | KDELR3 | AL035081 | KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 | hypothetical protein |
| 1240 37150_at | AB026190 | AB026190 | Kelch motif containing protein | Kelch motif containing protein |
| 1241 32329_at | KRTHB6 | X99142 | keratin, hair, basic, 6 (monilethrix) | type II intermediate filament of hair keratin |
| 1242 39346_at | KHDRBS1 | M88108 | KH domain containing, RNA binding, signal transduction associated 1 | p62 |

Fig 21

| | A | B | C | D | E |
|------|------------|----------|--------|--|-----------------------|
| 1243 | 32679_at | KIAA0009 | D13634 | KIAA0009 gene product | KIAA0009 gene product |
| 1244 | 34760_at | KIAA0022 | D14684 | KIAA0022 gene product | KIAA0022 gene product |
| 1245 | 41129_at | KIAA0033 | D26067 | KIAA0033 protein | |
| 1246 | 38797_at | KIAA0062 | D31887 | KIAA0062 protein | |
| 1247 | 36978_at | KIAA0077 | D38521 | KIAA0077 protein | |
| 1248 | 37718_at | KIAA0096 | D43636 | KIAA0096 protein | |
| 1249 | 37293_at | KIAA0097 | D43948 | KIAA0097 gene product | KIAA0097 protein |
| | | | | KIAA0098 is a human counterpart of mouse chaperonin containing TCP-1 gene. Start codon is not identified. ha01413 cDNA clone for KIAA0098 has a 2-bp insertion between 736-737 of the sequence of KIAA0098; Homo sapiens mRNA for KIAA0098 protein, partial cds. | |
| 1250 | 40417_at | KIAA0098 | D43950 | | KIAA0098 protein |
| 1251 | 39783_at | KIAA0100 | D43947 | KIAA0100 gene product | KIAA0100 protein |
| 1252 | 37359_at | KIAA0102 | D14658 | KIAA0102 gene product | KIAA0102 gene product |
| 1253 | 38031_at | KIAA0111 | D21853 | KIAA0111 gene product | KIAA0111 gene product |
| 1254 | 40279_at | KIAA0121 | D50911 | KIAA0121 gene product | KIAA0121 protein |
| 1255 | 36845_at | KIAA0136 | D50926 | KIAA0136 protein | |
| 1256 | 32099_at | KIAA0138 | D50928 | KIAA0138 gene product | KIAA0138 gene product |
| 1257 | 38472_at | KIAA0143 | D63477 | KIAA0143 protein | |
| 1258 | 41728_at | KIAA0152 | D63486 | KIAA0152 gene product | KIAA0152 gene product |
| 1259 | 37642_at | KIAA0157 | D63877 | KIAA0157 protein | KIAA0157 protein |
| 1260 | 32661_s_at | KIAA0170 | D79992 | KIAA0170 gene product | KIAA0170 gene product |
| 1261 | 37225_at | KIAA0172 | D79994 | KIAA0172 protein | |
| 1262 | 36942_at | KIAA0174 | D79996 | KIAA0174 gene product | KIAA0174 gene product |
| 1263 | 31863_at | KIAA0179 | D80001 | KIAA0179 protein | |
| 1264 | 37734_at | KIAA0184 | D80006 | KIAA0184 protein | |
| 1265 | 41669_at | KIAA0191 | D83776 | KIAA0191 protein | |
| 1266 | 36192_at | KIAA0193 | D83777 | KIAA0193 gene product | KIAA0193 gene product |
| 1267 | 38056_at | KIAA0195 | D83779 | KIAA0195 gene product | KIAA0195 gene product |
| 1268 | 38419_at | KIAA0196 | D83780 | KIAA0196 gene product | KIAA0196 gene product |
| 1269 | 38067_at | KIAA0202 | D86957 | KIAA0202 protein | |
| 1270 | 32586_at | KIAA0217 | D86971 | KIAA0217 protein | |
| 1271 | 38728_at | KIAA0225 | D86978 | KIAA0225 protein | |

Fig 21

| | A | B | C | D | E |
|------|------------|----------|----------|-----------------------|-----------------------|
| 1272 | 40971_at | KIAA0229 | D86982 | KIAA0229 protein | |
| 1273 | 37748_at | KIAA0232 | D86985 | KIAA0232 gene product | KIAA0232 protein |
| 1274 | 38892_at | KIAA0240 | D87077 | KIAA0240 protein | |
| 1275 | 40765_at | KIAA0251 | D87438 | KIAA0251 protein | |
| 1276 | 41634_at | KIAA0256 | D87445 | KIAA0256 gene product | KIAA0256 protein |
| 1277 | 36971_at | KIAA0257 | D87446 | KIAA0257 protein | |
| 1278 | 32237_at | KIAA0265 | D87454 | KIAA0265 protein | |
| 1279 | 39405_at | KIAA0266 | D87455 | KIAA0266 gene product | KIAA0266 gene product |
| 1280 | 35039_at | KIAA0276 | D87466 | KIAA0276 protein | |
| 1281 | 38592_s_at | KIAA0284 | A1828210 | KIAA0284 protein | |
| 1282 | 41381_at | KIAA0308 | AB002306 | KIAA0308 protein | |
| 1283 | 37943_at | KIAA0321 | AB002319 | KIAA0321 protein | |
| 1284 | 32592_at | KIAA0323 | AB002321 | KIAA0323 protein | |
| 1285 | 39797_at | KIAA0349 | AB002347 | KIAA0349 protein | |
| 1286 | 34661_at | KIAA0350 | AB002348 | KIAA0350 protein | KIAA0350 protein |
| 1287 | 32208_at | KIAA0355 | AB002353 | KIAA0355 gene product | KIAA0355 gene product |
| 1288 | 32223_at | KIAA0365 | AB002363 | KIAA0365 gene product | |
| 1289 | 33442_at | KIAA0367 | AB002365 | KIAA0367 protein | |
| 1290 | 35830_at | KIAA0370 | AB002368 | KIAA0370 protein | |
| 1291 | 40517_at | KIAA0372 | AB002370 | KIAA0372 gene product | KIAA0372 gene product |
| 1292 | 34837_at | KIAA0376 | AB002374 | KIAA0376 protein | |
| 1293 | 41457_at | KIAA0423 | AB007883 | KIAA0423 protein | |
| 1294 | 35167_at | KIAA0433 | AB007893 | KIAA0433 protein | KIAA0433 protein |
| 1295 | 33340_at | KIAA0438 | AB007898 | KIAA0438 gene product | KIAA0438 gene product |
| 1296 | 40805_at | KIAA0440 | AB007900 | KIAA0440 protein | KIAA0440 protein |
| 1297 | 32091_at | KIAA0446 | AB007915 | KIAA0446 gene product | KIAA0446 protein |
| 1298 | 41243_at | KIAA0447 | AB007916 | KIAA0447 gene product | KIAA0447 protein |
| 1299 | 32206_at | KIAA0451 | AB007920 | KIAA0451 gene product | KIAA0451 protein |
| 1300 | 36069_at | SRGAP2 | AB007925 | KIAA0456 protein | KIAA0456 protein |
| 1301 | 37230_at | KIAA0469 | AB007938 | KIAA0469 gene product | KIAA0469 protein |
| 1302 | 33893_r_at | KIAA0470 | AB007939 | KIAA0470 gene product | KIAA0470 protein |
| 1303 | 34445_at | KIAA0471 | AB007940 | KIAA0471 gene product | KIAA0471 protein |
| 1304 | 35318_at | KIAA0475 | AB007944 | KIAA0475 gene product | KIAA0475 protein |
| 1305 | 35786_at | KIAA0476 | AB007945 | KIAA0476 gene product | KIAA0476 protein |
| 1306 | 35762_at | KIAA0483 | AB007952 | KIAA0483 protein | KIAA0483 protein |
| 1307 | 41830_at | KIAA0494 | AB007963 | KIAA0494 gene product | KIAA0494 protein |

Fig 21

| | A | B | C | D | E |
|------|------------|----------|----------|-----------------------|----------------------|
| 1308 | 35534_at | KIAA0514 | AB011086 | KIAA0514 gene product | KIAA0514 protein |
| 1309 | 38724_at | KIAA0515 | AB011087 | KIAA0515 protein | KIAA0515 protein |
| 1310 | 34192_at | KIAA0532 | AB011104 | KIAA0532 protein | KIAA0532 protein |
| 1311 | 33787_at | KIAA0537 | AB011109 | KIAA0537 gene product | KIAA0537 protein |
| 1312 | 35184_at | KIAA0546 | AB011118 | KIAA0546 protein | KIAA0546 protein |
| 1313 | 31849_at | KIAA0564 | AB011136 | KIAA0564 protein | KIAA0564 protein |
| 1314 | 39434_at | KIAA0592 | AB011164 | KIAA0592 protein | KIAA0592 protein |
| 1315 | 41379_at | KIAA0594 | AB011166 | KIAA0594 protein | KIAA0594 protein |
| 1316 | 32866_at | KIAA0605 | AB011177 | KIAA0605 gene product | KIAA0605 protein |
| 1317 | 39852_at | KIAA0610 | AB011182 | KIAA0610 protein | KIAA0610 protein |
| 1318 | 40160_at | KIAA0618 | AL080109 | KIAA0618 gene product | hypothetical protein |
| 1319 | 40083_at | KIAA0625 | AB014525 | KIAA0625 protein | KIAA0625 protein |
| 1320 | 33241_at | KIAA0626 | AB014526 | KIAA0626 gene product | KIAA0626 protein |
| 1321 | 39376_at | KIAA0630 | AB014530 | KIAA0630 protein | KIAA0630 protein |
| 1322 | 34353_at | KIAA0648 | AB014548 | KIAA0648 protein | KIAA0648 protein |
| 1323 | 38082_at | KIAA0650 | AB014550 | KIAA0650 protein | KIAA0650 protein |
| 1324 | 39117_at | KIAA0662 | AB014562 | KIAA0662 gene product | KIAA0662 protein |
| 1325 | 41170_at | KIAA0663 | AB014563 | KIAA0663 gene product | KIAA0663 protein |
| 1326 | 31826_at | KIAA0674 | AB014574 | KIAA0674 protein | KIAA0674 protein |
| 1327 | 39403_at | KIAA0678 | AB014578 | KIAA0678 protein | KIAA0678 protein |
| 1328 | 39519_at | KIAA0692 | AB014592 | KIAA0692 protein | KIAA0692 protein |
| 1329 | 39380_at | KIAA0697 | AB014597 | KIAA0697 protein | KIAA0697 protein |
| 1330 | 39705_at | KIAA0700 | AB014600 | KIAA0700 protein | KIAA0700 protein |
| 1331 | 41620_at | KIAA0716 | AB018259 | KIAA0716 gene product | KIAA0716 protein |
| 1332 | 33835_at | KIAA0721 | AB018264 | KIAA0721 protein | KIAA0721 protein |
| 1333 | 35177_at | KIAA0725 | AB018268 | KIAA0725 protein | KIAA0725 protein |
| 1334 | 41218_at | KIAA0729 | AB018272 | KIAA0729 protein | KIAA0729 protein |
| 1335 | 38694_at | KIAA0738 | AB018281 | KIAA0738 gene product | KIAA0738 protein |
| 1336 | 39771_at | KIAA0740 | AB018283 | KIAA0740 gene product | KIAA0740 protein |
| 1337 | 41585_at | KIAA0746 | AB018289 | KIAA0746 protein | KIAA0746 protein |
| 1338 | 38424_at | KIAA0747 | AB018290 | KIAA0747 protein | KIAA0747 protein |
| 1339 | 40848_g_at | KIAA0750 | AB018293 | KIAA0750 gene product | KIAA0750 protein |
| 1340 | 32224_at | KIAA0769 | AB018312 | KIAA0769 gene product | KIAA0769 protein |
| 1341 | 36474_at | KIAA0776 | AB018319 | KIAA0776 protein | KIAA0776 protein |
| 1342 | 33251_at | KIAA0779 | AB018322 | KIAA0779 protein | KIAA0779 protein |
| 1343 | 35999_r_at | KIAA0781 | AB018324 | KIAA0781 protein | KIAA0781 protein |

GIS 21

| | A | B | C | D | E |
|------|------------|------------|----------|------------------|-----------------------------|
| 1344 | 41224_at | KIAA0788 | AB018331 | KIAA0788 protein | KIAA0788 protein |
| 1345 | 34285_at | KIAA0795 | AB018338 | KIAA0795 protein | KIAA0795 protein |
| 1346 | 39614_at | KIAA0802 | AB018345 | KIAA0802 protein | KIAA0802 protein |
| 1347 | 36588_at | KIAA0810 | AB018353 | KIAA0810 protein | KIAA0810 protein |
| 1348 | 40492_at | KIAA0826 | AB020633 | KIAA0826 protein | KIAA0826 protein |
| 1349 | 40455_at | KIAA0830 | AB020637 | KIAA0830 protein | KIAA0830 protein |
| 1350 | 41372_at | KIAA0831 | AB020638 | KIAA0831 protein | KIAA0831 protein |
| 1351 | 36888_at | KIAA0841 | AB020648 | KIAA0841 protein | KIAA0841 protein |
| 1352 | 39597_at | KIAA0843 | AB020650 | KIAA0843 protein | KIAA0843 protein |
| 1353 | 41503_at | KIAA0854 | AB020661 | KIAA0854 protein | KIAA0854 protein |
| 1354 | 38730_at | KIAA0864 | AB020671 | KIAA0864 protein | KIAA0864 protein |
| 1355 | 39021_at | KIAA0877 | AB020684 | KIAA0877 protein | KIAA0877 protein |
| 1356 | 32215_i_at | KIAA0878 | AB020685 | KIAA0878 protein | KIAA0878 protein |
| 1357 | 38254_at | KIAA0882 | AB020689 | KIAA0882 protein | KIAA0882 protein |
| 1358 | 35720_at | KIAA0893 | AB020700 | KIAA0893 protein | KIAA0893 protein |
| 1359 | 40423_at | KIAA0903 | AB020710 | KIAA0903 protein | KIAA0903 protein |
| 1360 | 41421_at | KIAA0909 | AB020716 | KIAA0909 protein | KIAA0909 protein |
| 1361 | 41498_at | KIAA0911 | AB020718 | KIAA0911 protein | KIAA0911 protein |
| 1362 | 39777_at | KIAA0916 | AF075587 | KIAA0916 protein | protein associated with Myc |
| 1363 | 32735_at | KIAA0931 | AB023148 | KIAA0931 protein | KIAA0931 protein |
| 1364 | 33408_at | KIAA0934 | AB023151 | KIAA0934 protein | KIAA0934 protein |
| 1365 | 35369_at | KIAA0937 | AB023154 | KIAA0937 protein | KIAA0937 protein |
| 1366 | 33235_at | KIAA0938 | AB023155 | KIAA0938 protein | KIAA0938 protein |
| 1367 | 32740_at | Rab11-FIP2 | AB023158 | KIAA0941 protein | KIAA0941 protein |
| 1368 | 35794_at | KIAA0942 | AB023159 | KIAA0942 protein | KIAA0942 protein |
| 1369 | 41595_at | KIAA0947 | AB023164 | KIAA0947 protein | KIAA0947 protein |
| 1370 | 38649_at | KIAA0970 | AB023187 | KIAA0970 protein | KIAA0970 protein |
| 1371 | 34396_at | KIAA0978 | AB023195 | KIAA0978 protein | KIAA0978 protein |
| 1372 | 32085_at | KIAA0981 | AB023198 | KIAA0981 protein | KIAA0981 protein |
| 1373 | 35199_at | KIAA0982 | AB023199 | KIAA0982 protein | KIAA0982 protein |
| 1374 | 32769_at | KIAA0993 | AB023210 | KIAA0993 protein | KIAA0993 protein |
| 1375 | 34751_at | KIAA0997 | A1970189 | KIAA0997 protein | KIAA0999 protein |
| 1376 | 34808_at | KIAA0999 | AB023216 | KIAA0999 protein | KIAA0999 protein |
| 1377 | 33193_at | KIAA1001 | AW052084 | KIAA1001 protein | KIAA1001 protein |
| 1378 | 36002_at | KIAA1012 | AB023229 | KIAA1012 protein | KIAA1012 protein |
| 1379 | 35802_at | KIAA1014 | AB023231 | KIAA1014 protein | KIAA1014 protein |

Fig 21

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| | A | B | C | D | E |
|------|------------|----------|----------|---|---------------------------------|
| 1380 | 39615_at | KIAA1026 | AB028949 | KIAA1026 protein | KIAA1026 protein |
| 1381 | 34089_at | KIAA1030 | AB028953 | KIAA1030 protein | KIAA1030 protein |
| 1382 | 41651_at | KIAA1033 | AB028956 | KIAA1033 protein | KIAA1033 protein |
| 1383 | 41708_at | KIAA1034 | AB028957 | KIAA1034 protein | KIAA1034 protein |
| 1384 | 35163_at | KIAA1041 | AB028964 | KIAA1041 protein | KIAA1041 protein |
| 1385 | 38778_at | KIAA1046 | AB028969 | KIAA1046 protein | KIAA1046 protein |
| 1386 | 41268_g_at | KIAA1049 | AB028972 | KIAA1049 protein | KIAA1049 protein |
| 1387 | 40855_at | KIAA1053 | AB028976 | KIAA1053 protein | KIAA1053 protein |
| 1388 | 39400_at | KIAA1055 | AB028978 | KIAA1055 protein | KIAA1055 protein |
| 1389 | 33877_s_at | KIAA1067 | AB028990 | KIAA1067 protein | KIAA1067 protein |
| 1390 | 34688_at | KIAA1078 | AB029001 | KIAA1078 protein | KIAA1078 protein |
| 1391 | 33924_at | KIAA1091 | AB029014 | KIAA1091 protein | KIAA1091 protein |
| 1392 | 32508_at | KIAA1096 | AL096857 | KIAA1096 protein | hypothetical protein |
| 1393 | 41179_at | KIAA1100 | AB029023 | KIAA1100 protein | KIAA1100 protein |
| 1394 | 34839_at | KIAA1104 | AB029027 | KIAA1104 protein | KIAA1104 protein |
| 1395 | 33457_at | RAP140 | AB029028 | KIAA1105 protein | KIAA1105 protein |
| 1396 | 36814_at | KIAA1109 | AB029032 | KIAA1109 protein | KIAA1109 protein |
| 1397 | 34274_at | KIAA1116 | AB029039 | KIAA1116 protein | KIAA1116 protein |
| 1398 | 37617_at | KIAA1128 | U90912 | KIAA1128 protein | |
| 1399 | 33358_at | KIAA1157 | W29087 | KIAA1157 protein | |
| 1400 | 40308_at | KIAA1240 | A1830496 | KIAA1240 protein | |
| 1401 | 33811_at | KIAA1254 | A1761557 | KIAA1254 protein | |
| 1402 | 38674_at | KIAA1354 | AA115140 | KIAA1354 protein | |
| 1403 | 32730_at | KIAA1750 | AL080059 | KIAA1750 protein | |
| 1404 | 32171_at | KIAA1856 | AL080102 | KIAA1856 protein | hypothetical protein |
| 1405 | 39897_at | KIAA1966 | N36997 | KIAA1966 protein | |
| 1406 | 32846_s_at | KTN1 | D13629 | kinectin 1 (kinesin receptor) | kinectin 1 |
| 1407 | 39057_at | KNS2 | LO4733 | kinectin 2 (60-70kD) | kinesin light chain |
| 1408 | 32079_at | KIF13B | AB014539 | kinesin family member 13B | KIAA0639 protein |
| 1409 | 33345_at | KIF3C | AF035621 | kinesin family member 3C | kinesin-related protein |
| 1410 | 34294_at | KIFC3 | AL041493 | kinesin family member C3 | |
| 1411 | 41474_at | KIF2 | Y08319 | kinesin heavy chain member 2 | kinesin-2 |
| 1412 | 40779_at | KIFAP3 | U59919 | kinesin-associated protein 3 | SMAP |
| 1413 | 34216_at | KLF7 | AA478904 | Kruppel-like factor 7 (ubiquitous) | |
| 1414 | 38768_at | HADHSC | X96752 | L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain | 3-hydroxyacyl-CoA dehydrogenase |

Cis 21

| | A | B | C | D | E |
|------|------------|----------|----------|---|--|
| 1415 | 41485_at | LDHA | X02152 | lactate dehydrogenase A | lactate dehydrogenase A |
| 1416 | 288_s_at | LBR | L25931 | lamin B receptor | lamin B receptor |
| 1417 | 256_s_at | LAMR1 | M14199 | laminin receptor 1 (67kD, ribosomal protein SA) | laminin receptor 1 |
| 1418 | 37671_at | LAMA4 | S78569 | laminin, alpha 4 | laminin alpha 4 chain |
| 1419 | 581_at | LAMB1 | M61916 | laminin, beta 1 | laminin B1 |
| 1420 | 39441_at | LANCL1 | Y11395 | LanC (antibiotic synthetase component C-like 1 (bacterial)) | lanthionine synthetase C-like protein. 1 |
| 1421 | 1495_at | LTBP1 | M34057 | latent transforming growth factor beta binding protein 1 | latent transforming growth factor beta binding protein 1 precursor |
| 1422 | 37906_at | LTBP2 | Z37976 | latent transforming growth factor beta binding protein 2 | LTBP-2 precursor |
| 1423 | 33412_at | LGALS1 | A1535946 | lectin, galactoside-binding, soluble, 1 (galectin 1) | |
| 1424 | 35367_at | LGALS3 | AB006780 | lectin, galactoside-binding, soluble, 3 (galectin 3) | galectin-3 |
| 1425 | 37754_at | LGALS3BP | L13210 | lectin, galactoside-binding, soluble, 3 binding protein | Mac-2 binding protein |
| 1426 | 1846_at | LGALS8 | L78132 | lectin, galactoside-binding, soluble, 8 (galectin 8) | prostate carcinoma tumor antigen |
| 1427 | 34267_r_at | LEPR | U50748 | leptin receptor | leptin receptor |
| 1428 | 33830_at | HSOBRGRP | AW026535 | leptin receptor gene-related protein | |
| 1429 | 33829_at | HSOBRGRP | Y12670 | leptin receptor gene-related protein | leptin receptor gene-related protein |
| 1430 | 38985_at | LEPROTL1 | AF063605 | leptin receptor overlapping transcript-like 1 | brain my047 protein |
| 1431 | 41320_s_at | LRRFIP1 | U69609 | leucine rich repeat (in FLI) interacting protein 1 | transcription repressor |
| 1432 | 39967_at | LDOC1 | AB019527 | leucine zipper, down-regulated in cancer 1 | LDOC1 protein |
| 1433 | 41754_at | LRPPRC | M92439 | leucine-rich PPR-motif containing | leucine-rich PPR-motif containing protein |
| 1434 | 37470_at | LAIR1 | AF013249 | leukocyte-associated Ig-like receptor 1 | leukocyte-associated Ig-like receptor-1 |
| 1435 | 38081_at | LT4H | J03459 | leukotriene A4 hydrolase | leukotriene A4 hydrolase |
| 1436 | 36062_at | LPXN | AF062075 | leupaxin | leupaxin |
| 1437 | 35278_at | RPS29 | A1541542 | libtest16.A02.r bvnorm Homo sapiens cDNA 5' mRNA sequence. | |
| 1438 | 39687_at | E46L | A1524873 | like mouse brain protein E46 | |

Gis 21

| | A | B | C | D | E |
|------|------------|-----------|----------|--|----------------------------------|
| 1439 | 39686_g_at | E46L | AL050282 | like mouse brain protein E46 | hypothetical protein |
| 1440 | 39685_at | E46L | AL050282 | like mouse brain protein E46 | hypothetical protein |
| 1441 | 39163_at | KIDINS220 | W27233 | likely homolog of rat kinase D-interacting substance of 220 kDa | |
| 1442 | 32669_at | SOC55 | AB014571 | likely ortholog of mouse suppressors of cytokine signalling 5 | KIAA0671 protein |
| 1443 | 40555_at | TC10 | AL043108 | likely ortholog of mouse TC10-alpha | |
| 1444 | 40844_at | TSBP | D63875 | likely ortholog of mouse TPR-containing, SH2-binding phosphoprotein | KIAA0155 gene product |
| 1445 | 41248_at | CSTF2T | AB014589 | likely ortholog of mouse variant polyadenylation protein CSTF-64 | KIAA0689 protein |
| 1446 | 35805_at | GRASP55 | AA447263 | likely ortholog of rat golgi stacking protein homolog GRASP55 | |
| 1447 | 39232_at | LIMS1 | U09284 | LIM and senescent cell antigen-like domains 1 | PINCH protein |
| 1448 | 36181_at | LASP1 | X82456 | LIM and SH3 protein 1 | LIM and SH3 domain protein |
| 1449 | 38617_at | LIMK2 | D45906 | LIM domain kinase 2 | LIMK-2 |
| 1450 | 1452_at | LMO4 | U24576 | LIM domain only 4 | breast tumor autoantigen |
| 1451 | 31936_s_at | LKAP | AB007890 | limkain b1 | KIAA0430 protein |
| 1452 | 38745_at | LIPA | X76488 | lipase A, lysosomal acid, cholesterol esterase (Wolman disease) | lysosomal acid lipase |
| 1453 | 38098_at | LPIN1 | D80010 | lipin 1 | |
| 1454 | 37542_at | LHFPL2 | D86961 | lipoma HMGIC fusion partner-like 2 | lipoprotein lipase precursor |
| 1455 | 41209_at | LPL | M15856 | lipoprotein lipase | estrogen regulated LIV-1 protein |
| 1456 | 1798_at | LIV-1 | U41060 | LIV-1 protein, estrogen regulated liver form; Homo sapiens glycogen phosphorylase (PYGL) gene, exon 20 and complete cds. | glycogen phosphorylase |
| 1457 | 37215_at | PYGL | AF046798 | | |

Fig 21

| A | B | C | D | E |
|-----------------|-----------|----------|--|--|
| 1458 40493_at | CD44 | L05424 | long tailed isoform; individual exons 6-14 are alternative exons any of which can be spliced out of the mRNA.; putative; long tailed isoform; putative; long tailed isoform; hemopoietic variant; putative; long tailed isoform; epithelial form; putative; Human cell surface glycoprotein CD44 (CD44) gene, 3' end of long tailed isoform. | cell surface glycoprotein CD44 |
| 1459 36194_at | LRPAP1 | M63959 | low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1) | alpha-2-macroglobulin receptor-associated protein |
| 1460 34400_at | QP-C | AI540957 | low molecular mass ubiquitinone-binding protein (9.5kD) | |
| 1461 37025_at | PIG7 | AL120815 | LPS-induced TNF-alpha factor | |
| 1462 39017_at | LSM1 | AJ238094 | Lsm1 protein | Lsm1 protein |
| 1463 38038_at | LUM | U21128 | lumican | lumican |
| 1464 38115_at | FUS1 | AF055479 | lung cancer candidate | lung cancer candidate FUS1 |
| 1465 39428_at | LNK | AF055581 | lymphocyte adaptor protein | adaptor protein Lnk |
| 1466 39396_at | LYPLA1 | AF081281 | lysophospholipase I | lysophospholipase |
| 1467 33788_at | LYSAL1 | AB002390 | lysosomal apyrase-like 1 | lysosomal apyrase-like 1 |
| 1468 39758_f_at | LAMP1 | J04182 | lysosomal-associated membrane protein 1 | lysosomal membrane glycoprotein-1 |
| 1469 38403_at | LAMP2 | X77196 | lysosomal-associated membrane protein 2 | lysosome-associated membrane protein-2 |
| 1470 38402_at | LAMP2 | U36336 | lysosomal-associated membrane protein 2 | lysosome-associated membrane protein-2b |
| 1471 39019_at | LAPTM4A | D14696 | lysosomal-associated protein | lysosomal-associated protein |
| 1472 33127_at | LOXL2 | U89942 | transmembrane 4 alpha | transmembrane 4 alpha |
| 1473 34336_at | KARS | D32053 | lysyl oxidase-like 2 | lysyl oxidase-related protein |
| 1474 32832_at | MAEA | AF084928 | lysyl-tRNA synthetase | Lysyl tRNA Synthetase |
| 1475 36174_at | MACMARCKS | X70326 | macrophage erythroblast attacher | erythroblast macrophage protein EMP |
| | | | macrophage myristoylated alanine-rich C kinase substrate | macrophage myristoylated alanine-rich C kinase substrate |

Fig 21

| | A | B | C | D | E |
|------|------------|----------|----------|---|--|
| 1476 | 1453_at | MADH2 | U68018 | MAD, mothers against decapentaplegic homolog 2 (Drosophila) | mad protein homolog |
| 1477 | 38944_at | MADH3 | U68019 | MAD, mothers against decapentaplegic homolog 3 (Drosophila) | mad protein homolog |
| 1478 | 1433_g_at | MADH3 | U68019 | MAD, mothers against decapentaplegic homolog 3 (Drosophila) | mad protein homolog |
| 1479 | 36953_at | MADH4 | U44378 | MAD, mothers against decapentaplegic homolog 4 (Drosophila) | Dpc4 |
| 1480 | 1013_at | MADH5 | U59913 | MAD, mothers against decapentaplegic homolog 5 (Drosophila) | Smad5 |
| 1481 | 1955_s_at | MADH6 | AF035528 | MAD, mothers against decapentaplegic homolog 6 (Drosophila) | Smad6 |
| 1482 | 1857_at | MADH7 | AF010193 | MAD, mothers against decapentaplegic homolog 7 (Drosophila) | MAD-related gene SMAD7 |
| 1483 | 41237_at | HLA-A | D32129 | major histocompatibility complex, class I, A | HLA-A26 |
| 1484 | 41609_at | HLA-DMB | U15085 | major histocompatibility complex, class II, DM beta | HLA-DMB |
| 1485 | 38096_f_at | HLA-DPB1 | M83664 | major histocompatibility complex, class II, DP beta 1 | HLA-DPB1 |
| 1486 | 38095_i_at | HLA-DPB1 | M83664 | major histocompatibility complex, class II, DP beta 1 | HLA-DPB1 |
| 1487 | 37039_at | HLA-DRA | J00194 | major histocompatibility complex, class II, DR alpha | major histocompatibility complex, class II, DR alpha precursor |
| 1488 | 33261_at | HLA-DRB1 | M16941 | major histocompatibility complex, class II, DR beta 1 | |
| 1489 | 34425_at | HLALS | AF031469 | major histocompatibility complex, class I-like sequence | MHC class I-related protein 1 isoform D |
| 1490 | 34003_at | CD4 | U47924 | major receptor for HIV-1; member of immunoglobulin supergene family; T cell surface glycoprotein T4 | protein 'A', isoform 1 |
| 1491 | 36608_at | MDH1 | D55654 | malate dehydrogenase 1, NAD (soluble) | cytosolic malate dehydrogenase |
| 1492 | 837_s_at | ME1 | U43944 | malic enzyme 1, NADP(+)-dependent, cytosolic | cytosolic NADP(+)-dependent malic enzyme |

Fig 21

| A | B | C | D | E |
|---------------|---------------|----------|---|---|
| 1493 36599_at | ME2 | M55905 | malic enzyme 2, NAD(+)-dependent, mitochondrial | mitochondrial NAD(P)+ -dependent malic enzyme |
| 1494 36673_at | MPI | X76057 | mannose phosphate isomerase | phosphomannose isomerase |
| 1495 35299_at | MKNK1 | AB000409 | MAP kinase-interacting serine/threonine kinase 1 | MNK1 |
| 1496 40826_at | MARK3 | M80359 | MAP/microtubule affinity-regulating kinase 3 | protein p78 |
| 1497 41506_at | MAPKAPK5; PRA | AF032437 | MAPK-activated protein kinase; PRK; Homo sapiens mitogen activated protein kinase activated protein kinase gene, complete cds. | mitogen activated protein kinase activated protein kinase |
| 1498 37009_at | CAT | AL035079 | match proteins: Sw:P04040 Sw:P04762 Sw:P24270 Tr:O62839 Sw:P00432 Sw:P17336 Tr:P90682 Tr:Q27487 Sw:O61235 Tr:O18193 Tr:O77229 Tr:Q49133 Sw:P26901 Sw:P55306 Sw:P30263 Tr:P95631 Sw:P44390 Tr:Q27710 Sw:Q96528 Sw:O13289 Sw:P07820 Sw:P30265 Sw:P77872 Tr:Q59602 Tr:P77924 Sw:Q59170 Sw:P15202 Tr:Q59296 Tr:O33613 Sw:Q92405 Sw:Q59635 Sw:P81138 match ESTs: W94164 N28621 match to ESTs AA316181 (NID:g3165221), AA032221 (NID:g1502183), and AI167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7q21, complete sequence. | dJ53C18.1 (Catalase) |
| 1499 40297_at | WUGSC:H_RG04 | AC005053 | | six transmembrane epithelial antigen of the prostate |

C's 21

| | A | B | C | D | E |
|------|------------|-------------|----------|---|---|
| 1500 | 34860_g_at | BCG1 | Z98046 | match: cDNAs X67055 X14690 D89287 X70393 S82800 X16260 M18192 Y11283 D38535 D38595 match: proteins Q06033 P97280 Q54882 Q35802 Q61704 Q14624 P79263 Q63416 Q42141 P19823 Q02668 Q61703 P97279 Q29052 | hepatocellular carcinoma associated protein; breast cancer associated gene 1 |
| 1501 | 35336_at | HS508115A | AL021707 | match: cDNAs: Em:AL050345 match: ESTs: Em:AA304885 Em:AA447346 Em:AA314213 Em:AA209368 Em:AA209372 Em:T84723 Em:H23039 Em:AA542125 Em:W41686 Em:AA384854 Em:AA492678 | chromosome 22 open reading frame 2 |
| 1502 | 32658_at | dJ1033B10.1 | AL031228 | match: protein O15214 | BING4 |
| 1503 | 31545_at | dJ1033B10.1 | AL031228 | match: protein O15214 | BING4 |
| 1504 | 36986_at | dJ886K2.1 | AL031295 | match: protein SPTREMBL; Q14241 match: proteins CE02000 Q59733 | UDP-galactose-4-epimerase |
| 1505 | 38072_at | dJ465N24.1 | AL031432 | match: proteins CE01999; supported by GENES and GENSCAN | hypothetical protein dJ465N24.2.1 |
| 1506 | 32478_f_at | dJ281H8.1 | AL031133 | match: proteins O15037 CE16881 supported by GENSCAN possibly this partial gene and dJ281H8.1 are part of one gene | dJ281H8.2 (PUTATIVE novel protein similar to KIAA0323 and worm C30F12.1) |

Fig 21

| A | B | C | D | E |
|---------------|-----------|----------|--|---|
| 1507 39759_at | dJ51J12.1 | AL031781 | <p>match: proteins O42476 Q94539; match: protein O88972; match: cDNA AF091047; owing to a different in-frame ORF, the translation of the last coding exon (8 C-terminal amino-acids) differs from that in mouse and is terminated more upstream; match: protein Q61110; Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.</p> | <p>dJ51J12.1 (human ortholog of zebrafish Quaking protein homolog ZKQ-1 (isoform 1)); dJ51J12.1.2 (human ortholog of mouse KH Domain RNA Binding protein QKI-7B (isoform 2)); dJ51J12.1.3 (human ortholog of mouse KH Domain RNA Binding protein QKI-7 (isoform 3))</p> |
| 1508 39760_at | dJ51J12.1 | AL031781 | <p>match: proteins O42476 Q94539; match: protein O88972; match: cDNA AF091047; owing to a different in-frame ORF, the translation of the last coding exon (8 C-terminal amino-acids) differs from that in mouse and is terminated more upstream; match: protein Q61110; Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.</p> | <p>dJ51J12.1 (human ortholog of zebrafish Quaking protein homolog ZKQ-1 (isoform 1)); dJ51J12.1.2 (human ortholog of mouse KH Domain RNA Binding protein QKI-7B (isoform 2)); dJ51J12.1.3 (human ortholog of mouse KH Domain RNA Binding protein QKI-7 (isoform 3))</p> |
| 1509 32573_at | COX6A | AL021546 | <p>match: proteins P13182 P1074 P10818 P43024 Q02221 P07471 P10817 P43023 P13182 O13085 O13082</p> | <p>cytochrome c oxidase subunit VIa polypeptide 1</p> |

6's 21

| | A | B | C | D | E |
|------|----------|------------|----------|---|---|
| 1510 | 33443_at | HSF2 | Z99129 | match: proteins P38533 Q03933 P38530 P41154 Q00613 P38529 P38531 Q63717 P38532 Q99472 | heat shock transcription factor 2 |
| 1511 | 36133_at | dJ512B11.1 | AL031058 | match: proteins Q14189 P15924 Q03001 P97395 P97396 P97394; Human DNA sequence from clone 512B11 on chromosome 6p24-25. Contains the Desmoplakin I (DPI) gene, ESTs, STSs and GSSs, complete sequence. | dJ512B11.1 (Desmoplakin I (DPI)) |
| 1512 | 37043_at | E2F-2 | AL021154 | match: proteins Q14209 Q16254 Q35261 Q00716 Q61501 Q90977 Q01094 Q27368 | E2F transcription factor 2 |
| 1513 | 41227_at | OCRL1 | AL022162 | match: proteins Q15774; match: protein Q01968 P32019; Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence. | dJ454M7.1.2 (Lowe Oculocerebrorenal Syndrome protein OCRL-1) (isoform 2); dJ454M7.1.1 (Lowe Oculocerebrorenal Syndrome protein OCRL-1) (isoform 1) |
| 1514 | 38990_at | dJ341E18.1 | AL031178 | match: proteins Q62726 P20793 Q04859 Q39423 P43294 Q49669 | dJ341E18.1 (Serine/Threonine Protein Kinase (presumptive isolog of Rat protein Q62726)) |

Fig 21

| A | B | C | D | E |
|-----------------|-------------|----------|---|--|
| 1515 34782_at | JUMONJI | AL021938 | match: proteins Q92833 Q62315; protein Q92833 has a different stop codon 19 aa further downstream because it jumps frame twice, circumventing the stopcodon in this entry. This could be due to a sequence error in the cDNA sequence; Homo sapiens DNA sequence from PAC 232K4 on chromosome 6p22.3. Contains the JUMONJI gene for a hypothetical 141.7 kD protein. Contains ESTs, STSs, a CA repeat polymorphism and genomic marker D6S260', complete sequence. | dJ232K4.1 (hypothetical 141.7 kD protein JUMONJI) |
| 1516 37350_at | dJ889N15.1 | AL031177 | match: proteins Q99795 Q91665 Q91664 O09052 P78310 P97792 Q91667 O60939 P54900 Q62861 Q61148 O00426 P06907 P25189 Q92677 P20938 P27573 P10522 P37301 match: patented sequence 180040 supported by GENSCAN and FGENES | dJ889N15.1 (novel protein similar to X. laevis Cortical Thymocyte Marker CTX) |
| 1517 39738_at | APOL2 | Z82215 | match: proteins: Sw:O14731 | apolipoprotein L |
| 1518 31824_at | ME1 | AL049699 | match: proteins: Sw:P06801 Sw:P28227 Sw:Q29558 Sw:P13697 Sw:P40927 Sw:Q16798 Tr:Q16797 Sw:P48163 | dJ747H23.1 (malic enzyme 1, soluble (NADP-dependent malic enzyme, malate oxidoreductase, EC 1.1.1.40)) |
| 1519 32766_at | OTK27 SSFA1 | Z83840 | match: proteins: Sw:P12956 | non-histone chromosome protein 2 (S. cerevisiae)-like 1 |
| 1520 39756_g_at | XBP1 | Z93930 | match: proteins: Sw:P17861 Tr:O35426; Human DNA sequence from clone CTA-292E10 on chromosome 22q11-12 Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island, complete sequence. | bK292E10.1 (X-box binding protein 1 (TREB5)) |

Fig 21

| | A | B | C | D | E |
|------|----------|------------|----------|---|---|
| 1521 | 39755_at | XBP1 | Z93930 | match: proteins: Sw:P17861 Tr:O35426; Human DNA sequence from clone CTA- 292E10 on chromosome 22q11-12 Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island, complete sequence. | bK292E10.1 (X-box binding protein 1 (TREB5)) |
| 1522 | 40771_at | MSN | Z98946 | match: proteins: Sw:P26038 Tr:O35763 Sw:P26041 Sw:P26042 Sw:P26044 Sw:P35241 Sw:P26043 Sw:P15311 Sw:P31976 Sw:P26040 Tr:Q26520 Tr:Q24788 Tr:Q24796 Tr:Q94815; Human DNA sequence from clone 376D21 on chromosome Xq11.1-12 Contains the MSN gene for Moesin (Membrane- organizing Extension Spike protein), ESTs, STSs, GSSs, genomic marker DXS8029 and a putative CpG island, complete sequence. | dJ376D21.1 (Moesin (Membrane-organizing Extension Spike protein)) |
| 1523 | 31722_at | RPL3 | AL022326 | match: proteins: Sw:P39023 Sw:O16797 Sw:P21531 Sw:P39872 Sw:P27659 Sw:Q92901 Sw:P49149 Sw:P22738 Sw:P35684 Sw:P17094 Wp:CE05598 | ribosomal protein L3 |
| 1524 | 33136_at | UBE21 | AL031714 | match: proteins: Sw:P50550 Sw:O09181 Tr:O62622 Sw:P40984 Sw:P50623 Tr:Q42551 Tr:O24240 Tr:Q42973 Sw:P52478 Sw:Q02159 Sw:P15732 Sw:O00102 Tr:O76542 Sw:P27949 Sw:P49427 Tr:O17424 Sw:P25867 Sw:P52490 | C358B7.1 (ubiquitin-conjugating enzyme E2) (homologous to yeast UBC9)) |
| 1525 | 36607_at | bK250D10.3 | Z99716 | match: proteins: Sw:Q12772 Sw:Q60429 Sw:P36956 Sw:Q60416 Tr:O15352 | sepin 3 |
| 1526 | 38399_at | SNRPB2 | AL034428 | match: proteins: Sw:Q28038 Sw:Q16674 Tr:P97591 Sw:Q61865 | small nuclear ribonucleoprotein polypeptide B" |

Fig 21

| A | B | C | D | E |
|---------------|------------------------|----------------------|--|--|
| 1527 36711_at | | | match: proteins: Tr:O54791 Sw:Q90595 Sw:Q61827 Sw:Q90596 Tr:O54790 Tr:O15525 Sw:Q90889 Tr:O73679 Tr:O75444 Sw:P54844 Sw:P54843 Sw:Q00056 Sw:Q10060 Sw:Q15427 | chromosome 22 open reading frame 5 |
| 1528 39561_at | HS5O6A DKFZP5 DNAL4 | AL021977 AL008583 | match: proteins: Tr:O54793 Tr:O44229 match: proteins: Tr:O75354 Tr:O75356 Tr:Q9QYC8 Tr:Q9WUZ9 Tr:O70214 Tr:Q9QYC9 | chromobox homolog 6 |
| 1529 39876_at | dJ738P15.1 | AL035252 | match: proteins: Tr:O94136 Sw:Q99798 Sw:P49609 Sw:P20004 Sw:P16276 Tr:O75809 Tr:O74699 Wp:CE00516 Sw:P19414 Tr:O75944 Sw:O13966 | dJ738P15.2 (CD39-like 2 (a nucleoside phosphatase)) |
| 1530 37189_at | ACO2 | AL023553 | match: proteins: Tr:P70386 Sw:Q02527 Sw:Q10470 Sw:Q09327 | dJ347H13.1 (aconitase 2, mitochondrial (Aconitate Hydratase, EC 4.2.1.3, Citrate Hydrolase)) |
| 1531 41235_at | TAXREB67 TXRE | AL022312 | match: proteins: Tr:Q00425 Sw:Q13671 Tr:O15010 Tr:P97680 | activating transcription factor 4 |
| 1532 36550_at | dJ117516.1 | AL049538 | match: proteins: Tr:Q14621 Tr:Q64012 Sw:P07910 Sw:P19600 Tr:O60812 Sw:Q14011 Sw:P26686 | dJ117516.1 (Ras inhibitor JC265 (Ras association (RalGDS/AF-6) domain containing protein)) |
| 1533 39368_at | P542 | AL031668 | match: proteins: Tr:Q9Y3M0 Tr:Q9WU14 Sw:P39540 Tr:Q9Y396 | RNA-binding protein (autoantigenic) long isoform |
| 1534 33821_at | dJ483K16.1 | AL034374 | maternal G10 transcript | dJ483K16.1.1 (novel protein (isoform 1)) |
| 1535 39029_at | G10 | U11861 | MAX binding protein | maternal G10 transcript |
| 1536 35145_at | MNT | X96401 | MAX interacting protein 1 | ROX protein |
| 1537 39072_at | MXI1 | L07648 | MAX interacting protein 1 | MAX interacting protein 1, isoform a, MAX interacting protein 1, isoform b |
| 1538 654_at | MXI1 | L07648 | MAX interacting protein 1 | MAX interacting protein 1, isoform a, MAX interacting protein 1, isoform b |
| 1539 35312_at | MCM2 | D21063 | MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisiae) | |
| 1540 40469_at | MCM3AP | AB011144 | MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) associated protein | KIAA0572 protein |

Fig 21

| | A | B | C | D | E |
|------|------------|---------|----------|--|---|
| 1541 | 40117_at | MCM6 | D84557 | MCM6 minichromosome maintenance deficient 6 (MIS5 homolog, <i>S. pombe</i>) (<i>S. cerevisiae</i>) | HsMcm6 |
| 1542 | 41388_at | MEIS2 | AF017418 | Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) | homeobox protein MEIS2 |
| 1543 | 37486_f_at | MEIS3 | U68385 | Meis1, myeloid ecotropic viral integration site 1 homolog 3 (mouse) | Meis1-related protein 2 |
| 1544 | 35340_at | MEL | AI819948 | mel transforming oncogene (derived from cell line NK14)- RAB8 homolog | |
| 1545 | 36500_at | MAGEA2A | AF027974 | melanoma antigen, family A, 2, copy a; similar to GenBank Accession Number L18920 | melanoma antigen family A2a |
| 1546 | 41139_at | MAGED1 | W26633 | melanoma antigen, family D, 1 | |
| 1547 | 39327_at | D2S448 | D86983 | Melanoma associated gene | |
| 1548 | 38441_s_at | MCP | X59408 | membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen) | membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen) |
| 1549 | 39471_at | M11S1 | Z48042 | membrane component, chromosome 11, surface marker 1 | GPI-anchored protein p137 |
| 1550 | 33444_at | M17S2 | D30756 | membrane component, chromosome 17, surface marker 2 (ovarian carcinoma antigen CA125) | membrane component, chromosome 17, surface marker 2 |
| 1551 | 1389_at | MME | J03779 | membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) | membrane metallo-endopeptidase |
| 1552 | 40399_r_at | MEOX2 | AI743406 | mesenchyme homeo box 2 (growth arrest-specific homeo box) | |
| 1553 | 37697_s_at | por | L08666 | Met at bp 328 also used as initiation codon in vitro; Met at bp 248 also used as initiation codon in vitro; Homo sapiens porin (por) mRNA, complete cds and truncated cds. | porin |
| 1554 | 40244_s_at | MPPE1 | AI743654 | metallo phosphoesterase | |

Fig 21

| A | B | C | D | E |
|-----------------|--------|----------|--|---|
| 1555 31975_at | | X55503 | metallothionein (MT)-like gene; H.sapiens pseudogene for metallothionein and AG/CT repetitive element. | metallothionein |
| 1556 39081_at | MT2A | AI547258 | metallothionein 2A | |
| 1557 38945_at | MTF1 | X78710 | metal-regulatory transcription factor 1 | metal-regulatory transcription factor |
| 1558 1643_g_at | MTA1 | U35113 | metastasis associated 1 | metastasis associated protein |
| 1559 35642_at | MTX2 | AF053551 | metaxin 2 | metaxin 2 |
| 1560 39342_at | MARS | X94754 | methionine-tRNA synthetase | yeast methionyl-tRNA synthetase homolog |
| 1561 37619_at | METAP1 | D42084 | methionyl aminopeptidase 1 | |
| 1562 41828_at | MBD1 | Y10746 | methyl-CpG binding domain protein 1 | methyl-CpG binding protein |
| 1563 33905_at | MBD2 | AF072242 | methyl-CpG binding domain protein 2 | methyl-CpG binding protein MBD2 |
| 1564 34386_at | MBD4 | AF072250 | methyl-CpG binding domain protein 4 | methyl-CpG binding protein MBD4 |
| 1565 40074_at | MTHFD2 | X16396 | methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase | methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase, precursor |
| 1566 674_g_at | MTHFD1 | J04031 | methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase | methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase |
| 1567 40105_at | MUT | M65131 | methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase | methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase |
| 1568 35937_at | MICB | U65416 | MHC class I chain-related gene B; cDNA sequence deposited under GenBank Accession Number X91625; Human MHC class I molecule (MICB) gene, complete cds. | MHC class I molecule |
| 1569 36535_at | MFAP1 | U04209 | microfibrillar-associated protein 1 | associated microfibrillar protein |
| 1570 38228_g_at | MITF | AB006909 | microphthalmia-associated transcription factor | A-type microphthalmia associated transcription factor |
| 1571 820_at | MGST2 | U77604 | microsomal glutathione S-transferase 2 | microsomal glutathione S-transferase 2 |
| 1572 38704_at | MACF1 | AB007934 | microtubule-actin crosslinking factor 1 | KIAA0465 protein |
| 1573 35917_at | MAP1A | W26631 | microtubule-associated protein 1A | |
| 1574 33850_at | MAP4 | W28892 | microtubule-associated protein 4 | |

613 21

| | A | B | C | D | E |
|------|------------|-------------|----------|--|---|
| 1575 | 33456_at | MAPRE1 | U24166 | microtubule-associated protein, RP/EB family, member 1 | EB1 |
| 1576 | 39370_at | MAP1A/1BLC3 | W28807 | microtubule-associated proteins 1A/1B light chain 3 | |
| 1577 | 34296_at | MID1 | AF041210 | midline 1 (Opitz/BBB syndrome) | midline 1 fetal kidney isoform 3 |
| 1578 | 34403_at | MFGE8 | U58516 | milk fat globule-EGF factor 8 protein | BA46 |
| 1579 | 40027_at | ATPW | W52999 | mitochondrial ATP synthase regulatory component factor B | |
| 1580 | 37174_at | MRPL19 | D14660 | mitochondrial ribosomal protein L19 | mitochondrial ribosomal protein L19 |
| 1581 | 37726_at | MRPL3 | X06323 | mitochondrial ribosomal protein L3 | mitochondrial ribosomal protein L3 |
| 1582 | 39717_g_at | MRPL33 | AI597616 | mitochondrial ribosomal protein L33 | |
| 1583 | 32221_at | MRPS18B | AL050361 | mitochondrial ribosomal protein S18B | mitochondrial ribosomal protein S18B |
| 1584 | 38899_s_at | MFN1 | U95822 | mitofusin 1 | putative transmembrane GTPase |
| 1585 | 34369_at | MFN2 | D86987 | mitofusin 2 | KIAA0214 protein |
| 1586 | 36577_at | MIG2 | Z24725 | mitogen inducible 2 | mitogen inducible gene mig-2 |
| 1587 | 37733_at | MAPK14 | L35263 | mitogen-activated protein kinase 14 | CSAids binding protein |
| 1588 | 36926_at | MAPK6 | X80692 | mitogen-activated protein kinase 6 | p97mapk |
| 1589 | 38431_at | MAPK9 | U09759 | mitogen-activated protein kinase 9 | protein kinase |
| 1590 | 1238_at | MAPK9 | U09759 | mitogen-activated protein kinase 9 | protein kinase |
| 1591 | 1130_at | MAP2K1 | L11284 | mitogen-activated protein kinase kinase 1 | mitogen-activated protein kinase kinase 1 |
| 1592 | 1327_s_at | MAP3K5 | U67156 | mitogen-activated protein kinase kinase kinase 5 | mitogen-activated kinase kinase kinase 5 |
| 1593 | 36905_at | MAP3K7 | AB009356 | mitogen-activated protein kinase kinase kinase 7 | TGF-beta activated kinase 1a |
| 1594 | 38980_at | MAP3K7IP2 | AB018276 | mitogen-activated protein kinase kinase kinase 7 interacting protein 2 | KIAA0733 protein |
| 1595 | 35694_at | MAP4K4 | AB014587 | mitogen-activated protein kinase kinase kinase 4 | KIAA0687 protein |
| 1596 | 36179_at | MAPKAPK2 | U12779 | mitogen-activated protein kinase-activated protein kinase 2 | MAP kinase activated protein kinase 2 |
| 1597 | 1637_at | MAPKAPK3 | U09578 | mitogen-activated protein kinase-activated protein kinase 3 | MAPKAP kinase |
| 1598 | 41220_at | MSF | AB023208 | MLL septin-like fusion | KIAA0991 protein |
| 1599 | 38437_at | MLN51 | X80199 | MLN51 protein | MLN51 protein |

G's 21

| | A | B | C | D | E |
|------|------------|-----------|----------|--|--|
| 1600 | 35273_at | MMS19L | AF007151 | MMS19-like (MET18 homolog, <i>S. cerevisiae</i>) | MMS19 (MET18 <i>S. cerevisiae</i>)-like |
| 1601 | 34767_at | MAP-1 | A1670788 | modulator of apoptosis 1 | |
| 1602 | 41771_g_at | MAOA | AA420624 | monoamine oxidase A | monoamine oxidase A |
| 1603 | 41772_at | MAOA | M68840 | monoamine oxidase A | |
| 1604 | 41770_at | MAOA | AA420624 | monoamine oxidase A | monoamine oxidase B |
| 1605 | 37628_at | MAOB | M69177 | monoamine oxidase B | monocyte to macrophage differentiation-associated, precursor |
| 1606 | 37565_at | MMD | X85750 | associated | MORF-related gene X |
| 1607 | 40861_at | MRGX | D14812 | MORF-related gene X | |
| 1608 | 33797_at | MPHOSPH10 | X98494 | M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein) | M phase phosphoprotein 10 |
| 1609 | 34306_at | MBNL | AB007888 | muscleblind-like (Drosophila) | muscleblind (Drosophila)-like |
| 1610 | 35992_at | MSC | AF087036 | musculin (activated B-cell factor-1) | musculin |
| 1611 | 31884_at | MLH3 | L40399 | mutL homolog 3 (E. coli) | mutL homolog 3 |
| 1612 | 860_at | MSH2 | U03911 | mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli) | mutS homolog 2 |
| 1613 | 2003_s_at | MSH6 | U28946 | mutS homolog 6 (E. coli) | G/T mismatch binding protein |
| 1614 | 33769_at | MPZL1 | AF087020 | myelin protein zero-like 1 | protein zero related protein |
| 1615 | 33146_at | MCL1 | L08246 | myeloid cell leukemia sequence 1 (BCL2-related) | myeloid cell leukemia sequence 1 (BCL2-related) |
| 1616 | 277_at | MCL1 | L08246 | myeloid cell leukemia sequence 1 (BCL2-related) | myeloid cell leukemia sequence 1 (BCL2-related) |
| 1617 | 39037_at | MLLT2 | L13773 | myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2 | myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2 |
| 1618 | 41637_at | MYLE | AF108145 | translocated to, 2 | DEXI |
| 1619 | 41439_at | MYO1B | AJ001381 | MYLE protein | myh-1c |
| 1620 | 35729_at | MYO1D | AB018270 | myosin IB | KIAA0727 protein |
| 1621 | 37631_at | MYO1E | U14391 | myosin ID | myosin-1C |
| 1622 | 38251_at | MLC1SA | A1127424 | myosin IE | |
| 1623 | 41187_at | MLC-B | U26162 | myosin light chain 1 slow a | myosin regulatory light chain |
| 1624 | 35362_at | MYO10 | AB018342 | myosin regulatory light chain | KIAA0799 protein |
| 1625 | 33447_at | MLCB | X54304 | myosin X | myosin, light polypeptide, regulatory, non-sarcomeric (20kD) |
| 1626 | 35739_at | MTMR3 | AB002369 | myosin, light polypeptide, regulatory, non-sarcomeric (20kD) | myotubularin related protein 3 |

Fig. 21

| | A | B | C | D | E |
|------|------------|--------|----------|---|---|
| 1627 | 39707_at | MTMR4 | AB014547 | myotubularin related protein 4 | KIAA0647 protein |
| 1628 | 38035_at | MTMR6 | AF072928 | myotubularin related protein 6 | myotubularin related protein 6 |
| 1629 | 39607_at | MTMR8 | AL080178 | myotubularin related protein 8 | hypothetical protein |
| 1630 | 36692_at | MTMR8 | AF052099 | myotubularin related protein 8 | |
| 1631 | 32434_at | MARCKS | D10522 | myristoylated alanine-rich protein kinase C substrate | 80K-L protein |
| 1632 | 39267_at | AGM1 | AF102265 | N-acetylglucosamine-phosphate mutase | N-acetylglucosamine-phosphate mutase |
| 1633 | 36938_at | ASAH | U70063 | N-acylsphingosine amidohydrolase (acid ceramidase) | acid ceramidase |
| 1634 | 461_at | ASAH | U70063 | N-acylsphingosine amidohydrolase (acid ceramidase) | acid ceramidase |
| 1635 | 36169_at | NDUFA1 | N47307 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 (7.5kD, MWFE) | |
| 1636 | 40546_s_at | NDUFA2 | AF047185 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8) | NADH-ubiquinone oxidoreductase subunit C1B8 |
| 1637 | 38462_at | NDUFA5 | U64028 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (13kD, B13) | NADPH:ubiquinone oxidoreductase subunit B13 |
| 1638 | 32752_at | NDUFA7 | W72440 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (14.5kD, B14.5a) | |
| 1639 | 38605_at | NDUFB1 | AI345944 | NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1 (7kD, MNLL) | |
| 1640 | 38981_at | NDUFB3 | AA203354 | NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3 (12kD, B12) | |
| 1641 | 32232_at | NDUFB5 | AF047181 | NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (16kD, SGDH) | NADH-ubiquinone oxidoreductase subunit C1SGDH |
| 1642 | 32774_at | NDUFB8 | AI541050 | NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1) | |
| 1643 | 38485_at | NDUFC1 | AA760866 | NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1 (6kD, KFYI) | |
| 1644 | 38395_at | NDUFS1 | X61100 | NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) | 75 kDa subunit NADH dehydrogenase precursor |
| 1645 | 38695_at | NDUFS4 | AA203303 | NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase) | |

6-15 21

| A | B | C | D | E |
|-----------------|---------------|----------|---|---|
| 1646 38060_at | NDUFS5 | AI541336 | NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase) | |
| 1647 34893_at | NDUFV2 | AI557064 | NADH dehydrogenase (ubiquinone) flavoprotein 2 (24kD) | |
| 1648 34519_at | NPR3 | M59305 | natriuretic peptide receptor C/guanylate cyclase C (atrialnatriuretic peptide receptor C) | atrial natriuretic peptide clearance receptor |
| 1649 34234_l_at | NKTR | AI688640 | natural killer-tumor recognition sequence | |
| 1650 41795_at | NCK1 | X17576 | NCK adaptor protein 1 | NCK adaptor protein 1 |
| 1651 33357_at | NCKAP1 | AB011159 | NCK-associated protein 1 | KIAA0587 protein |
| 1652 36073_at | NDN | U35139 | necdin homolog (mouse) | NECDIN related protein |
| 1653 34202_at | DKFZP566B0846 | AL050071 | nectin 3 | hypothetical protein |
| 1654 34264_at | NESCA | AB026894 | nesca protein | NESCA |
| 1655 38719_at | NSF | U03985 | N-ethylmaleimide-sensitive factor | N-ethylmaleimide-sensitive factor |
| 1656 39356_at | NEDD4L | AB007899 | neural precursor cell expressed, developmentally down-regulated 4-like | ubiquitin-protein ligase NEDD4-like |
| 1657 40281_at | NEDD5 | D63878 | neural precursor cell expressed, developmentally down-regulated 5 | neural precursor cell expressed, developmentally down-regulated 5 |
| 1658 1695_at | NEDD8 | D23662 | neural precursor cell expressed, developmentally down-regulated 8 | ubiquitin-like protein |
| 1659 37005_at | NBL1 | D28124 | neuroblastoma, suppression of tumorigenicity 1 | neuroblastoma, suppression of tumorigenicity 1 |
| 1660 31896_at | NAG | AL050281 | neuroblastoma-amplified protein | hypothetical protein |
| 1661 37286_at | NRCAM | AB002341 | neuronal cell adhesion molecule | neuronal cell adhesion molecule |
| 1662 37673_at | NSMAF | X96586 | neural sphingomyelinase (N-SMase) activation associated factor | FAN protein |
| 1663 38692_at | NAB1 | AF045451 | NGFI-A binding protein 1 (EGR1 binding protein 1) | transcriptional regulatory protein p54 |
| 1664 34835_at | NCSTN | D87442 | nicastatin | |
| 1665 37032_at | NNMT | U08021 | nicotinamide N-methyltransferase | nicotinamide N-methyltransferase |
| 1666 41722_at | NNT | U40490 | nicotinamide nucleotide transhydrogenase | nicotinamide nucleotide transhydrogenase |
| 1667 35366_at | NID | M30269 | nidogen (enactin) | nidogen |
| 1668 753_at | NID2 | D86425 | nidogen 2 | osteonidogen |

Fig 21

| | A | B | C | D | E |
|------|------------|----------|----------|--|-------------------------------------|
| 1669 | 37047_at | NPC1 | AF002020 | Niemann-Pick disease, type C1 | Niemann-Pick C disease protein |
| 1670 | 980_at | NPC1 | AF002020 | Niemann-Pick disease, type C1 | Niemann-Pick C disease protein |
| 1671 | 39345_at | NPC2 | AI525834 | Niemann-Pick disease, type C2 | |
| 1672 | 35153_at | NBS1 | AF058696 | Nijmegen breakage syndrome 1 (nibrin) | cell cycle regulatory protein p95 |
| 1673 | 36047_at | NEK1 | AL050385 | NIMA (never in mitosis gene a)-related kinase 1 | |
| 1674 | 35843_at | Nek8 | L40402 | NIMA-related kinase Nek8 | |
| 1675 | 40866_at | NIPSNAP1 | AJ001258 | nipsnap homolog 1 (C. elegans) | NIPSNAP1 protein |
| 1676 | 33916_at | NISCH | AB023192 | nischarin | KIAA0975 protein |
| 1677 | 39165_at | NIFU | U47101 | nitrogen fixation cluster-like | NifU-like protein |
| 1678 | 36472_at | NMI | U32849 | N-myc (and STAT) interactor | Nmi |
| 1679 | 36933_at | NDRG1 | D87953 | N-myc downstream regulated gene 1 | RTP |
| 1680 | 41656_at | NMT2 | AF043325 | N-myristoyltransferase 2 | N-myristoyltransferase 2 |
| 1681 | 39040_at | NCUBE1 | W28360 | non-canonical ubiquitin conjugating enzyme 1 | |
| 1682 | 39039_s_at | NCUBE1 | AI557497 | non-canonical ubiquitin conjugating enzyme 1 | |
| 1683 | 1521_at | NME1 | X17620 | non-metastatic cells 1, protein (NM23A) expressed in | Nm23 protein |
| 1684 | 33415_at | NME2 | X58965 | non-metastatic cells 2, protein (NM23B) expressed in | NM23-H2 protein |
| 1685 | 1980_s_at | NME2 | X58965 | non-metastatic cells 2, protein (NM23B) expressed in | NM23-H2 protein |
| 1686 | 38527_at | NONO | U02493 | non-POU domain containing, octamer-binding | 54 kDa protein |
| 1687 | 38750_at | NOTCH3 | U97669 | Notch homolog 3 (Drosophila) | Notch3 |
| 1688 | 34781_at | WS-3 | D84145 | novel RGD-containing protein | novel RGD-containing protein |
| 1689 | 40122_at | NSAP1 | AF037448 | NS1-associated protein 1 | Gry-rbp |
| 1690 | 33752_at | NS1-BP | AB020657 | NS1-binding protein | KIAA0850 protein |
| 1691 | 35626_at | SGSH | U30894 | N-sulfoglucosamine sulfohydrolase (sulfamidase) | N-sulphoglucosamine sulphonydrolase |
| 1692 | 37352_at | SP100 | M60618 | nuclear antigen Sp100 | nuclear autoantigen |
| 1693 | 37353_g_at | SP100 | M60618 | nuclear antigen Sp100 | nuclear autoantigen |
| 1694 | 40901_at | GS2NA | U17989 | nuclear autoantigen | GS2NA |
| 1695 | 32789_at | NCBP2 | AA149428 | nuclear cap binding protein subunit 2, 20kD | |

Fig 21

| A | B | C | D | E |
|---------------|-------------------|----------|---|---|
| 1696 35836_at | NUDC | AB019408 | nuclear distribution gene C homolog (A. nidulans) | nuclear distribution gene C (A. nidulans) homolog |
| 1697 39782_at | C1D | X95592 | nuclear DNA-binding protein | C1D protein |
| 1698 40063_at | NDP52 | U22897 | nuclear domain 10 protein | NDP52 |
| 1699 853_at | NFE2L2 | S74017 | nuclear factor (erythroid-derived 2)-like 2 | Nrf2 |
| 1700 38354_at | CEBPB; LAP; C/EBP | X52560 | nuclear factor NF-IL6 (AA 1-345); Human gene for nuclear factor NF-IL6. | C/EBP |
| 1701 40822_at | NFATC3 | L41067 | nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 | nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 |
| 1702 38438_at | NFKB1 | M58603 | nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) | nuclear factor kappa-B DNA binding subunit |
| 1703 1377_at | NFKB1 | M58603 | nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) | nuclear factor kappa-B DNA binding subunit |
| 1704 1461_at | NFKBIA | M69043 | nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha | nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha |
| 1705 37544_at | NFIL3 | X64318 | nuclear factor, interleukin 3 regulated | nuclear factor, interleukin 3 regulated |
| 1706 38648_at | CIZ | U80760 | nuclear matrix transcription factor 4 | CAGH1 alternate open reading frame |
| 1707 40816_at | PWP1 | L07758 | nuclear phosphoprotein similar to S. cerevisiae PWP1 | IEF SSP 9502 |
| 1708 34312_at | NCOA2 | A1040324 | nuclear receptor coactivator 2 | Amplified in Breast Cancer |
| 1709 33381_at | NCOA3 | AFO12108 | nuclear receptor coactivator 3 | Ret fused gene |
| 1710 39174_at | NCOA4 | X77548 | nuclear receptor coactivator 4 | nuclear factor RIP140 |
| 1711 40088_at | NRIP1 | X84373 | nuclear receptor interacting protein 1 | |
| 1712 39397_at | NR2F2 | M64497 | nuclear receptor subfamily 2, group F, member 2 | apolipoprotein A1 regulatory protein-1 |
| 1713 36690_at | NR3C1 | M10901 | nuclear receptor subfamily 3, group C, member 1 | nuclear receptor subfamily 3, group C, member 1 |
| 1714 35302_at | NXF1 | AJ132712 | nuclear RNA export factor 1 | nuclear RNA export factor 1 |
| 1715 37928_at | NFYB | AA621555 | nuclear transcription factor Y, beta | |
| 1716 34667_at | NFX1 | U15306 | nuclear transcription factor, X-box binding 1 | NFX1 |
| 1717 33413_at | PRL-1 | AF051160 | nuclear; Homo sapiens tyrosine phosphatase (PRL-1) gene, complete cds. | tyrosine phosphatase |

fig-21

| | A | B | C | D | E |
|------|------------|------------|----------|--|--|
| 1718 | 32340_s_at | NSEP1 | M85234 | nuclease sensitive element binding protein 1 | nuclease sensitive element binding protein-1 |
| 1719 | 35643_at | NUCB2 | X76732 | nucleobindin 2 | NEFA protein |
| 1720 | 36597_at | NOLC1 | D21262 | nucleolar and coiled-body phosphoprotein 1 | ORF |
| 1721 | 37520_at | HSA6591 | AJ006591 | nucleolar cysteine-rich protein | cysteine-rich protein |
| 1722 | 36930_at | HUMAUANTIG | L05425 | nucleolar GTPase | nucleolar GTPase |
| 1723 | 39390_at | NUP133 | AF052123 | nucleoporin 133kD | |
| 1724 | 32850_at | NUP153 | Z25535 | nucleoporin 153kD | nuclear pore complex protein hnup153 |
| 1725 | 39024_at | NUP98 | AF042357 | nucleoporin 98kD | |
| 1726 | 571_at | NAP1L1 | M86667 | nucleosome assembly protein 1-like 1 | nucleosome assembly protein 1-like 1 |
| 1727 | 743_at | NAP1L3 | D50370 | nucleosome assembly protein 1-like 3 | nucleosome assembly protein |
| 1728 | 32575_at | NAP1L4 | U77456 | nucleosome assembly protein 1-like 4 | nucleosome assembly protein 2 |
| 1729 | 36127_g_at | NBP | U18919 | nucleotide binding protein | nucleotide binding protein |
| 1730 | 41584_at | NUDT3 | AF062529 | nudix (nucleoside diphosphate linked moiety X)-type motif 3 | diphosphoinositol polyphosphate phosphohydrolase |
| 1731 | 37693_at | NUMB | L40393 | numb homolog (Drosophila) | numb homolog |
| 1732 | 35916_s_at | INHBC | AA877215 | ob15e02.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1323770 3' similar to SW:ROA3_HUMAN P51991 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A3.; mRNA sequence. | |
| 1733 | 34169_s_at | OCRL | U57627 | oculocerebrorenal syndrome of Lowe | ocr11 |
| 1734 | 31921_at | OLF3 | U56421 | olfactory receptor; Human olfactory receptor (OLF3) gene, complete cds. O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase) | HsOLF3 |
| 1735 | 39507_at | OGT | AL050366 | opioid growth factor receptor | hypothetical protein |
| 1736 | 40332_at | OGFR | AF109134 | optic atrophy 1 (autosomal dominant) | Jul-60 |
| 1737 | 39745_at | OPA1 | AB011139 | optineurin | KIAA0567 protein |
| 1738 | 41744_at | OPTN | AF070533 | OR11-3; olfactory receptor; Homo sapiens OR7E12P pseudogene, complete sequence. | optineurin |
| 1739 | 34539_at | OR7E12P | AF065854 | | |

Fig-21

| | A | B | C | D | E |
|------|----------------|-------------|----------|--|---|
| 1740 | AFFX-BioC-3_at | bioA | J04423 | ORF 1 | 7,8-diamino-pelargonic acid aminotransferase |
| 1741 | AFFX-BioB-M_at | bioA | J04423 | ORF 1 | 7,8-diamino-pelargonic acid aminotransferase |
| 1742 | AFFX-BioDn-5_a | bioA | J04423 | ORF 1 | 7,8-diamino-pelargonic acid aminotransferase |
| 1743 | AFFX-BioDn-3_a | bioA | J04423 | ORF 1 | 7,8-diamino-pelargonic acid aminotransferase |
| 1744 | AFFX-BioC-5_at | bioA | J04423 | ORF 1 | 7,8-diamino-pelargonic acid aminotransferase |
| 1745 | 32412_at | RPS14 | M13934 | ORF; putative; Human ribosomal protein S14 gene, complete cds. | unknown protein; ribosomal protein S14 |
| 1746 | 1315_at | OAZ1 | D78361 | ORF1; ORF 2; no start codon; Human mRNA for ornithine decarboxylase antizyme, ORF 1 and ORF 2. | ornithine decarboxylase antizyme 1 |
| 1747 | 32800_at | RXRA; NR2B1 | U66306 | ORF-2; ORF-3; Human retinoid X receptor alpha mRNA, 3' UTR, partial sequence. | retinoid X receptor, alpha |
| 1748 | 38155_at | ORC5L | U92538 | origin recognition complex, subunit 5-like (yeast) | origin recognition complex subunit 5 homolog |
| 1749 | 36636_at | OAT | M12267 | ornithine aminotransferase (gyrate atrophy) | ornithine aminotransferase |
| 1750 | 1959_at | OAZIN | D88674 | ornithine decarboxylase antizyme inhibitor | antizyme inhibitor |
| 1751 | 33367_s_at | OAZIN | D88674 | ornithine decarboxylase antizyme inhibitor | antizyme inhibitor |
| 1752 | 1081_at | ODC1 | M33764 | ornithine decarboxylase; Human ornithine decarboxylase gene, complete cds. | ornithine decarboxylase 1 |
| 1753 | 31700_at | GPR35 | AF027957 | orphan G protein-coupled receptor; Homo sapiens G protein-coupled receptor (GPR35) gene, complete cds. | G protein-coupled receptor |
| 1754 | 1451_s_at | OSF-2 | D13666 | osteoblast specific factor 2 (fascin 1-like) | osteoblast specific factor 2 |
| 1755 | 39774_at | OXA1L | X80695 | oxidase (cytochrome c) assembly 1-like | oxidase (cytochrome c) assembly 1-like |

Fig-21

| A | B | C | D | E |
|-----------------|----------------|----------|---|--|
| 1756 39136_at | OSR1 | AB017642 | oxidative-stress responsive 1 | oxidative-stress responsive 1 |
| 1757 41438_at | OSBPL8 | AL049923 | oxysterol binding protein-like 8 | oxysterol-binding protein-like protein 8 |
| 1758 34329_at | PAK2 | N25547 | p21 (CDKN1A)-activated kinase 2 | |
| 1759 39710_at | P311 | U30521 | P311 protein | P311 HUM |
| 1760 36136_at | PIG11 | AF010315 | p53-induced protein | Pig11 |
| 1761 40441_g_at | PAI-RBP1 | AL080119 | PAI-1 mRNA-binding protein | hypothetical protein |
| 1762 40440_at | PAI-RBP1 | AL080119 | PAI-1 mRNA-binding protein | hypothetical protein |
| 1763 32001_s_at | PACE4 | M80482 | paired basic amino acid cleaving system 4 | subtilisin-like protease |
| | | | | paired box gene 8, isoform PAX8A; paired box gene 8, isoform PAX8B; paired box gene 8, isoform PAX8C; paired box gene 8, isoform PAX8D; paired box gene 8, isoform PAX8E |
| 1764 121_at | PAX8 | X69699 | paired box gene 8 | homeobox protein |
| 1765 40127_at | PMX1 | M95929 | paired mesoderm homeo box 1 | KIAA0992 protein |
| 1766 41191_at | KIAA0992 | AB023209 | palladin | paraoxonase |
| 1767 40504_at | PON2 | AF001601 | paraoxonase 2 | hypothetical protein |
| | | | partially supported by FGENES and GENSCAN | DFS70 |
| 1768 36032_at | dJ167A19.1 | AL031427 | PC4 and SFRS1 interacting protein 2 | KIAA0824 protein |
| 1769 39243_s_at | PSIP2 | U94319 | PCF11p homolog | |
| 1770 41665_at | PCF11 | AB020631 | PDGFA associated protein 1 | carboxyl terminal LIM domain protein |
| 1771 38758_at | PDAP1 | R98910 | PDZ and LIM domain 1 (elfin) | PDZ domain containing guanine nucleotide exchange factor(GEF)1 |
| 1772 36937_s_at | PDLIM1 | U90878 | PDZ domain containing guanine nucleotide exchange factor(GEF)1 | |
| 1773 32026_s_at | PDZ-GEF1 | AB002311 | PDZ domain containing guanine nucleotide exchange factor(GEF)1 | |
| 1774 34745_at | PDZ-GEF1 | AF070570 | PDZ domain containing guanine nucleotide exchange factor(GEF)1 | |
| 1775 40856_at | SERPINF1; PEDF | U29953 | PEDF; Human pigment epithelium-derived factor gene, complete cds. | pigment epithelium-derived factor |
| 1776 1491_at | PTX3 | M31166 | pentaxin-related gene, rapidly induced by IL-1 beta | tumor necrosis factor |
| 1777 38465_at | PAM | M37721 | peptidylglycine alpha-amidating monooxygenase | peptidylglycine alpha-amidating monooxygenase |
| 1778 35823_at | PPIB | M63573 | peptidylprolyl isomerase B (cyclophilin B) | secreted cyclophilin-like protein |

fig-21

| A | B | C | D | E |
|-----------------|----------------|----------|--|---|
| 1779 37422_at | PPIC | S71018 | peptidylprolyl isomerase C (cyclophilin C) | cyclophilin C |
| 1780 37385_at | PPIG | U40763 | peptidyl-prolyl isomerase G (cyclophilin G) | CARS-Cyp |
| 1781 36829_at | PER1 | AF022991 | period homolog 1 (Drosophila) | Rigi |
| 1782 35835_at | PDL-108 | AB019409 | periodontal ligament fibroblast protein | |
| | | | peripheral benzodiazepine receptor; Human peripheral benzodiazepine receptor (hpbbs) mRNA, complete cds. | peripheral benzodiazepine receptor; peripheral benzodiazepine receptor short form |
| 1783 32806_at | BZRP; MBR; PBR | M36035 | | PMP-22(PAS-II/SR13/Gas-3) |
| 1784 36653_at | PMP22 | D11428 | peripheral myelin protein 22 | |
| 1785 41213_at | PRDX1 | X67951 | peroxiredoxin 1 | peroxiredoxin 1 |
| 1786 36631_at | PRDX3 | D49396 | peroxiredoxin 3 | Aop1_Human, MER5(Aop1_Mouse)-like protein |
| 1787 38435_at | PRDX4 | U25182 | peroxiredoxin 4 | antioxidant enzyme AOE37-2 |
| 1788 37900_at | PEX11B | AF093670 | peroxisomal biogenesis factor 11B | peroxisomal biogenesis factor |
| 1789 36864_at | PEX3 | AJ001625 | peroxisomal biogenesis factor 3 | Pex3 protein |
| 1790 36625_at | ZAP128 | L40401 | peroxisomal long-chain acyl-coA thioesterase | peroxisomal long-chain acyl-coA thioesterase |
| 1791 33265_at | PXMP3 | M86852 | peroxisomal membrane protein 3 (35kD, Zellweger syndrome) | peroxisome assembly factor-1 |
| 1792 36502_at | PFTK1 | AB020641 | PFTAIRE protein kinase 1 | KIAA0834 protein |
| 1793 37694_at | PHF3 | D87685 | PHD finger protein 3 | PHD finger protein 3 |
| 1794 39381_at | XAP135 | AF055030 | PHD zinc finger protein XAP135 | PHD zinc finger protein XAP135, isoform a; PHD zinc finger protein XAP135, isoform b |
| 1795 1434_at | PTEN | U92436 | phosphatase and tensin homolog (mutated in multiple advanced cancers 1) | MMAC1 |
| 1796 34797_at | PPAP2A | AF014402 | phosphatidic acid phosphatase type 2A | type-2 phosphatidic acid phosphatase alpha- 1 |
| 1797 33862_at | PPAP2B | AF017786 | phosphatidic acid phosphatase type 2B | phosphatidic acid phosphohydrolase homolog |
| 1798 40783_s_at | PIK4CA | L36151 | phosphatidylinositol 4-kinase, catalytic, alpha polypeptide | phosphatidylinositol 4-kinase |
| 1799 37685_at | PICALM | U45976 | phosphatidylinositol binding clathrin assembly protein | CALM |

Fig. 21

| | A | B | C | D | E |
|------|------------|---------|----------|--|--|
| 1800 | 39993_at | PIGA | D11466 | phosphatidylinositol glycan, class A (paroxysmal nocturnal hemoglobinuria) | PIG-A protein |
| 1801 | 314_at | PIGB | D42138 | phosphatidylinositol glycan, class B | PIG-B |
| 1802 | 751_at | PIGC | D85418 | phosphatidylinositol glycan, class C | phosphatidylinositol-glycan-class C (PIG-C) |
| 1803 | 776_at | PIGF | D13435 | phosphatidylinositol glycan, class F | PIG-F |
| 1804 | 40629_at | PIGH | L19783 | phosphatidylinositol glycan, class H | phosphatidylinositol glycan, class H |
| 1805 | 38297_at | PITPNM | X98654 | phosphatidylinositol transfer protein, membrane-associated | homologue of Drosophila retinal degeneration B gene |
| 1806 | 35741_at | PIP5K2B | U85245 | phosphatidylinositol-4-phosphate 5-kinase, type II, beta | phosphatidylinositol-4-phosphate 5-kinase type II beta |
| 1807 | 37320_at | PTDSS1 | D14694 | phosphatidylserine synthase 1 | phosphatidylserine synthase 1 |
| 1808 | 33705_at | PDE4B | L20971 | phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homologue, Drosophila) | phosphodiesterase |
| 1809 | 39422_at | PDE4DIP | AB007923 | phosphodiesterase 4D interacting protein (myomegalin) | KIAA0454 protein |
| 1810 | 37676_at | PDE8A | AF056490 | phosphodiesterase 8A | cAMP-specific phosphodiesterase 8A |
| 1811 | 37188_at | PCK2 | X92720 | phosphoenolpyruvate carboxykinase 2 (mitochondrial) | phosphoenolpyruvate carboxykinase (GTP) |
| 1812 | 39175_at | PFKP | D25328 | phosphofructokinase, platelet | platelet-type phosphofructokinase |
| 1813 | 32210_at | PGM1 | M83088 | phosphoglucomutase 1 | phosphoglucomutase 1 |
| 1814 | 36963_at | PGD | U30255 | phosphogluconate dehydrogenase | phosphogluconate dehydrogenase |
| 1815 | 37677_at | PGK1 | V00572 | phosphoglycerate kinase 1 | phosphoglycerate kinase 1 |
| 1816 | 41221_at | PGAM1 | J04173 | phosphoglycerate mutase 1 (brain) | phosphoglycerate mutase 2 |
| 1817 | 35665_at | PIK3C3 | Z46973 | phosphoinositide-3-kinase, class 3 | phosphatidylinositol 3-kinase |
| 1818 | 1269_at | PIK3R1 | M61906 | phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha) | |
| 1819 | 37961_at | PIK3R3 | U90907 | phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma) | |
| 1820 | 32775_r_at | PLSCR1 | AB006746 | phospholipid scramblase 1 | phospholipid scramblase 1 |
| 1821 | 32260_at | PEA15 | X86809 | phosphoprotein enriched in astrocytes 15 | |
| 1822 | 36489_at | PRPS1 | D00860 | phosphoribosyl pyrophosphate synthetase 1 | phosphoribosyl pyrophosphate synthetase subunit I |

Fig. 21

| A | B | C | D | E |
|-----------------|----------|----------|--|---|
| 1823 37338_at | PRPSAP1 | D61391 | phosphoribosyl pyrophosphate synthetase-associated protein 1 | phosphoribosyl pyrophosphate synthetase-associated protein 39 |
| 1824 39056_at | | | phosphoribosylaminoimidazole carboxylase, | phosphoribosylaminoimidazole carboxylase, |
| 1825 37392_at | PAICS | X53793 | phosphoribosylaminoimidazole succinocarboxamide synthetase | phosphoribosylaminoimidazole succinocarboxamide synthetase |
| 1826 36667_at | PHKB | X84908 | phosphorylase kinase, beta | phosphorylase kinase |
| 1827 32724_at | PYGB | U47025 | phosphorylase, glycogen; brain | glycogen phosphorylase B |
| 1828 33543_s_at | PHYH | AF023462 | phytanoyl-CoA hydroxylase (Refsum disease) | peroxisomal phytanoyl-CoA alpha-hydroxylase |
| 1829 39003_at | PNN | U77718 | pinin, desmosome associated protein | pinin |
| 1830 34793_s_at | PTTG1IP | Z50022 | pituitary tumor-transforming 1 interacting protein | putative surface glycoprotein |
| 1831 32569_at | PLS3 | M22299 | plasmin 3 (T isoform) | T-plasmin polypeptide |
| 1832 1731_at | PAFAH1B1 | L13385 | platelet-activating factor acetylhydrolase, isoform 1b, alpha subunit (45kD) | Miller-Dieker lissencephaly protein |
| 1833 38666_at | PDGFRA | M21574 | platelet-derived growth factor receptor, alpha polypeptide | platelet-derived growth factor receptor A chain |
| 1834 38741_at | PSCD1 | M85169 | pleckstrin homology, Sec7 and coiled/coiled domains 1 (cytohesin 1) | cytohesin 1, isoform 1; cytohesin 1, isoform 2 |
| 1835 36943_r_at | PSCD2 | U70728 | pleckstrin homology, Sec7 and coiled/coiled domains 2 (cytohesin-2) | cytohesin-2 |
| 1836 34780_at | PLAGL1 | U81992 | pleiomorphic adenoma gene-like 1 | C2H2 zinc finger protein PLAGL1 |
| 1837 32193_at | PLXNB2 | AB002313 | plexin B2 | plexin B2 |
| 1838 38270_at | PLXNC1 | AF030339 | plexin C1 | VESPR |
| 1839 31951_s_at | PARG | AF005043 | poly (ADP-ribose) glycohydrolase | poly(ADP-ribose) glycohydrolase |
| 1840 31950_at | PABPC1 | Z48501 | poly(A) binding protein, cytoplasmic 1 | polyadenylate binding protein II |
| 1841 36003_at | PABPC1 | Y00345 | poly(A) binding protein, cytoplasmic 1 | poly(A) binding protein, cytoplasmic 1 |
| 1842 34305_at | PARN | AJ005698 | poly(A)-specific ribonuclease (deadenylation nuclease) | poly(A)-specific ribonuclease |
| 1843 35746_r_at | PCBP1 | Z29505 | poly(rC) binding protein 1 | sub2.3 |
| 1844 35745_f_at | PCBP2 | X78136 | poly(rC) binding protein 2 | hnRNP-E2 |
| 1845 39868_at | PCBP3 | AL046394 | poly(rC) binding protein 3 | hnRNP-E2 |

fig. 21

| | A | B | C | D | E |
|------|----------------|--------|----------|--|--|
| 1846 | 38120_at | PKD2 | U50928 | polycystic kidney disease 2 (autosomal dominant) | polycystin 2 |
| 1847 | 33380_at | POLS | AB005754 | polymerase (DNA directed) sigma | LAK-1 |
| 1848 | 38702_at | POLE3 | AF070640 | polymerase (DNA directed), epsilon 3 (p17 subunit) | polymerase (DNA directed), epsilon 3 (p17 subunit) |
| 1849 | 40791_at | POLR2A | X63564 | polymerase (RNA) II (DNA directed) polypeptide A (220kD) | RNA polymerase II largest subunit |
| 1850 | 39746_at | POLR2B | X63563 | polymerase (RNA) II (DNA directed) polypeptide B (140kD) | RNA polymerase II 140 kDa subunit |
| 1851 | 36027_at | POLR2F | AA418779 | polymerase (RNA) II (DNA directed) polypeptide F | |
| 1852 | 35631_at | POLR2H | U37689 | polymerase (RNA) II (DNA directed) polypeptide H | RNA polymerase II subunit |
| 1853 | 1248_at | POLR2H | U37689 | polymerase (RNA) II (DNA directed) polypeptide H | RNA polymerase II subunit |
| 1854 | 503_at | POLR2L | U37690 | polymerase (RNA) II (DNA directed) polypeptide L (7.6kD) | RNA polymerase II subunit |
| 1855 | 35841_at | POLR2L | N24355 | polymerase (RNA) II (DNA directed) polypeptide L (7.6kD) | |
| 1856 | 34320_at | PTRF | AL050224 | polymerase I and transcript release factor | |
| 1857 | 34005_at | PIGR | X73079 | polymeric immunoglobulin receptor | Polymeric immunoglobulin receptor |
| 1858 | 40593_at | PTBP1 | X66975 | polypyrimidine tract binding protein 1 | nuclear ribonucleoprotein |
| 1859 | 31600_s_at | PMS2L1 | D38435 | postmeiotic segregation increased 2-like 1 | |
| 1860 | AFFX-CreX-5_at | | | pot. ORF1 (aa 1-73); ORF2, put. cre protein (aa 1-343); Bacteriophage P1 cre gene for recombinase protein. | |
| 1861 | AFFX-CreX-3_at | | X03453 | pot. ORF1 (aa 1-73); ORF2, put. cre protein (aa 1-343); Bacteriophage P1 cre gene for recombinase protein. | |
| 1862 | 315_at | PRDM2 | D45132 | PR domain containing 2, with ZNF domain | zinc-finger DNA-binding protein |
| 1863 | 32696_at | PBX3 | X59841 | pre-B-cell leukemia transcription factor 3 | homeobox protein |

Fig. 21

| | A | B | C | D | E |
|------|------------|--------|----------|--|--|
| 1864 | 36666_at | P4HB | M22806 | precursor; Human prolyl 4-hydroxylase beta-subunit and disulfide isomerase (P4HB) gene, exon 11, clones 6B-(1,3,5,6). | prolyl 4-hydroxylase beta-subunit |
| 1865 | 34321_i_at | GS3786 | D87120 | predicted osteoblast protein | GS3786 |
| 1866 | 41003_at | PFDN4 | U41816 | prefoldin 4 | C-1 |
| 1867 | 38698_at | PREI3 | AL080070 | preimplantation protein 3 | hypothetical protein |
| 1868 | 40269_at | PRP18 | U51990 | pre-mRNA processing factor 18 | hPrp18 |
| 1869 | 38291_at | PENK | J00123 | preproenkephalin (: Human enkephalin gene: exon 3 and 3'flank. | proenkephalin |
| 1870 | 641_at | PSEN1 | L76517 | presenilin 1 (Alzheimer disease 3) | presenilin 1 |
| 1871 | 40621_at | PAWR | U63809 | PRKC, apoptosis, WT1, regulator | prostate apoptosis response protein par-4 |
| 1872 | 41773_at | PCOLN3 | U58048 | procollagen (type III) N-endopeptidase | PRSM1 |
| 1873 | 31609_s_at | PCOLCE | L33799 | procollagen C-endopeptidase enhancer | procollagen C-proteinase enhancer protein |
| 1874 | 34795_at | PLOD2 | U84573 | procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2 | lysyl hydroxylase isoform 2 |
| 1875 | 36184_at | PLOD | L06419 | procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) | lysyl hydroxylase |
| 1876 | 37037_at | P4HA1 | M24486 | procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I | procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I |
| 1877 | 34390_at | P4HA2 | U90441 | procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II | prolyl 4-hydroxylase alpha (II) subunit |
| 1878 | 691_g_at | P4HB | J02783 | procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55) | procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55) |
| 1879 | 38840_s_at | PFN2 | L10678 | profilin 2 | profilin II |
| 1880 | 38839_at | PFN2 | AL096719 | profilin 2 | profilin 2 isoform b; profilin 2 isoform a |
| 1881 | 38802_at | PGRMC1 | Y12711 | progesterone receptor membrane component 1 | putative progesterone binding protein |
| 1882 | 38821_at | PGRMC2 | AJ002030 | progesterone receptor membrane component 2 | progesterone binding protein |

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| | A | B | C | D | E |
|------|------------|---------|----------|---|---|
| 1883 | 39035_at | DD5 | AF006010 | progesterone induced protein | progesterone induced protein |
| 1884 | 39036_g_at | DD5 | AF006010 | progesterone induced protein | progesterone induced protein |
| 1885 | 35218_at | PDCD10 | AF022385 | programmed cell death 10 | TFAR15 |
| 1886 | 37569_at | PDCD6 | AF035606 | programmed cell death 6 | calcium binding protein |
| 1887 | 32212_at | PDCD8 | AL049703 | programmed cell death 8 (apoptosis-inducing factor) | hypothetical protein |
| 1888 | 36592_at | PHB | S85655 | prohibitin | prohibitin |
| 1889 | 1884_s_at | PCNA | M15796 | proliferating cell nuclear antigen | proliferating cell nuclear antigen |
| 1890 | 41600_at | PA2G4 | U59435 | proliferation-associated 2G4, 38kD | cell cycle protein p38-2G4 homolog |
| 1891 | 35978_at | PRRG1 | AF009242 | proline-rich Gla (G-carboxyglutamic acid) polypeptide 1 | proline-rich Gla protein 1 |
| 1892 | 36023_at | PRH1 | AI864120 | proline-rich protein Haelll subfamily 1 | |
| 1893 | 40803_at | PORIMIN | AL050161 | pro-oncogene receptor inducing membrane injury gene | pro-oncogene receptor inducing membrane injury gene |
| 1894 | 1348_s_at | PCCA | S79219 | propionyl Coenzyme A carboxylase, alpha polypeptide | Propionyl-Coenzyme A carboxylase, alpha polypeptide precursor |
| 1895 | 36561_at | PCCB | X73424 | propionyl Coenzyme A carboxylase, beta polypeptide | propionyl-CoA carboxylase |
| 1896 | 41032_at | PCSK5 | U56387 | proprotein convertase subtilisin/kexin type 5 | protease PC6 isoform A |
| 1897 | 36795_at | PSAP | J03077 | prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) | prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) |
| 1898 | 38406_f_at | PTGDS | AI207842 | prostaglandin D2 synthase (21kD, brain) | |
| 1899 | 828_at | PTGER2 | U19487 | prostaglandin E receptor 2 (subtype EP2), 53kD | prostaglandin E2 receptor |
| 1900 | 1890_at | PLAB | AB000584 | prostate differentiation factor | TGF-beta superfamily protein |
| 1901 | 32611_at | PBP | X75252 | prostatic binding protein | phosphatidylethanolamine binding protein |
| 1902 | 719_g_at | PRSS11 | D87258 | protease, serine, 11 (IGF binding) | serin protease with IGF-binding motif |
| 1903 | 718_at | PRSS11 | D87258 | protease, serine, 11 (IGF binding) | serin protease with IGF-binding motif |
| 1904 | 33368_at | PRSS15 | X76040 | protease, serine, 15 | Lon protease-like protein |
| 1905 | 40078_at | SPUVE | AF015287 | protease, serine, 23 | serine protease |
| 1906 | 39845_at | PRSS25 | AF020760 | protease, serine, 25 | serine protease |
| 1907 | 688_at | PSMC1 | L02426 | proteasome (prosome, macropain) 26S subunit, ATPase, 1 | 26S protease (S4) regulatory subunit |

Fig. 21

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| A | B | C | D | E |
|-----------------|--------|----------|--|--|
| 1908 35353_at | PSMC2 | D11094 | proteasome (prosome, macropain) 26S subunit, ATPase, 2 | MSS1 protein |
| 1909 592_at | PSMC3 | M34079 | proteasome (prosome, macropain) 26S subunit, ATPase, 3 | proteasome (prosome, macropain) 26S subunit, ATPase, 3 |
| 1910 37766_s_at | PSMC5 | AF035309 | proteasome (prosome, macropain) 26S subunit, ATPase, 5 | |
| 1911 949_s_at | PSMC6 | D78275 | proteasome (prosome, macropain) 26S subunit, ATPase, 6 | proteasome subunit p42 |
| 1912 1314_at | PSMD1 | D44466 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 | proteasome subunit p112 |
| 1913 1192_at | PSMD12 | AB003103 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 | 26S proteasome subunit p55 |
| 1914 32240_at | PSMD5 | D31889 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 |
| 1915 945_at | PSMD7 | D50063 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog) | proteasome subunit p40 / Mov34 protein |
| 1916 40276_at | PSMD7 | D50063 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog) | proteasome subunit p40 / Mov34 protein |
| 1917 32584_at | PSMD8 | D38047 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 8 | 26S proteasome subunit p31 |
| 1918 36492_at | PSMD9 | AI347155 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 9 | |
| 1919 41171_at | PSME2 | D45248 | proteasome (prosome, macropain) activator subunit 2 (PA28 beta) | proteasome activator hPA28 suunit beta |
| 1920 1184_at | PSME2 | D45248 | proteasome (prosome, macropain) activator subunit 2 (PA28 beta) | proteasome activator hPA28 suunit beta |
| 1921 36974_at | PSMIF1 | D88378 | proteasome (prosome, macropain) inhibitor subunit 1 (PI31) | proteasome inhibitor hPI31 subunit |
| 1922 38371_at | PSMA1 | M64992 | proteasome (prosome, macropain) subunit, alpha type, 1 | prosomeal protein P30-33K |
| 1923 1446_at | PSMA2 | D00760 | proteasome (prosome, macropain) subunit, alpha type, 2 | proteasome (prosome, macropain) subunit, alpha type, 2 |
| 1924 1448_at | PSMA3 | D00762 | proteasome (prosome, macropain) subunit, alpha type, 3 | proteasome (prosome, macropain) subunit, alpha type, 3 |

Fig. 21

| | A | B | C | D | E |
|------|-----------|---------|----------|--|---|
| 1925 | 1450_g_at | PSMA4 | D00763 | proteasome (prosome, macropain) subunit, alpha type, 4 | proteasome (prosome, macropain) subunit, alpha type, 4 |
| 1926 | 1449_at | PSMA4 | D00763 | proteasome (prosome, macropain) subunit, alpha type, 4 | proteasome (prosome, macropain) subunit, alpha type, 4 |
| 1927 | 37046_at | PSMA5 | A1246726 | proteasome (prosome, macropain) subunit, alpha type, 5 | |
| 1928 | 36122_at | PSMA6 | X59417 | proteasome (prosome, macropain) subunit, alpha type, 6 | prosome P27K protein |
| 1929 | 1447_at | PSMB1 | D00761 | proteasome (prosome, macropain) subunit, beta type, 1 | proteasome (prosome, macropain) subunit, beta type, 1 |
| 1930 | 1310_at | PSMB2 | D26599 | proteasome (prosome, macropain) subunit, beta type, 2 | proteasome subunit HsC7-l |
| 1931 | 33154_at | PSMB4 | D26600 | proteasome (prosome, macropain) subunit, beta type, 4 | proteasome subunit HsN3 |
| 1932 | 1311_at | PSMB4 | D26600 | proteasome (prosome, macropain) subunit, beta type, 4 | proteasome subunit HsN3 |
| 1933 | 37666_at | PSMB5 | D29011 | proteasome (prosome, macropain) subunit, beta type, 5 | proteasome subunit X |
| 1934 | 941_at | PSMB6 | D29012 | proteasome (prosome, macropain) subunit, beta type, 6 | proteasome subunit Y |
| 1935 | 39060_at | PSMB7 | D38048 | proteasome (prosome, macropain) subunit, beta type, 7 | proteasome subunit z |
| 1936 | 1313_at | PSMB7 | D38048 | proteasome (prosome, macropain) subunit, beta type, 7 | proteasome subunit z |
| 1937 | 38287_at | PSMB9 | AA808961 | proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2) | |
| 1938 | 41750_at | P5 | D49489 | protein disulfide isomerase-related protein | human P5 |
| 1939 | 32558_at | PIAS3 | AB021868 | protein inhibitor of activated STAT3 | protein inhibitor of activated STAT3 |
| 1940 | 34376_at | PKIG | AB019517 | protein kinase (cAMP-dependent, catalytic) inhibitor gamma | protein kinase inhibitor gamma |
| 1941 | 36957_at | PRKCBP1 | W22296 | protein kinase C binding protein 1 | |
| 1942 | 1602_at | PRKCI | L33881 | protein kinase C, iota | protein kinase C iota |
| 1943 | 1603_g_at | PRKCI | L33881 | protein kinase C, iota | protein kinase C iota |
| 1944 | 36835_at | PRKCL2 | U33052 | protein kinase C-like 2 | PRK2 |

Fig. 21

| | A | B | C | D | E |
|------|----------|----------|----------|--|--|
| 1945 | 41768_at | PRKAR1A | M33336 | protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1) | cAMP-dependent protein kinase type I-alpha subunit |
| 1946 | 227_g_at | PRKAR1A | M33336 | protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1) | cAMP-dependent protein kinase type I-alpha subunit |
| 1947 | 226_at | PRKAR1A | M33336 | protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1) | cAMP-dependent protein kinase type I-alpha subunit |
| 1948 | 32205_at | PRKRA | AF072860 | protein kinase, interferon-inducible double stranded RNA dependent activator | protein activator of the interferon-induced protein kinase |
| 1949 | 37725_at | PPP1CC | X74008 | protein phosphatase 1, catalytic subunit, gamma isoform | serine /threonine specific protein phosphatase |
| 1950 | 40438_at | PPP1R12A | D87930 | protein phosphatase 1, regulatory (inhibitor) subunit 12A | myosin phosphatase target subunit 1 |
| 1951 | 39366_at | PPP1R3C | N36638 | protein phosphatase 1, regulatory (inhibitor) subunit 3C | |
| 1952 | 41540_at | PPP1R7 | Z50749 | protein phosphatase 1, regulatory subunit 7 | yeast sds22 homolog |
| 1953 | 857_at | PPM1A | S87759 | protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform | protein phosphatase 2C alpha |
| 1954 | 36501_at | PPM1A | S87759 | protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform | protein phosphatase 2C alpha |
| 1955 | 37107_at | PPM1D | U78305 | protein phosphatase 1D magnesium-dependent, delta isoform | Wip1 |
| 1956 | 924_s_at | PPP2CB | J03805 | protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform | |
| 1957 | 41167_at | PPP2R2A | M64929 | protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform | protein phosphatase-2A subunit-alpha |
| 1958 | 1383_at | PPP2R2A | M64929 | protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform | protein phosphatase-2A subunit-alpha |
| 1959 | 32734_at | PPP2R5E | L76703 | protein phosphatase 2, regulatory subunit B (B56), epsilon isoform | protein phosphatase B56-epsilon |

Fig. 21

| | A | B | C | D | E |
|------|------------|---------|----------|--|--|
| 1960 | 40786_at | PPP2R5C | U37352 | protein phosphatase 2, regulatory subunit B (B56), gamma isoform | protein phosphatase 2A B'alpha1 regulatory subunit |
| 1961 | 176_at | PPP2R5C | U37352 | protein phosphatase 2, regulatory subunit B (B56), gamma isoform | protein phosphatase 2A B'alpha1 regulatory subunit |
| 1962 | 39127_f_at | PPP2R4 | X73478 | protein phosphatase 2A, regulatory subunit B' (PR 53) | phosphotyrosyl phosphatase activator |
| 1963 | 38277_at | PPP3CB | M29550 | protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta) | protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta) |
| 1964 | 32541_at | PPP3CC | S46622 | protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma) | calcineurin A catalytic subunit |
| 1965 | 34371_at | PPP4R1 | U79267 | protein phosphatase 4, regulatory subunit 1 | |
| 1966 | 37581_at | PPP6C | X92972 | protein phosphatase 6, catalytic subunit | protein phosphatase 6 |
| 1967 | 35752_s_at | PROS1 | M15036 | protein S (alpha) | protein S (alpha) |
| 1968 | 32564_at | SEC61B | AA083129 | protein translocation complex beta | |
| 1969 | 1064_at | PTK9 | U02680 | protein tyrosine kinase 9 | protein tyrosine kinase |
| 1970 | 843_at | PTP4A1 | U48296 | protein tyrosine phosphatase type IVA, member 1 | protein tyrosine phosphatase PTPCAAX1 |
| 1971 | 38415_at | PTP4A2 | U14603 | protein tyrosine phosphatase type IVA, member 2 | protein-tyrosine phosphatase |
| 1972 | 1241_at | PTP4A2 | U14603 | protein tyrosine phosphatase type IVA, member 2 | protein-tyrosine phosphatase |
| 1973 | 40137_at | PTPN1 | M31724 | protein tyrosine phosphatase, non-receptor type 1 | protein tyrosine phosphatase, non-receptor type 1 |
| 1974 | 1463_at | PTPN12 | M93425 | protein tyrosine phosphatase, non-receptor type 12 | protein tyrosine phosphatase |
| 1975 | 34198_at | PTPN13 | U12128 | protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase) | protein tyrosine phosphatase 1E |
| 1976 | 1496_at | PTPRA | M34668 | protein tyrosine phosphatase, receptor type, A | protein tyrosine phosphatase, receptor type, A, isoform 1 precursor; protein tyrosine phosphatase, receptor type, A, isoform 2 precursor |

Fig. 21

| | A | B | C | D | E |
|-----------------|---|----------|----------|--|--|
| 1977 36204_at | | PTPRF | Y00815 | protein tyrosine phosphatase, receptor type, F | put. LAR preprotein (AA -16 to 1881) |
| 1978 41780_at | | PPFIA1 | U22816 | protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 | LAR-interacting protein 1b |
| 1979 1488_at | | PTPRK | L77886 | protein tyrosine phosphatase, receptor type, K | protein tyrosine phosphatase |
| 1980 995_g_at | | PTPRM | X58288 | protein tyrosine phosphatase, receptor type, M | protein-tyrosine phosphatase |
| 1981 31892_at | | PTPRM | X58288 | protein tyrosine phosphatase, receptor type, M | protein-tyrosine phosphatase |
| 1982 41141_at | | PRKRIR | AL049970 | protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor) | hypothetical protein |
| 1983 37737_at | | PCMT1 | D25547 | protein-L-isoaspartate (D-aspartate) O-methyltransferase | PIMT isozyme I |
| 1984 37736_at | | PCMT1 | D13892 | protein-L-isoaspartate (D-aspartate) O-methyltransferase | carboxyl methyltransferase |
| 1985 32227_at | | PRG1 | X17042 | proteoglycan 1, secretory granule | proteoglycan 1, secretory granule |
| 1986 38590_r_at | | PTMA | M14630 | prothymosin, alpha (gene sequence 28) | prothymosin, alpha (gene sequence 28) |
| 1987 38589_i_at | | PTMA | M14630 | prothymosin, alpha (gene sequence 28) | prothymosin, alpha (gene sequence 28) |
| 1988 37936_at | | HPRP4P | A1184802 | PRP4/STK/WD splicing factor | |
| 1989 31697_s_at | | FTHP1 | J04755 | pseudoferritin H protein; Human ferritin H processed pseudogene, complete cds. | |
| 1990 36117_at | | PTK2 | L13616 | PTK2 protein tyrosine kinase 2 | focal adhesion kinase |
| 1991 40048_at | | PUM1 | D43951 | pumilio homolog 1 (Drosophila) | KIAA0099 protein |
| 1992 35359_at | | PUM2 | D87078 | pumilio homolog 2 (Drosophila) | KIAA0235 protein |
| 1993 35221_at | | PURA | X91648 | purine-rich element binding protein A | |
| 1994 33341_at | | GNB1 | X04526 | put. ORFX (AA 1-75); beta subunit (AA 1-340); Human liver mRNA for beta-subunit | guanine nucleotide-binding protein, beta-1 subunit |
| 1995 33720_at | | LOC56902 | L48692 | signal transducing proteins Gs/Gi (beta-G). | |
| 1996 39363_at | | BC-2 | AF042384 | putative 28 kDa protein putative breast adenocarcinoma marker (32kD) | BC-2 protein |

Fig. 21

| A | B | C | D | E |
|-----------------|----------|----------|--|--|
| 1997 39884_g_at | HSA9761 | AF091078 | putative dimethyladenosine transferase | putative dimethyladenosine transferase |
| 1998 38841_at | GDBR1 | AF068195 | putative glioblastoma cell differentiation-related | putative glioblastoma cell differentiation-related protein |
| 1999 41188_at | LC27 | W28186 | putative integral membrane transporter | |
| 2000 38984_at | KIAA0436 | AB007896 | putative L-type neutral amino acid transporter | |
| 2001 39116_at | LOC54499 | AF070626 | putative membrane protein | |
| 2002 35286_r_at | RY1 | X76302 | putative nucleic acid binding protein RY-1 | nucleic acid binding protein |
| 2003 36852_at | N33 | U42349 | Putative prostate cancer tumor suppressor | |
| 2004 33710_at | C3F | U72515 | putative protein similar to nesso (Drosophila) | C3f |
| 2005 40203_at | SUI1 | AJ012375 | putative translation initiation factor | putative translation initiation factor |
| 2006 37678_at | NMA | U23070 | putative transmembrane protein | putative transmembrane protein |
| 2007 35326_at | 54TM | AF004876 | putative transmembrane protein; homolog of yeast Golgi membrane protein Yif1p (Yip1p-interacting factor) | 54TMp |
| 2008 35697_at | PTS | L76259 | putative; Homo sapiens PTS gene, complete cds. | 6-pyruvoyltetrahydropterin synthase |
| 2009 40887_g_at | PTI-1 | L41498 | putative; originally identified as an 'oncogene', product renamed by NCBI staff; Homo sapiens longation factor 1-alpha 1 (PTI-1) mRNA, complete cds. | longation factor 1-alpha 1 |
| 2010 40886_at | PTI-1 | L41498 | putative; originally identified as an 'oncogene', product renamed by NCBI staff; Homo sapiens longation factor 1-alpha 1 (PTI-1) mRNA, complete cds. | longation factor 1-alpha 1 |
| 2011 33219_at | VDU1 | AB029020 | pVHL-interacting deubiquitinating enzyme 1 | KIAA1097 protein |
| 2012 36164_at | PDX1 | U82328 | Pyruvate dehydrogenase complex, lipoyl-containing component X; E3-binding protein | pyruvate dehydrogenase complex protein X subunit precursor |
| 2013 32378_at | PKM2 | M28252 | pyruvate kinase, muscle | pyruvate kinase, muscle |
| 2014 260_at | QDPR | M16447 | quinoid dihydropteridine reductase | quinoid dihydropteridine reductase |

Fig-21

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| | A | B | C | D | E |
|-----------------|---|---------|----------|--|--|
| 2015 36610_at | | R3HDM | D21852 | R3H domain (binds single-stranded nucleic acids) containing | KIAA0029 protein |
| 2016 39030_at | | RABAC1 | AJ133534 | Rab acceptor 1 (prenylated) | prenylated Rab acceptor 1 (PRA1) |
| 2017 37703_at | | RABGGTB | Y08201 | Rab geranylgeranyltransferase, beta subunit | rab geranylgeranyl transferase |
| 2018 38264_at | | RABIF | U74324 | RAB interacting factor | guanine nucleotide exchange factor mss4 |
| 2019 36660_at | | RAB11A | AF000231 | RAB11A, member RAS oncogene family | rab11a |
| 2020 35325_at | | RAB14 | AF052113 | RAB14, member RAS oncogene family | |
| 2021 34393_r_at | | RAB1A | AL050268 | RAB1A, member RAS oncogene family | hypothetical protein |
| 2022 34392_s_at | | RAB1A | AL050268 | RAB1A, member RAS oncogene family | hypothetical protein |
| 2023 33326_at | | RAB21 | D42087 | RAB21, member RAS oncogene family | RAB21, member RAS oncogene family |
| 2024 809_at | | RAB27A | U57094 | RAB27A, member RAS oncogene family | Rab27a |
| 2025 33371_s_at | | RAB31 | U59877 | RAB31, member RAS oncogene family | low-Mr GTP-binding protein Rab31 |
| 2026 36110_at | | RAB5A | M28215 | RAB5A, member RAS oncogene family | GTP-binding protein |
| 2027 35289_at | | GAPCENA | AJ011679 | rab6 GTPase activating protein (GAP and centrosome-associated) | Rab6 GTPase activating protein, GAPCena |
| 2028 35304_at | | RAB6A | AF052130 | RAB6A, member RAS oncogene family | |
| 2029 39628_at | | RAB9A | AI671547 | RAB9A, member RAS oncogene family | |
| 2030 41716_at | | RC3 | AB020663 | rabconnectin-3 | KIAA0856 protein |
| 2031 37543_at | | ARHGEF6 | D25304 | Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 | |
| 2032 36857_at | | RAD1 | AF084513 | RAD1 homolog (S. pombe) | DNA repair exonuclease |
| 2033 38114_at | | RAD21 | D38551 | RAD21 homolog (S. pombe) | RAD21 homolog |
| 2034 1874_at | | RAD23B | D21090 | RAD23 homolog B (S. cerevisiae) | XP-C repair complementing protein (p58/HHR23B) |
| 2035 32757_at | | RAE1 | U84720 | RAE1 RNA export 1 homolog (S. pombe) | mRNA export protein |
| 2036 1524_at | | | U46194 | RAGE-4 ORF2; one of 2 possible coding regions; RAGE-4 ORF3; one of 2 possible coding regions; Human renal cell carcinoma antigen RAGE-4 mRNA, complete putative cds. | |
| 2037 36628_at | | RALBP1 | L42542 | ralA binding protein 1 | RLIP76 protein |
| 2038 37539_at | | RGL | AB023176 | RalGDS-like gene | KIAA0959 protein |

Fig. 21

| | A | B | C | D | E |
|------|-----------|----------|----------|---|---|
| 2039 | 41342_at | RANBP1 | D38076 | RAN binding protein 1 | Ran-BP1(Ran-binding protein 1) |
| 2040 | 40824_at | RANBP16 | AB018288 | RAN binding protein 16 | KIAA0745 protein |
| 2041 | 41174_at | RANBP2L1 | AF012086 | RAN binding protein 2-like 1 | Ran binding protein 2 |
| 2042 | 35255_at | RANBP7 | AF098799 | RAN binding protein 7 | RanBP7/importin 7 |
| 2043 | 32602_at | RAP1GDS1 | X63465 | RAP1, GTP-GDP dissociation stimulator 1 | smg GDS |
| 2044 | 1848_at | RAP1A | M22995 | RAP1A, member of RAS oncogene family | ras-related protein |
| 2045 | 40146_at | RAP1B | AL080212 | RAP1B, member of RAS oncogene family | hypothetical protein |
| 2046 | 39601_at | RASSF1 | AF061836 | Ras association (RalGDS/AF-6) domain family 1 | putative tumor suppressor protein |
| 2047 | 37598_at | RASSF2 | D79990 | Ras association (RalGDS/AF-6) domain family 2 | Ras association (RalGDS/AF-6) domain family 2 |
| 2048 | 1659_s_at | RHEB2 | D78132 | Ras homolog enriched in brain 2 | ras-related GTP-binding protein |
| 2049 | 37309_at | ARHA | L09159 | ras homolog gene family, member A | multidrug resistance protein |
| 2050 | 1394_at | ARHA | L25080 | ras homolog gene family, member A | GTP-binding protein |
| 2051 | 35803_at | ARHE | S82240 | ras homolog gene family, member E | RhoE |
| 2052 | 36935_at | RASA1 | M23379 | RAS p21 protein activator (GTPase activating protein) 1 | GTPase-activating protein |
| 2053 | 1675_at | RASA1 | M23379 | RAS p21 protein activator (GTPase activating protein) 1 | GTPase-activating protein |
| 2054 | 35793_at | G3BP2 | AB014560 | Ras-GTPase activating protein SH3 domain-binding protein 2 | KIAA0660 protein |
| 2055 | 40864_at | RAC1 | D25274 | ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1) | |
| 2056 | 2050_s_at | RAC1 | M29870 | ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1) | ras-related C3 botulinum toxin substrate 1 isoform Rac1; ras-related C3 botulinum toxin substrate 1 isoform Rac1b |
| 2057 | 35316_at | RAGA | U41654 | Ras-related GTP-binding protein | adenovirus E3-14.7K interacting protein 1 |
| 2058 | 33234_at | BCAA | AA887480 | RBP1-like protein | |
| 2059 | 41407_at | RDBP | L03411 | RD RNA-binding protein | RD protein |
| 2060 | 34684_at | RECQL | L36140 | RecQ protein-like (DNA helicase Q1-like) | DNA helicase |

Fig. 21

| | A | B | C | D | E |
|------|------------|------------|----------|--|--|
| 2061 | 34685_at | RECQL | Al685944 | RecQ protein-like (DNA helicase Q1-like) regulated at the translational level; contains l-mfa domain; utilizes unique GTG start codon; Homo sapiens HIC protein isoform p40 and HIC protein isoform p32 mRNAs, complete cds. | HIC protein isoform p40; HIC protein isoform p32 |
| 2062 | 37842_at | HIC | AF054589 | regulator of G-protein signalling 19 | RGS-GAIP interacting protein GIPC |
| 2063 | 35756_at | RGS19IP1 | AF089816 | interacting protein 1 | helix-loop-helix phosphoprotein |
| 2064 | 37701_at | RGS2 | L13463 | regulator of G-protein signalling 2, 24kD | hypothetical protein |
| 2065 | 35722_at | RENT2 | AL080198 | regulator of nonsense transcripts 2 | |
| 2066 | 32827_at | RRAS2 | Al365215 | related RAS viral (r-ras) oncogene homolog 2 | |
| 2067 | 34845_at | dJ796117.4 | AL035398 | remainder of gene in clone 549K18 (AL023654) | CGI-51 protein |
| 2068 | 1055_g_at | RFC4 | M87339 | replication factor C (activator 1) 4 (37kD) | replication factor C, 37-kDa subunit |
| 2069 | 38481_at | RPA1 | M63488 | replication protein A1 (70kD) | replication protein A, 70-kDa subunit |
| 2070 | 652_g_at | RPA3 | L07493 | replication protein A3 (14kD) | replication protein A 14kDa subunit |
| 2071 | 37651_at | RCOR | D31888 | REST corepressor | REST corepressor |
| 2072 | 34350_at | RSN | X64838 | restin (Reed-Steinberg cell-expressed intermediate filament-associated protein) | restin |
| 2073 | 31851_at | RFP2 | AJ224819 | ret finger protein 2 | tumor suppressor |
| 2074 | 40556_at | RCN1 | D42073 | reticulocalbin 1, EF-hand calcium binding domain | reticulocalbin |
| 2075 | 37727_i_at | RCN2 | X78669 | reticulocalbin 2, EF-hand calcium binding domain | EF-hand protein |
| 2076 | 37728_r_at | RCN2 | X78669 | reticulocalbin 2, EF-hand calcium binding domain | EF-hand protein |
| 2077 | 31536_at | RTN4 | AB020693 | reticulon 4 | KIAA0886 protein |
| 2078 | 39964_at | RP2 | AJ007590 | retinitis pigmentosa 2 (X-linked recessive) | XRP2 protein |
| 2079 | 38164_at | RPGR | U57629 | retinitis pigmentosa GTPase regulator | retinitis pigmentosa GTPase regulator |
| 2080 | 2044_s_at | RB1 | M15400 | retinoblastoma 1 (including osteosarcoma) | retinoblastoma 1 (including osteosarcoma) |

Fig. 21

| | A | B | C | D | E |
|------|------------|---------------|----------|---|---|
| 2081 | 35227_at | RBBP8 | U72066 | retinoblastoma binding protein 8 | CtBP interacting protein CtIP |
| 2082 | 33860_at | RBAF600 | AB007931 | retinoblastoma-associated factor 600 | KIAA0462 protein |
| 2083 | 32597_at | RBL2 | X76061 | retinoblastoma-like 2 (p130) | 130K protein |
| 2084 | 35848_at | RAI17 | AL049432 | retinoic acid induced 17 | |
| | | | | retropseudogene; Human | |
| | | | | retropseudogene MSSP-1 DNA, complete cds. | MSSP-1 |
| 2085 | 31672_g_at | RBMS1P; MSSP1 | D82351 | REV3-like, catalytic subunit of DNA polymerase zeta (yeast) | hypothetical protein |
| 2086 | 39908_s_at | REV3L | AL096744 | reversion-inducing-cysteine-rich protein with kazal motifs | |
| 2087 | 35236_g_at | RECK | AA099265 | reversion-inducing-cysteine-rich protein with kazal motifs | |
| 2088 | 35235_at | RECK | AA099265 | reversion-inducing-cysteine-rich protein with kazal motifs | |
| 2089 | 35234_at | RECK | D50406 | reversion-inducing-cysteine-rich protein with kazal motifs | RECK protein precursor |
| 2090 | 553_g_at | ARHGAP1 | U02570 | Rho GTPase activating protein 1 | CDC42 GTPase-activating protein |
| 2091 | 39700_at | ARHGAP1 | A1961929 | Rho GTPase activating protein 1 | |
| | | | | Rho guanine nucleotide exchange factor (GEF) 10 | Rho guanine nucleotide exchange factor 10 |
| 2092 | 34180_at | ARHGEF10 | AB002292 | Rho guanine nucleotide exchange factor (GEF) 7 | PAK-interacting exchange factor beta |
| 2093 | 40828_at | ARHGEF7 | D63476 | rho/rac guanine nucleotide exchange factor (GEF) 2 | guanine nucleotide regulatory factor |
| 2094 | 40100_at | ARHGEF2 | U72206 | Rho-specific guanine nucleotide exchange factor p114 | KIAA0521 protein |
| 2095 | 36537_at | P114-RHO-GEF | AB011093 | ribonuclease P (38kD) | RNaseP protein P38 |
| 2096 | 41040_at | RPP38 | U77664 | ribonuclease, RNase A family, 4 | RNase 4 |
| 2097 | 32664_at | RNASE4 | D37931 | ribonuclease/angiogenesis inhibitor | ribonuclease/angiogenesis inhibitor |
| 2098 | 36187_at | RNH | X13973 | ribonuclease M1 polypeptide | M1 subunit of ribonuclease |
| 2099 | 34314_at | RRM1 | X59543 | ribosomal protein L10 | Wilms' tumor-related protein |
| 2100 | 2016_s_at | RPL10 | M64241 | ribosomal protein L11 | ribosomal protein L11 |
| 2101 | 41178_at | RPL11 | X79234 | ribosomal protein L12 | ribosomal protein L13 |
| 2102 | 33668_at | RPL12 | AF037643 | ribosomal protein L13 | 23 kD highly basic protein |
| 2103 | 31509_at | RPL13 | X64707 | ribosomal protein L13a | ribosomal protein L14 |
| 2104 | 35119_at | RPL13A | X56932 | ribosomal protein L14 | |
| 2105 | 31907_at | RPL14 | D87735 | | |

Fig. 21

| | A | B | C | D | E |
|------|------------|--------|----------|------------------------|---|
| 2106 | 32432_f_at | RPL15 | L25899 | ribosomal protein L15 | ribosomal protein L10 |
| 2107 | 32440_at | RPL17 | X53777 | ribosomal protein L17 | ribosomal protein L17 |
| 2108 | 31546_at | RPL18 | L11566 | ribosomal protein L18 | ribosomal protein L18 |
| 2109 | 33614_at | RPL18A | X80822 | ribosomal protein L18a | ribosomal protein L18a |
| 2110 | 32435_at | RPL19 | X63527 | ribosomal protein L19 | ribosomal protein L19 |
| 2111 | 32337_at | RPL21 | U25789 | ribosomal protein L21 | ribosomal protein L21 |
| 2112 | 33451_s_at | RPL22 | A1526079 | ribosomal protein L22 | |
| 2113 | 32395_r_at | RPL23 | X55954 | ribosomal protein L23 | HL23 ribosomal protein |
| 2114 | 32394_s_at | RPL23 | X55954 | ribosomal protein L23 | HL23 ribosomal protein |
| 2115 | 32341_f_at | RPL23A | U37230 | ribosomal protein L23a | ribosomal protein L23a |
| 2116 | 33677_at | RPL24 | M94314 | ribosomal protein L24 | ribosomal protein L30 |
| 2117 | 32444_at | RPL26 | X69392 | ribosomal protein L26 | ribosomal protein L26 |
| 2118 | 39830_at | RPL27 | AA044823 | ribosomal protein L27 | |
| 2119 | 32436_at | RPL27A | U14968 | ribosomal protein L27a | ribosomal protein L27a |
| 2120 | 31708_at | RPL30 | L05095 | ribosomal protein L30 | ribosomal protein L30 |
| 2121 | 33676_at | RPL31 | X15940 | ribosomal protein L31 | ribosomal protein L31 |
| 2122 | 32276_at | RPL32 | X03342 | ribosomal protein L32 | ribosomal protein L32 |
| 2123 | 33657_at | RPL34 | L38941 | ribosomal protein L34 | ribosomal protein L34 |
| 2124 | 41765_at | RPL35 | A1541285 | ribosomal protein L35 | |
| 2125 | 41152_f_at | RPL36A | T89551 | ribosomal protein L36a | |
| 2126 | 33656_at | RPL37 | D23661 | ribosomal protein L37 | ribosomal protein L37 |
| 2127 | 31962_at | RPL37A | L06499 | ribosomal protein L37a | ribosomal protein L37a |
| 2128 | 34085_at | RPL38 | Z26876 | ribosomal protein L38 | ribosomal protein |
| 2129 | 33485_at | RPL4 | D23660 | ribosomal protein L4 | ribosomal protein |
| 2130 | 32466_at | RPL41 | Z12962 | ribosomal protein L41 | human homologue to yeast ribosomal protein YL41 |
| 2131 | 33660_at | RPL5 | U14966 | ribosomal protein L5 | ribosomal protein L5 |
| 2132 | 31952_at | RPL6 | X69391 | ribosomal protein L6 | ribosomal protein L6 |
| 2133 | 36333_at | RPL7 | X57958 | ribosomal protein L7 | ribosomal protein L7 |
| 2134 | 31505_at | RPL8 | Z28407 | ribosomal protein L8 | ribosomal protein L8 |
| 2135 | 31568_at | RPS10 | U14972 | ribosomal protein S10 | ribosomal protein S10 |
| 2136 | 32330_at | RPS11 | X06617 | ribosomal protein S11 | ribosomal protein S11 |
| 2137 | 33116_f_at | RPS12 | AA977163 | ribosomal protein S12 | |
| 2138 | 33619_at | RPS13 | L01124 | ribosomal protein S13 | ribosomal protein S13 |
| 2139 | 34317_g_at | RPS15A | W52024 | ribosomal protein S15a | ribosomal protein S15a |
| 2140 | 38061_at | RPS16 | A1541256 | ribosomal protein S16 | |

Fig. 21

| | A | B | C | D | E |
|------|------------|-----------|----------|---|---------------------------------------|
| 2141 | 34593_g_at | RPS17 | M13932 | ribosomal protein S17 | ribosomal protein S17 |
| 2142 | 34592_at | RPS17 | M13932 | ribosomal protein S17 | ribosomal protein S17 |
| 2143 | 31330_at | RPS19 | M81757 | ribosomal protein S19 | S19 ribosomal protein |
| 2144 | 31527_at | RPS2 | X17206 | ribosomal protein S2 | ribosomal protein S2 |
| 2145 | 32438_at | RPS20 | L06498 | ribosomal protein S20 | ribosomal protein S20 |
| 2146 | 347_s_at | RPS23 | D14530 | ribosomal protein S23 | ribosomal protein |
| 2147 | 32315_at | RPS24 | M31520 | ribosomal protein S24 | ribosomal protein S24 |
| 2148 | 31573_at | RPS25 | M64716 | ribosomal protein S25 | ribosomal protein |
| 2149 | 32748_at | RPS27 | A1557852 | ribosomal protein S27 (metalloprotein 1) | |
| 2150 | 34570_at | RPS27A | S79522 | ribosomal protein S27a | ubiquitin carboxyl extension protein |
| 2151 | 39798_at | RPS28 | R87876 | ribosomal protein S28 | |
| 2152 | 34645_at | RPS3 | X55715 | ribosomal protein S3 | ribosomal protein S3 |
| 2153 | 1653_at | RPS3A | M84711 | ribosomal protein S3A | v-fos transformation effector protein |
| 2154 | 34643_at | RPS4X | M58458 | ribosomal protein S4, X-linked | ribosomal protein S4X isoform |
| 2155 | 32437_at | RPS5 | U14970 | ribosomal protein S5 | ribosomal protein S5 |
| 2156 | 31511_at | RPS9 | U14971 | ribosomal protein S9 | ribosomal protein S9 |
| 2157 | 31538_at | RPLP0 | M17885 | ribosomal protein, large, P0 | ribosomal protein P0 |
| 2158 | 31956_f_at | RPLP1 | M17886 | ribosomal protein, large, P1 | ribosomal protein P1 |
| 2159 | 31957_r_at | RPLP1 | M17886 | ribosomal protein, large, P1 | ribosomal protein P1 |
| 2160 | 33213_g_at | RRBP1 | AF006751 | ribosome binding protein 1 homolog 180kD (dog) | ES/130 |
| 2161 | 38331_at | RIT | Y07566 | Ric-like, expressed in many tissues (Drosophila) | Ric-like, expressed in many tissues |
| 2162 | 35656_at | RNF6 | AJ010346 | ring finger protein (C3H2C3 type) 6 | RING-H2 |
| 2163 | 39150_at | RNF11 | U69559 | ring finger protein 11 | |
| 2164 | 35811_at | RNF13 | AF037204 | ring finger protein 13 | RING zinc finger protein |
| 2165 | 33343_at | RNF14 | AB022663 | ring finger protein 14 | ring finger protein 14 |
| 2166 | 33484_at | RNF2 | Y10571 | ring finger protein 2 | ring finger protein 2 |
| 2167 | 37964_at | RNF3 | W25793 | ring finger protein 3 | |
| 2168 | 35777_at | RNF4 | AB000468 | ring finger protein 4 | zinc finger protein |
| | | | | ring zinc-finger protein; escapes X chromosome inactivation; Human ring zinc finger protein (ZNF127-Xp) gene and 5' flanking sequence. | |
| 2169 | 37650_at | ZNF127-Xp | U41315 | | ZNF127-Xp |
| 2170 | 37732_at | RYBP | AL049940 | RING1 and YY1 binding protein | |

Fig. 21

| A | B | C | D | E |
|-----------------|----------|----------|--|---|
| 2171 38073_at | RNMT | AB007858 | RNA (guanine-7-) methyltransferase | RNA (guanine-7-) methyltransferase |
| 2172 41460_at | RBM14 | AF080561 | RNA binding motif protein 14 | SYT interacting protein SIP |
| 2173 41741_at | RBM3 | U28686 | RNA binding motif protein 3 | RNPL |
| 2174 35351_at | RBM4 | U89505 | RNA binding motif protein 4 | Hlark |
| 2175 32804_at | RBM5 | AF091263 | RNA binding motif protein 5 | RNA binding motif protein 5 |
| 2176 40870_g_at | RBM6 | AF089517 | RNA binding motif protein 6 | RNA binding protein DEF-3 |
| 2177 40260_g_at | RBM9 | AL009266 | RNA binding motif protein 9 | hypothetical protein |
| 2178 39731_at | RBMX | Z23064 | RNA binding motif protein, X chromosome | hnRNP G protein |
| 2179 33867_s_at | RBMS1 | X77494 | RNA binding motif, single stranded interacting protein 1 | RNA binding motif, single stranded interacting protein 1, isoform a |
| 2180 36186_at | RNPS1 | L37368 | RNA binding protein S1, serine-rich domain | RNA-binding protein |
| 2181 35202_at | RNGTT | AF025654 | RNA guanylyltransferase and 5'-phosphatase | mRNA capping enzyme |
| 2182 33237_at | KIAA0801 | AB018344 | RNA helicase | KIAA0801 protein |
| 2183 36045_at | RNAH | AJ223948 | RNA helicase family | RNA helicase |
| 2184 38762_at | RNAHP | AF083255 | RNA helicase-related protein | RNA helicase-related protein |
| 2185 38049_g_at | RBPM5 | D84110 | RNA-binding protein gene with multiple splicing | RBP-MS/type 4 |
| 2186 38047_at | RBPM5 | D84109 | RNA-binding protein gene with multiple splicing | RBP-MS/type 3 |
| 2187 38974_at | DJ-1 | AF021819 | RNA-binding protein regulatory subunit containing 2 | RNA-binding protein regulatory subunit |
| 2188 39725_at | RNPC2 | L10910 | RNA-binding region (RNP1, RRM) containing 2 | splicing factor |
| 2189 38011_at | RMP | AB006572 | RPB5-mediated protein | RPB5 mediating protein |
| 2190 35195_at | RTCD1 | Y11651 | RTC domain containing 1 | phosphate cyclase |
| 2191 943_at | RUNX1 | D43968 | runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) | AML1b protein |
| 2192 40124_at | RUVBL1 | Y18418 | RuvB-like 1 (E. coli) | erythrocyte cytosolic protein of 54 kDa, ECP-54 |
| 2193 35758_at | RUVBL2 | AB024301 | RuvB-like 2 (E. coli) | RuvB-like DNA helicase TIP49b |
| 2194 39338_at | S100A10 | AI201310 | S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide [p11]) | |

Fig. 21

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| A | B | C | D | E |
|-----------------|----------|----------|---|---|
| 2195 36089_at | SAC2 | AB023183 | Sac domain-containing inositol phosphatase 2 | KIAA0966 protein |
| 2196 41101_at | SAC3 | D87464 | Sac domain-containing inositol phosphatase 3 | KIAA0274 gene product |
| 2197 36511_at | SACM1L | AB020658 | SAC1 suppressor of actin mutations 1-like (yeast) | KIAA0851 protein |
| 2198 34792_at | AHCYL1 | AL049954 | S-adenosylhomocysteine hydrolase-like 1 | hypothetical protein |
| 2199 41302_at | AHCYL1 | R59606 | S-adenosylhomocysteine hydrolase-like 1 | |
| 2200 36685_at | AMD1 | W63793 | S-adenosylmethionine decarboxylase 1 | S-adenosylmethionine decarboxylase 1 precursor |
| 2201 263_g_at | AMD1 | M21154 | S-adenosylmethionine decarboxylase 1 sarcoglycan, epsilon | epsilon-sarcoglycan |
| 2202 41449_at | SGCE | AJ000534 | sarcoma amplified sequence | SAS |
| 2203 36083_at | SAS | U01160 | schwannomin interacting protein 1 | schwannomin interacting protein 1 |
| 2204 36536_at | SCHIP1 | AF070614 | SEC13-like 1 (S. cerevisiae) | SEC13 (S. cerevisiae)-like 1 |
| 2205 33423_g_at | SEC13L1 | AF052155 | SEC13-like 1 (S. cerevisiae) | SEC13 (S. cerevisiae)-like 1 |
| 2206 33422_at | SEC13L1 | AF052155 | SEC13-like 1 (S. cerevisiae) | SEC13 (S. cerevisiae)-like 1 |
| 2207 36207_at | SEC14L1 | D67029 | SEC14-like 1 (S. cerevisiae) | SEC14 (S. cerevisiae)-like 1 |
| 2208 39099_at | SEC23A | X97064 | Sec23 homolog A (S. cerevisiae) | Sec23 protein |
| 2209 34199_at | SEC24A | AJ131244 | SEC24 related gene family, member A (S. cerevisiae) | Sec24A protein |
| 2210 35845_at | SEC24B | AJ131245 | SEC24 related gene family, member B (S. cerevisiae) | Sec24B protein |
| 2211 32770_at | SEC24D | AB018298 | SEC24 related gene family, member D (S. cerevisiae) | KIAA0755 protein |
| 2212 34349_at | SEC63L | AJ011779 | SEC63 protein | SEC63 protein |
| 2213 32521_at | SFRP1 | AF056087 | secreted frizzled-related protein 1 | secreted frizzled related protein |
| 2214 34342_s_at | SPP1 | AF052124 | secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1) | osteopontin |
| 2215 671_at | SPARC | J03040 | secreted protein, acidic, cysteine-rich (osteonectin) | secreted protein, acidic, cysteine-rich (osteonectin) |
| 2216 34265_at | SGNE1 | Y00757 | secretory granule, neuroendocrine protein 1 (7B2 protein) | secretory granule, neuroendocrine protein 1 (7B2 protein) |
| 2217 37405_at | SELENBP1 | U29091 | selenium binding protein 1 | selenium-binding protein |

fig. 21

| | A | B | C | D | E |
|------|------------|----------|----------|--|--|
| 2218 | 39078_at | SPS2 | U43286 | selenophosphate synthetase 2 | selenophosphate synthetase 2 |
| 2219 | 34363_at | SEPP1 | Z11793 | selenoprotein P, plasma, 1 | selenoprotein P |
| 2220 | 377_g_at | SEMA3C | AB000220 | sema domain, immunoglobulin domain (lg), short basic domain, secreted, (semaphorin) 3C | semaphorin E |
| 2221 | 376_at | SEMA3C | AB000220 | sema domain, immunoglobulin domain (lg), short basic domain, secreted, (semaphorin) 3C | semaphorin E |
| 2222 | 35666_at | SEMA3F | U38276 | sema domain, immunoglobulin domain (lg), short basic domain, secreted, (semaphorin) 3F | semaphorin III family homolog |
| 2223 | 38826_at | 2-Sep | D50918 | septin 6 | septin 2 |
| 2224 | 40898_at | SQSTM1 | U46751 | sequestosome 1 | phosphotyrosine independent ligand for the Lck SH2 domain p62 |
| 2225 | 34789_at | SERPINE6 | S69272 | serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6 | cytoplasmic antiproteinase |
| 2226 | 38125_at | SERPINE1 | M14083 | serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1 | serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1 |
| 2227 | 39167_r_at | SERPINE2 | D83174 | serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 2 | collagen binding protein 2 |
| 2228 | 38818_at | SPTLC1 | Y08685 | serine palmitoyltransferase, long chain base subunit 1 | serine palmitoyltransferase, subunit I |
| 2229 | 40966_at | STK39 | AF099989 | serine threonine kinase 39 (STE20/SPS1 homolog, yeast) | Ste-20 related kinase SPAK |
| 2230 | 41737_at | SRM1 | AF048977 | serine/arginine repetitive matrix 1 | Ser/Arg-related nuclear matrix protein |
| 2231 | 36019_at | STK19 | L26260 | serine/threonine kinase 19 | RP protein |
| 2232 | 40473_at | STK24 | AF024636 | serine/threonine kinase 24 (STE20 homolog, yeast) | STE20-like kinase 3 |
| 2233 | 32142_at | STK3 | U26424 | serine/threonine kinase 3 (STE20 homolog, yeast) | MST2 |
| 2234 | 32784_at | PRP4 | AB011108 | serine/threonine-protein kinase PRP4 homolog | KIAA0536 protein |

Fig. 21

| A | B | C | D | E |
|---------------|---------|----------|--|---|
| 2235 40109_at | SRF | J03161 | serum response factor (c-fos serum response element-binding transcription factor) | serum response factor (c-fos serum response element-binding transcription factor) |
| 2236 1409_at | SRF | J03161 | serum response factor (c-fos serum response element-binding transcription factor) | serum response factor (c-fos serum response element-binding transcription factor) |
| 2237 41544_at | SNK | AF059617 | serum-inducible kinase | serum-inducible kinase |
| 2238 34849_at | SARS | X91257 | seryl-tRNA synthetase | seryl-tRNA synthetase |
| 2239 40189_at | SET | M93651 | SET translocation (myeloid leukemia-associated) | SET translocation (myeloid leukemia-associated) |
| 2240 32160_at | SIAH1 | U76247 | seven in absentia homolog 1 (Drosophila) | hSIAH1 |
| 2241 33799_at | SIAH2 | U76248 | seven in absentia homolog 2 (Drosophila) | hSIAH2 |
| 2242 39088_at | NIFIE14 | Y18007 | seven transmembrane domain protein | seven transmembrane domain protein |
| 2243 39747_at | tpb-7 | U52427 | seventh largest subunit; Human RNA polymerase II seventh subunit (rpb-7) gene, complete cds. | RNA polymerase II seventh subunit |
| 2244 38518_at | SCML2 | Y18004 | sex comb on midleg-like 2 (Drosophila) | SCML2 protein |
| 2245 36040_at | SH3BGR | A1337192 | SH3 domain binding glutamic acid-rich protein | SH3 domain binding glutamic acid-rich-like protein |
| 2246 39714_at | SH3BGRL | AF042081 | SH3 domain binding glutamic acid-rich protein like | SH3 domain binding glutamic acid-rich-like protein |
| 2247 38968_at | SH3BP5 | AB005047 | SH3-domain binding protein 5 (BTK-associated) | SH3 binding protein |
| 2248 39691_at | SH3GLB1 | AB007960 | SH3-domain GRB2-like endophilin B1 | SH3-containing protein SH3GLB1 |
| 2249 38118_at | SHC1 | U73377 | SHC (Src homology 2 domain containing) transforming protein 1 | p66shc |
| 2250 34256_at | SIAT9 | AB018356 | sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) | GM3 synthase |
| 2251 39139_at | SPC18 | A1357653 | signal peptidase complex (18kD) | |
| 2252 41194_at | SRP14 | A1525652 | signal recognition particle 14kD (homologous Alu RNA binding protein) | |
| 2253 35231_at | SRP19 | X12791 | signal recognition particle 19kD | signal recognition particle 19kD |
| 2254 36060_at | SRP54 | U51920 | signal recognition particle 54kD | signal recognition particle |

fig. 21

| | A | B | C | D | E |
|------|--------------|-------|----------|--|--|
| 2255 | 33837_at | SRP72 | AF069765 | signal recognition particle 72kD | signal recognition particle 72 |
| 2256 | 36981_at | SRP9 | AF070649 | signal recognition particle 9kD | signal recognition particle receptor (docking protein) |
| 2257 | 36679_at | SRPR | X06272 | signal recognition particle receptor ('docking protein') | transcription factor ISGF-3 |
| 2258 | AFFX-HUMISGF | STAT1 | M97935 | signal transducer and activator of transcription 1, 91kD | transcription factor ISGF-3 |
| 2259 | 32860_g_at | STAT1 | M97935 | signal transducer and activator of transcription 1, 91kD | transcription factor ISGF-3 |
| 2260 | 32859_at | STAT1 | M97935 | signal transducer and activator of transcription 1, 91kD | transcription factor ISGF-3 |
| 2261 | 33338_at | STAT1 | M97936 | signal transducer and activator of transcription 1, 91kD | |
| | | | | signal transducer and activator of transcription 3 (acute-phase response factor) | DNA-binding protein |
| 2262 | 39708_at | STAT3 | L29277 | signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 | STAM |
| 2263 | 160_at | STAM | U43899 | similar to Drosophila ash2 gene; Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene. | |
| 2264 | 35804_at | ASH2L | AB022785 | similar to S. cerevisiae RER1 | |
| 2265 | 41552_g_at | RER1 | AW044624 | similar to S. cerevisiae RER1 | |
| 2266 | 41551_at | RER1 | AW044624 | similar to S. pombe dim1+ | Dim1p homolog |
| 2267 | 33632_g_at | DIM1 | AF023612 | similar to SW:GOL DROME Q06003 | ring finger protein 24 |
| 2268 | 35083_at | G1L | AL031670 | GOLIATH PROTEIN' | |
| 2269 | 37178_at | na | M74089 | similar to TB1 | |
| | | | | similar to Wiskott-Aldrich syndrome protein interacting protein | |
| 2270 | 40787_at | WIRE | U90911 | similar to yeast BET3 (S. cerevisiae) | hBET3 protein |
| 2271 | 34705_at | BET3 | AJ224335 | similar to yeast Upl3, variant A | |
| 2272 | 39131_at | UPF3A | N36842 | sin3-associated polypeptide, 18kD | |
| 2273 | 41277_at | SAP18 | AW021542 | sin3-associated polypeptide, 18kD | sin3 associated polypeptide p18 |
| 2274 | 33859_at | SAP18 | U96915 | sin3-associated polypeptide, 30kD | mSin3A associated polypeptide p30 |
| 2275 | 40992_s_at | SAP30 | AF055993 | sin3-associated polypeptide, 30kD | sin3 associated polypeptide p30 |
| 2276 | 40004_at | SIX1 | X91868 | sine oculis homeobox homolog 1 (Drosophila) | sine oculis homeobox (Drosophila) homolog 1 |

Fig. 21

| A | B | C | D | E |
|-----------------|-------------|----------|---|---|
| 2277 39070_at | SNL | U03057 | singed-like (fascin homolog, sea urchin) (Drosophila) | actin bundling protein |
| 2278 39086_g_at | SSBP1 | AA768912 | single-stranded DNA binding protein | |
| 2279 32668_at | SSBP2 | AL080076 | single-stranded DNA binding protein 2 | hypothetical protein |
| 2280 35294_at | SSA2 | M25077 | Siogren syndrome antigen A2 (60kD, ribonucleoprotein autoantigen SS-A/Ro) | 60kD Ro/SSA autoantigen |
| 2281 35295_g_at | SSA2 | M25077 | Siogren syndrome antigen A2 (60kD, ribonucleoprotein autoantigen SS-A/Ro) | 60kD Ro/SSA autoantigen |
| 2282 38450_at | SSB | X69804 | Siogren syndrome antigen B (autoantigen La) | Siogren syndrome antigen B (autoantigen La) |
| 2283 37715_at | SNW1 | AF045184 | SKI-interacting protein | nuclear receptor coactivator NCoA-62 |
| 2284 37389_at | IMAGE145052 | AI346580 | small acidic protein | |
| 2285 40875_s_at | SNRP70 | X06815 | small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen) | hU1-70K-like protein (216 AA) |
| 2286 38679_g_at | SNRPE | AA733050 | small nuclear ribonucleoprotein polypeptide E | |
| 2287 37337_at | SNRPG | AI803447 | small nuclear ribonucleoprotein polypeptide G | |
| 2288 34842_at | SNRPN | U41303 | small nuclear ribonucleoprotein polypeptide N | small nuclear ribonucleoprotein particle N |
| 2289 35247_at | SNAPC5 | AI557062 | small nuclear RNA activating complex, polypeptide 5, 19kD | |
| 2290 32172_at | SHARP | AL096858 | SMART/HDAC1 associated repressor protein | hypothetical protein |
| 2291 32849_at | SMC1L1 | D80000 | SMC1 structural maintenance of chromosomes 1-like 1 (yeast) | |
| 2292 38738_at | SMT3H1 | X99584 | SMT3 suppressor of mif two 3 homolog 1 (yeast) | SMT3A protein |
| 2293 41185_f_at | SMT3H2 | AI971724 | SMT3 suppressor of mif two 3 homolog 2 (yeast) | |
| 2294 38288_at | SNAI2 | U69196 | snail homolog 2 (Drosophila) | |
| 2295 38659_at | SHOC2 | AB020669 | soc-2 suppressor of clear homolog (C. elegans) | KIAA0862 protein |
| 2296 40928_at | WSB1 | W26496 | SOCS box-containing WD protein SWIP-1 | |

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| A | B | C | D | E |
|-----------------|---------|----------|---|---|
| 2297 36609_at | SLC1A3 | D26443 | solute carrier family 1 (glial high affinity glutamate transporter), member 3 | glutamate transporter |
| 2298 35320_at | SLC11A2 | AB004857 | solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 | NRAMP2 |
| 2299 33143_s_at | SLC16A3 | U81800 | solute carrier family 16 (monocarboxylic acid transporters), member 3 | monocarboxylate transporter |
| 2300 39260_at | SLC16A4 | U59185 | solute carrier family 16 (monocarboxylic acid transporters), member 4 | solute carrier family 16 (monocarboxylic acid transporters), member 4 |
| 2301 36979_at | SLC2A3 | M20681 | solute carrier family 2 (facilitated glucose transporter), member 3 | solute carrier family 2 (facilitated glucose transporter), member 3 |
| 2302 32084_at | SLC22A5 | AF057164 | solute carrier family 22 (organic cation transporter), member 5 | organic cation transporter OCTN2 |
| 2303 38122_at | SLC23A1 | D87075 | solute carrier family 23 (nucleobase transporters), member 1 | |
| 2304 32822_at | SLC25A4 | J02966 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4 |
| 2305 37740_r_at | SLC25A5 | J02683 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 |
| 2306 40436_g_at | SLC25A6 | J03592 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6 | |
| 2307 40435_at | SLC25A6 | J03592 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6 | |
| 2308 37675_at | SLC25A3 | X60036 | solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3 | phosphate carrier protein |
| 2309 33901_at | SLC29A1 | U81375 | solute carrier family 29 (nucleoside transporters), member 1 | equilibrative nucleoside transporter 1 |
| 2310 40364_at | SLC31A1 | U83460 | solute carrier family 31 (copper transporters), member 1 | high-affinity copper uptake protein |

Fig. 21

| A | B | C | D | E |
|-----------------|---------|----------|--|--|
| 2311 34749_at | SLC31A2 | U83461 | solute carrier family 31 (copper transporters), member 2 | putative copper uptake protein |
| 2312 37895_at | SLC35A1 | D87969 | solute carrier family 35 (CMP-sialic acid transporter), member 1 | CMP-sialic acid transporter |
| 2313 38208_at | SLC35A3 | AB021981 | solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3 | UDP-N-acetylglucosamine transporter |
| 2314 34936_at | SLC4A7 | AB012130 | solute carrier family 4, sodium bicarbonate cotransporter, member 7 | sodium bicarbonate cotransporter2 |
| 2315 34166_at | SLC6A7 | S80071 | solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 | brain-specific L-proline transporter |
| 2316 32186_at | SLC7A5 | M80244 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 |
| 2317 39533_at | SLC7A6 | D87432 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 |
| 2318 32681_at | SLC9A1 | S68616 | solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na+/H+, amiloride sensitive) | Na+/H+ exchanger NHE-1 isoform |
| 2319 36542_at | SLC9A6 | AF030409 | solute carrier family 9 (sodium/hydrogen exchanger), isoform 6 | sodium-hydrogen exchanger 6 |
| 2320 39097_at | SON | X63753 | SON DNA binding protein | SON DNA-binding protein |
| 2321 32857_at | SOS2 | L13858 | son of sevenless homolog 2 (Drosophila) | guanine nucleotide exchange factor |
| 2322 41462_at | SNX2 | AF065482 | sorting nexin 2 | sorting nexin 2 |
| 2323 39360_at | SNX3 | AF034546 | sorting nexin 3 | sorting nexin 3 |
| 2324 40605_at | SNX4 | AA524345 | sorting nexin 4 | |
| 2325 37808_at | SNX7 | AL049989 | sorting nexin 7 | hypothetical protein |
| 2326 33352_at | H2A | X57985 | Source: H.sapiens genes for histones H2B.1 and H2A. | histone H2A |
| 2327 36112_r_at | SC-35 | X75755 | Source: H.sapiens PR264 gene. | splicing factor, arginine/serine-rich 2 |
| 2328 36111_s_at | SC-35 | X75755 | Source: H.sapiens PR264 gene. | splicing factor, arginine/serine-rich 2 |

fig. 21

| | A | B | C | D | E |
|------|------------|-----------|--------------|--|--|
| 2329 | 1173_g_at | | HG172-HT3924 | Source: Homo sapiens chromosome 10 clone RP11-96B5, WORKING DRAFT SEQUENCE, 8 unordered pieces. | |
| 2330 | 40617_at | 44M2.1 | AC004381 | Source: Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence. | hypothetical protein FLJ20274 |
| 2331 | 33740_at | COTE1 | AF023268 | Source: Homo sapiens clk2 kinase (CLK2), propin1, cote1, glucocerebrosidase (GBA), and metaxin genes, complete cds; metaxin pseudogene and glucocerebrosidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds. | chromosome 1 open reading frame 2 |
| 2332 | 41834_g_at | HJTB PAR | AB016492 | Source: Homo sapiens hJTB gene, complete cds. | jumping translocation breakpoint |
| 2333 | 41833_at | HJTB PAR | AB016492 | Source: Homo sapiens hJTB gene, complete cds. | jumping translocation breakpoint |
| 2334 | 32335_r_at | UbC2 | AB009010 | Source: Homo sapiens mRNA for polyubiquitin UbC, complete cds. | polyubiquitin UbC |
| 2335 | 32334_f_at | UbC2 | AB009010 | Source: Homo sapiens mRNA for polyubiquitin UbC, complete cds. | polyubiquitin UbC |
| 2336 | 32194_at | CBF | M37197 | Source: Human CCAAT-box-binding factor (CBF) mRNA, complete cds. | CCAAT-box-binding transcription factor |
| 2337 | 229_at | CBF | M37197 | Source: Human CCAAT-box-binding factor (CBF) mRNA, complete cds. | CCAAT-box-binding transcription factor |
| 2338 | 41791_at | 101F10.3 | AC002550 | Source: Human Chromosome 16 BAC clone CIT987SK-A-101F10, complete sequence. | hypothetical protein |
| 2339 | 41488_at | A-211C6.1 | AC002394 | Source: Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence. | hypothetical protein A-211C6.1 |
| 2340 | 35742_at | A-362G6.1 | U95740 | Source: Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete sequence. | hypothetical protein A-362G6.1 |

Fig. 21

| | A | B | C | D | E |
|------|------------|---------------------|----------|--|---|
| 2341 | 41733_at | 61E3.1 | AC003007 | Source: Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence. | Unknown gene product (partial) |
| 2342 | 36894_at | | AL031846 | Source: Human DNA sequence from clone RP4-742C19 on chromosome 22, complete sequence. | |
| 2343 | 37383_f_at | HLA class I - locus | X58536 | Source: Human mRNA for HLA class I locus C heavy chain. | HLA class I heavy chain |
| 2344 | 39778_at | GLYT1 GLCNAC- | M55621 | Source: Human N-acetylglucosaminyltransferase I (GlcNAc-TI) mRNA, complete cds. | mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase |
| 2345 | 41573_at | SP3 | X68560 | Sp3 transcription factor | |
| 2346 | 32102_at | SACS | AB018273 | spastic ataxia of Charlevoix-Saguenay (sacsin) | KIAA0730 protein |
| 2347 | 35171_at | SPG4 | AB029006 | spastic paraplegia 4 (autosomal dominant; spastin) | KIAA1083 protein |
| 2348 | 39423_f_at | SPOP | AJ000644 | speckle-type POZ protein | SPOP |
| 2349 | 38924_s_at | SSH3BP1 | AF001628 | spectrin SH3 domain binding protein 1 | interactor protein AbIBP4 |
| 2350 | 33886_at | SSH3BP1 | AF006516 | spectrin SH3 domain binding protein 1 | e3B1 |
| 2351 | 39556_at | SPTBN1 | M96803 | spectrin, beta, non-erythrocytic 1 | beta-spectrin |
| 2352 | 34304_s_at | SAT | AL050290 | spermidine/spermine N1-acetyltransferase | |
| 2353 | 32574_at | SMPD1 | X59960 | sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase) | sphingomyelin phosphodiesterase |
| 2354 | 36142_at | SCA1 | X79204 | spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1) | ataxin-1 |
| 2355 | 36998_s_at | SCA2 | Y08262 | spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant, ataxin 2) | ataxin 2 |
| 2356 | 38040_at | SPF30 | AF107463 | splicing factor 30, survival of motor neuron related | splicing factor |
| 2357 | 36973_at | SF3B2 | U41371 | splicing factor 3b, subunit 2, 145kD | spliceosome associated protein |

fig. 21

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| | A | B | C | D | E |
|------|------------|---------------|----------|--|--|
| 2358 | 36224_g_at | SFPQ | A1827895 | splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) | |
| 2359 | 40638_at | SFPQ | X70944 | splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) | PTB-associated splicing factor |
| 2360 | 36098_at | SFRS1 | M72709 | splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor) | splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor) |
| 2361 | 140_s_at | SFRS10 | U68063 | splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila) | transformer-2 beta |
| 2362 | 32183_at | SFRS11 | M74002 | splicing factor, arginine/serine-rich 11 | arginine-rich nuclear protein |
| 2363 | 35258_f_at | SFRS21P | AF030234 | splicing factor, arginine/serine-rich 2, interacting protein | splicing factor Sip1 |
| 2364 | 40457_at | SFRS3 | AF038250 | splicing factor, arginine/serine-rich 3 | |
| 2365 | 36991_at | SFRS4 | L14076 | splicing factor, arginine/serine-rich 4 | pre-mRNA splicing factor |
| 2366 | 40453_s_at | SFRS5 | U30826 | splicing factor, arginine/serine-rich 5 | SRp40-1 |
| 2367 | 40262_at | SRP46 | AF031166 | Splicing factor, arginine/serine-rich, 46kD | SRp46 splicing factor |
| 2368 | 35839_at | SOLE | D78130 | squalene epoxidase | squalene epoxidase |
| 2369 | 39047_at | SART3 | AB020880 | squamous cell carcinoma antigen recognised by T cells 3 | squamous cell carcinoma antigen SART-3 |
| 2370 | 41784_at | DKFZp564B0769 | AL080186 | SR rich protein | hypothetical protein |
| 2371 | 36091_at | SCAP2 | AF051323 | src family associated phosphoprotein 2 | Src-associated adaptor protein |
| 2372 | 41354_at | STC1 | U25997 | stanniocalcin 1 | stanniocalcin precursor |
| 2373 | 32043_at | STC2 | AF098462 | stanniocalcin 2 | stanniocalcin-related protein |
| 2374 | 41295_at | STARD7 | AL041780 | START domain containing 7 | |
| 2375 | 38800_at | STMN2 | D45352 | stathmin-like 2 | |
| 2376 | 41823_at | STAU | AJ132258 | stauflin, RNA binding protein (Drosophila) | stauflin protein |
| 2377 | 38669_at | SLK | D86959 | Sle20-related serine/threonine kinase | KIAA0204 protein |
| 2378 | 37147_at | SCGF | AF020044 | stem cell growth factor; lymphocyte secreted C-type lectin | lymphocyte secreted C-type lectin precursor |
| 2379 | 36913_at | SLBP | U75679 | stem-loop (histone) binding protein | histone stem-loop binding protein |
| 2380 | 38034_at | STS | M16505 | steroid sulfatase (microsomal), arylsulfatase C, isozyme S | steroid sulfatase (microsomal), arylsulfatase C, isozyme S |

Fig. 21

| | A | B | C | D | E |
|-----------------|---|----------|----------|--|--|
| 2381 589_at | | SRD5A1 | | steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1) | steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1) |
| 2382 33369_at | | SC4MOL | M32313 | steroid-C4-methyl oxidase-like | |
| 2383 33421_s_at | | SC5DL | AB016247 | steroid-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like | sterol-C5-desaturase |
| 2384 40419_at | | EPB72 | X85116 | stomatol; H.sapiens epb72 gene exon 1. | band 7 integral membrane protein |
| 2385 33322_i_at | | SFN | X57348 | stratillin | stratillin |
| 2386 37035_at | | SERP1 | AI557272 | stress-associated endoplasmic reticulum protein 1; ribosome associated membrane protein 4 | |
| 2387 35747_at | | SDFR1 | AF035287 | stromal cell derived factor receptor 1 | stromal cell derived factor receptor 1 isoform b; stromal cell derived factor receptor 1 isoform a |
| 2388 32666_at | | SDF1 | U19495 | stromal cell-derived factor 1 | intercrine-alpha |
| 2389 33834_at | | SDF1 | L36033 | stromal cell-derived factor 1 | pre-B cell stimulating factor homologue |
| 2390 41627_at | | SDF2 | D50645 | stromal cell-derived factor 2 | SDF2 |
| 2391 34826_at | | SDHA | L21936 | succinate dehydrogenase complex, subunit A, flavoprotein (Fp) | succinate dehydrogenase flavoprotein subunit |
| 2392 34385_at | | SDHC | U57877 | succinate dehydrogenase complex, subunit C; integral membrane protein, 15kD | integral membrane protein CII-3 |
| 2393 40467_at | | SDHD | AB006202 | succinate dehydrogenase complex, subunit D; integral membrane protein | cytochrome b small subunit of complex II |
| 2394 40893_at | | SUCLA2 | AF058953 | succinate-CoA ligase, ADP-forming, beta subunit | ATP-specific succinyl-CoA synthetase beta subunit |
| 2395 35832_at | | KIAA1077 | AB029000 | sulfatase FP | KIAA1077 protein |
| 2396 33712_at | | SULT4A1 | N63574 | sulfotransferase family 4A, member 1 | |
| 2397 34814_at | | UBA2 | AL041443 | SUMO-1 activating enzyme subunit 2 | |
| 2398 37998_at | | SKIV2L | U09877 | superkiller viralicidic activity 2-like (S. cerevisiae) | helicase-like protein |
| 2399 36620_at | | SOD1 | X02317 | superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult)) | superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult)) |
| 2400 40069_at | | SVIL | AF051850 | supervillin | supervillin |
| 2401 36676_at | | GHRF GRF | AL031659 | supported by FGENESH | growth hormone releasing hormone |

Fig. 21

| A | B | C | D | E |
|-----------------|---------------------------|----------|---|---|
| 2402 33297_at | CBF-B HAP2 NF- κ B | AL031778 | supported by GENEWISE, GENSCAN and FGENES | nuclear transcription factor Y, alpha, isoform 1 |
| 2403 34825_at | TTRAP | AL031775 | supported by GENSCAN | TRAF and TNF receptor-associated protein |
| 2404 1640_at | ST13 | U17714 | suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein) | putative tumor suppressor ST13 |
| 2405 37745_s_at | ST5 | U15780 | suppression of tumorigenicity 5 | p82 |
| 2406 37805_at | SRPUL | AF060567 | sushi-repeat protein | sushi-repeat protein |
| 2407 31855_at | SRPX | U61374 | sushi-repeat-containing protein, X chromosome | |
| 2408 31869_at | KIAA0640 | AB014540 | SWAP-70 protein | KIAA0640 protein |
| 2409 40213_at | SMARCA1 | M88163 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 | transcription activator |
| 2410 40961_at | SMARCA2 | X72889 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 | HBRM |
| 2411 32579_at | SMARCA4 | U29175 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 | transcriptional activator |
| 2412 39132_at | SMARCA5 | AB010882 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 | hSNF2H |
| 2413 34753_at | SYBL1 | X92396 | synaptobrevin-like 1 | synaptobrevin-like 1 |
| 2414 41692_at | SYNJ1 | AB020717 | synaptotagmin 1 | KIAA0910 protein |
| 2415 38075_at | SYPL | X68194 | synaptophysin-like protein | synaptophysin-like protein |
| 2416 36452_at | KIAA1029 | AB028952 | synaptopodin | KIAA1029 protein |
| 2417 32178_r_at | SNAP23 | AJ011915 | synaptosomal-associated protein, 23kD | synaptosome associated protein of 23 kilodaltons, isoform A |
| 2418 39757_at | SDC2 | J04621 | syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan) | |
| 2419 32092_at | SDC3 | AB007937 | syndecan 3 (N-syndecan) | KIAA0468 protein |
| 2420 38110_at | SDCBP | AF000652 | syndecan binding protein (syntenin) | syntenin |
| 2421 38685_at | STX12 | AL035306 | syntaxin 12 | hypothetical protein |
| 2422 38381_at | STX3A | U32315 | syntaxin 3A | syntaxin 3 |

Fig. 2

| A | B | C | D | E |
|-----------------|---------------------|----------|--|--|
| 2423 38774_at | STX7 | U77942 | syntaxin 7 | syntaxin 7 |
| 2424 37510_at | STX8 | AF036715 | syntaxin 8 | syntaxin 8 |
| 2425 33942_s_at | STXBP1 | AF004563 | syntaxin binding protein 1 | hUNC18b |
| 2426 37962_r_at | STXBP3 | D63506 | syntaxin binding protein 3 | unc-18homologue |
| 2427 33315_at | | M29204 | Synthetic construct chimeric DNA-binding factor mRNA, complete cds. | chimeric DNA-binding factor |
| 2428 192_at | TAF7 | U18062 | TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55 kD | TFIID subunit TAFII55 |
| 2429 193_at | TAF9 | U21858 | TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32 kD | TAFII32 precursor |
| 2430 37620_at | TAF12; TAF2J; TAF11 | U57693 | TAFII20; contains homology to histone H2B; TFIID subunit; TAFII15; contains homology to histone H2B; TFIID subunit; Human TFIID subunits TAF20 and TAF15 mRNA, complete cds. | TAF20; TAF15 |
| 2431 32166_at | TLN1 | AB028950 | taln 1 | KIAA1027 protein |
| 2432 39765_at | TLN2 | AB002318 | taln 2 | tapasin |
| 2433 41168_at | TAPBP | AF029750 | TAP binding protein (tapasin) | TAR RNA loop binding protein |
| 2434 39779_at | TARBP1 | U38847 | TAR (HIV) RNA binding protein 1 | hypothetical protein |
| 2435 32241_at | TARDBP | AL050265 | TAR DNA binding protein | Tax interaction protein 1 |
| 2436 39416_at | TIP-1 | U90913 | Tax interaction protein 1 | tax1-binding protein TXBP151 |
| 2437 498_at | TAX1BP1 | U33821 | Tax1 (human T-cell leukemia virus type I) binding protein 1 | tax1-binding protein TXBP151 |
| 2438 35279_at | TAX1BP1 | U33821 | Tax1 (human T-cell leukemia virus type I) binding protein 1 | TBX19 protein |
| 2439 36702_at | TBX19 | AJ010277 | T-box 19 | KIAA0829 protein |
| 2440 32196_at | TIP120A | AB020636 | TBP-interacting protein | t-complex 1 |
| 2441 34791_at | TCP1 | X52882 | t-complex 1 | t-complex-associated-testis-expressed 1-like |
| 2442 36921_at | TCTE1L | U02556 | t-complex-associated-testis-expressed 1-like | t-complex-associated-testis-expressed 1-like |
| 2443 946_at | TCTEL1 | D50663 | t-complex-associated-testis-expressed 1-like 1 | 1 |

Fig. 21

| | A | B | C | D | E |
|------|------------|--------------------------|----------|---|--|
| 2444 | 38374_at | TIEG; EGRA; KLF AF050110 | | TEIG; EGRA; Homo sapiens TGFb inducible early protein and early growth response protein alpha genes, complete cds. | TGFb inducible early protein; early growth response protein alpha |
| 2445 | 32255_i_at | TERF1 | U40705 | telomeric repeat binding factor (NIMA-interacting) 1 | telomeric repeat binding factor 1, isoform 2; telomeric repeat binding factor 1, isoform 1 |
| 2446 | 32134_at | TES | AL050162 | testis derived transcript (3 LIM domains) | hypothetical protein |
| 2447 | 33988_at | TEGT | X75861 | testis enhanced gene transcript (BAX inhibitor 1) | testis enhanced gene transcript (BAX inhibitor 1) |
| 2448 | 32080_at | TETRA | L11669 | tetracycline transporter-like protein | tetracycline transporter-like protein |
| 2449 | 38612_at | TSPAN-3 | M69023 | tetraspan 3 | |
| 2450 | 37321_at | TTC1 | U46570 | tetratricopeptide repeat domain 1 | tetratricopeptide repeat protein |
| 2451 | 39065_s_at | TTC3 | D83077 | tetratricopeptide repeat domain 3 | TPRD |
| 2452 | 224_at | TIEG | S81439 | TGFb inducible early growth response | zinc finger transcription factor |
| 2453 | 38805_at | TGIF | X89750 | TGFB-induced factor (TALE family homeobox) | TGIF protein |
| 2454 | 37319_at | IGFBP3 | M35878 | The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds. | growth factor-binding protein-3 precursor |
| 2455 | 1586_at | IGFBP3 | M35878 | The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds. | growth factor-binding protein-3 precursor |

Fig. 21

| A | B | C | D | E |
|-----------------|-----------------|----------|--|--|
| | | | The first in-frame ATG codon is located at nucleotides 17-19, followed by a second ATG codon 52 codons downstream. And the second ATG codon is potential initiation point for translation of NPPase.; Human mRNA for nucleotide pyrophosphatase, complete cds. | NPPase |
| 2456 342_at | ENPP1; M6S1; NF | D12485 | thioredoxin | |
| 2457 36992_at | TXN | AI653621 | thioredoxin domain-containing | hypothetical protein |
| 2458 34768_at | TXNDC | AL080080 | | |
| 2459 31508_at | TXNIP | S73591 | thioredoxin interacting protein | brain-expressed HHCPA78 homolog VDUP1 |
| 2460 39425_at | TXNRD1 | X91247 | thioredoxin reductase 1 | thioredoxin reductase (NADPH) |
| 2461 32214_at | TXNL | AF003938 | thioredoxin-like, 32kD | thioredoxin-like protein |
| 2462 38473_at | TARS | M63180 | threonyl-tRNA synthetase | threonyl-tRNA synthetase |
| 2463 659_g_at | THBS2 | L12350 | thrombospondin 2 | thrombospondin 2 |
| 2464 658_at | THBS2 | L12350 | thrombospondin 2 | thrombospondin 2 |
| 2465 40865_at | TDG | U51166 | thymine-DNA glycosylase | G/T mismatch-specific thymine DNA glycosylase |
| 2466 31557_at | TMSB4X | M17733 | thymosin, beta 4, X chromosome | thymosin, beta 4 |
| 2467 32654_g_at | SMAP | AW020536 | thyroid hormone receptor coactivating protein | |
| 2468 39699_at | TRIP12 | D28476 | thyroid hormone receptor interactor 12 | thyroid hormone receptor interactor 12 |
| 2469 41251_at | TRIP3 | L40410 | thyroid hormone receptor interactor 3 | thyroid receptor interactor |
| 2470 39341_at | TRIP6 | AJ001902 | thyroid hormone receptor interactor 6 | TRIP6 |
| 2471 37348_s_at | TRIP7 | AA845349 | thyroid hormone receptor interactor 7 | |
| 2472 41625_at | TRAP240 | AB011165 | thyroid hormone receptor-associated protein, 240 kDa subunit | KIAA0593 protein |
| 2473 34323_at | TRIP15 | AF084260 | thyroid receptor interacting protein 15 | signalosome subunit 2 |
| 2474 33852_at | TIA1 | M77142 | TIA1 cytotoxic granule-associated RNA binding protein | TIA1 protein, isoform 1; TIA1 protein, isoform 2 |
| 2475 41763_g_at | TIAL1 | D64015 | TIA1 cytotoxic granule-associated RNA binding protein-like 1 | T-cluster binding protein |
| 2476 36655_at | TJP2 | L27476 | tight junction protein 2 (zona occludens 2) | tight junction protein 2 (zona occludens 2) |
| 2477 37801_at | TJ6 | AF112972 | TJ6 protein | TJ6 |

Fig-21

| | A | B | C | D | E |
|------|-----------|----------|----------|--|---|
| 2478 | 35238_at | TRAF5 | AB000509 | TNF receptor-associated factor 5 | TRAF5 |
| 2479 | 33243_at | GG2-1 | AF099935 | TNF-induced protein | MDC-3.13 isoform 2 |
| 2480 | 40310_at | TLR2 | AF051152 | tol-like receptor 2 | Toll/interleukin-1 receptor-like protein 4 |
| 2481 | 1030_s_at | TOP1 | U07806 | topoisomerase (DNA) I | DNA topoisomerase I |
| 2482 | 36571_at | TOP2B | X68060 | topoisomerase (DNA) II beta (180kD) | DNA topoisomerase II |
| 2483 | 32233_at | TOR1B | AF007872 | torsin family 1, member B (torsin B) | torsinB |
| 2484 | 32219_at | TLK1 | D50927 | tousled-like kinase 1 | KIAA0137 protein |
| 2485 | 35321_at | TLK2 | AB004884 | tousled-like kinase 2 | PKU-alpha |
| 2486 | 39742_at | TANK | U59863 | TRAF family member-associated NFKB activator | I-TRAF |
| 2487 | 40051_at | KIAA0057 | D31762 | TRAM-like protein | TRAM-like protein |
| 2488 | 1073_at | TCEA1 | M81601 | transcription elongation factor A (SII), 1 | transcription elongation factor SII |
| 2489 | 38317_at | TCEAL1 | M99701 | transcription elongation factor A (SII)-like 1 | transcription elongation factor A (SII)-like 1 |
| 2490 | 1399_at | TCEB1 | L34587 | transcription elongation factor B (SIII), polypeptide 1 (15kD, elongin C) | RNA polymerase II elongation factor SIII, p15 subunit |
| 2491 | 41759_at | TCEB1L | Z47087 | transcription elongation factor B (SIII), polypeptide 1-like | RNA polymerase II elongation factor-like protein |
| 2492 | 39426_at | TCERG1 | AF017789 | transcription elongation regulator 1 (CA150) | putative transcription factor CA150 |
| 2493 | 33348_at | TCF12 | M80627 | transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) | helix-loop-helix protein |
| 2494 | 1373_at | TCF3 | M31523 | transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47) | |
| 2495 | 33440_at | TCF8 | U19969 | transcription factor 8 (represses interleukin 2 expression) | ZEB |
| 2496 | 39638_at | TFAP4 | S73885 | transcription factor AP-4 (activating enhancer binding protein 4) | AP-4 |
| 2497 | 37757_at | TFDP1 | L23959 | transcription factor Dp-1 | E2F-related transcription factor |
| 2498 | 32578_at | TCFL4 | AW005997 | transcription factor-like 4 | |
| 2499 | 35614_at | TCFL5 | AB012124 | transcription factor-like 5 (basic helix-loop-helix) | transcription factor-like 5 |
| 2500 | 35749_at | TADA3L | AF069733 | transcriptional adaptor 3-like | ADA3-like protein |

Fig. 21

| | A | B | C | D | E |
|------|------------|-----------|----------|--|---|
| 2501 | 35297_at | GGA2 VEAR | AC002400 | Transcriptional coactivator P15 like | KIAA1080 protein; Golgi-associated, gamma-adaplin ear containing, ARF-binding protein 2 |
| 2502 | 33876_at | TAZ | AL050107 | transcriptional co-activator with PDZ-binding motif (TAZ) | hypothetical protein |
| 2503 | 39358_at | SMRT | U37146 | transcriptional co-repressor; Human silencing mediator of retinoid and thyroid hormone action (SMRT) mRNA, complete cds. | silencing mediator of retinoid and thyroid hormone action |
| 2504 | 37312_at | TRIP-Br2 | D50917 | transcriptional regulator interacting with the PHS-bromodomain 2 | KIAA0127 gene product |
| 2505 | 40631_at | TOB1 | D38305 | transducer of ERBB2, 1 | Tob |
| 2506 | 32554_s_at | TBL1 | Y12781 | transducin (beta)-like 1 | transducin (beta) like 1 protein |
| 2507 | 37324_at | TFRC | X01060 | transferrin receptor (p90, CD71) | transferrin receptor (p90, CD71) |
| 2508 | 39344_at | HSU53209 | U53209 | transformer-2 alpha (htra-2 alpha) | transformer-2 alpha |
| 2509 | 39032_at | TSC22 | AJ222700 | transforming growth factor beta-stimulated protein TSC-22 | TSC-22 |
| 2510 | 41445_at | TGFB1 | X02812 | transforming growth factor, beta 1 (Camurati-Engelmann disease) | transforming growth factor, beta 1 (Camurati-Engelmann disease) |
| 2511 | 1815_g_at | TGFBR2 | D50683 | transforming growth factor, beta receptor II (70-80kD) | TGF-betaIIr alpha |
| 2512 | 1814_at | TGFBR2 | D50683 | transforming growth factor, beta receptor II (70-80kD) | TGF-betaIIr alpha |
| 2513 | 1385_at | TGFBI | M77349 | transforming growth factor, beta-induced, 68kD | transforming growth factor induced protein |
| 2514 | 40841_at | TACC1 | AF049910 | transforming, acidic coiled-coil containing protein 1 | TACC1 |
| 2515 | 38816_at | TACC2 | AF095791 | transforming, acidic coiled-coil containing protein 2 | TACC2 protein |
| 2516 | 36931_at | TAGLN | M95787 | transgelin | smooth muscle protein |
| 2517 | 36678_at | TAGLN2 | D21261 | transgelin 2 | transgelin 2 |
| 2518 | 31829_r_at | TGOLN2 | AF027515 | trans-golgi network protein 2 | hTGN48 |
| 2519 | 39124_r_at | TRPC1 | X89066 | transient receptor potential cation channel, subfamily C, member 1 | TRPC1 protein |
| 2520 | 39123_s_at | TRPC1 | X89066 | transient receptor potential cation channel, subfamily C, member 1 | TRPC1 protein |

Fig. 21

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| A | B | C | D | E |
|---------------|-------|----------|--|---|
| | | | RETICULUM ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN) (VCP); Human homolog of spIQ01853TERA_MOUSE TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN) (VCP) pirlS25197 transitional endoplasmic reticulum ATPase - mouse gil55217 (Z14044) murine valosin- containing protein; 99% identical to mouse, rat, and pig homologs; X-ray cross- complementing gene 9; Putative DNA repair protein; Hypothetical 96.6 kDa putative membrane protein; Most similar to hypothetical proteins in fission and budding yeast, and C. elegans: (AB004539) ORF YLL031c [Schizosaccharomyces pombe] producing hypothetical protein (AL021766) [Schizosaccharomyces pombe]; probable membrane protein YLL031c - yeast (Saccharomyces cerevisiae) gnlPIDle245463 (Z73136) ORF YLL031c [Saccharomyces cerevisiae]; (AF003137) C27A12.9 [Caenorhabditis elegans]; Hypothetical 38.8 kDa putative membrane protein; Most similar to hypothetical proteins: PIDle276130 (Z81072) F30A10.5 [Caenorhabditis elegans]; spIP72655YB28 translation factor sufi1 homolog translation initiation factor IF2 | |
| 2521 34380_at | XRCC9 | AC004472 | | TERA_HUMAN; XRCC9; P1.11659_3; |
| 2522 33351_at | GC20 | AF064607 | | P1.11659_4; P1.11659_5 |
| 2523 40537_at | IF2 | AB018284 | | GC20 protein KIAA0741 protein |
| 2524 32173_at | UK114 | X95384 | translational inhibitor protein p14.5 | 14.5 kDa translational inhibitor protein, p14.5 |

Fig. 21

| | A | B | C | D | E |
|------|------------|---------------|----------|--|---|
| 2525 | 41051_at | TSNAX | X95073 | translin-associated factor X | Translin associated protein X |
| 2526 | 32831_at | TIMM17A | AA453183 | translocase of inner mitochondrial membrane 17 homolog A (yeast) | |
| 2527 | 36198_at | TOMM20-PENDIN | D13641 | translocase of outer mitochondrial membrane 20 (yeast) homolog | mitochondrial outer membrane protein 19 |
| 2528 | 37050_r_at | TOMM34 | AI130910 | translocase of outer mitochondrial membrane 34 | |
| 2529 | 32853_at | TOMM70A | AB018262 | translocase of outer mitochondrial membrane 70 homolog A (yeast) | KIAA0719 protein |
| 2530 | 34796_at | TRAM | X63679 | translocating chain-associating membrane protein | TRAM protein |
| 2531 | 38100_at | TLOC1 | D87127 | translocation protein 1 | translocation protein-1 |
| 2532 | 950_at | TLOC1 | D87127 | translocation protein 1 | translocation protein-1 |
| 2533 | 41531_at | TM4SF1 | AI445461 | transmembrane 4 superfamily member 1 | |
| 2534 | 39362_r_at | TM4SF6 | AF043906 | transmembrane 4 superfamily member 6 | T245 protein |
| 2535 | 32083_at | TM7SF1 | AF027826 | transmembrane 7 superfamily member 1 (upregulated in kidney) | putative seven pass transmembrane protein |
| 2536 | 38835_at | TM9SF1 | U94831 | transmembrane 9 superfamily member 1 | multispanning membrane protein |
| 2537 | 34307_at | TM9SF2 | U81006 | transmembrane 9 superfamily member 2 | p76 |
| 2538 | 37955_at | TMEM4 | AB015631 | transmembrane protein 4 | type II membrane protein |
| 2539 | 37445_at | TMEM5 | AB015633 | transmembrane protein 5 | type II membrane protein |
| 2540 | 36128_at | TMP21 | L40397 | transmembrane trafficking protein | |
| 2541 | 38982_at | RAP1 | W28865 | TRF2-interacting telomeric RAP1 protein | |
| 2542 | 39382_at | TRIM2 | AB011089 | tripartite motif-containing 2 | KIAA0517 protein |
| 2543 | 36825_at | TRIM22 | X82200 | tripartite motif-containing 22 | gpStat50 |
| 2544 | 38537_at | TRIM32 | U18543 | tripartite motif-containing 32 | zinc-finger protein |
| 2545 | 32635_at | TRIM33 | AB029036 | tripartite motif-containing 33 | KIAA1113 protein |
| 2546 | 33107_at | TRIM37 | AB020705 | tripartite motif-containing 37 | KIAA0898 protein |
| 2547 | 40461_at | TIX1 | AB007855 | triple homeobox 1 | |
| 2548 | 36791_g_at | TPM1 | M19267 | tropomyosin 1 (alpha) | tropomyosin 1 (alpha) |
| 2549 | 36790_at | TPM1 | M19267 | tropomyosin 1 (alpha) | tropomyosin 1 (alpha) |

Fig. 21

| | A | B | C | D | E |
|------|------------|-----------|----------|---------------------------------------|--------------------------------------|
| 2550 | 36792_at | TPM1 | Z24727 | tropomyosin 1 (alpha) | tropomyosin isoform |
| 2551 | 32313_at | TPM2 | M12125 | tropomyosin 2 (beta) | tropomyosin 2 (beta) |
| 2552 | 32777_at | WRB | Y12478 | tryptophan rich basic protein | congenital heart disease 5 protein |
| 2553 | 38121_at | WARS | X59892 | tryptophanyl-tRNA synthetase | 471 aa polypeptide (gamma2) |
| 2554 | 39867_at | TUFM | S75463 | Tu translation elongation factor, | |
| 2555 | 31944_at | TULP3 | AI028290 | mitochondrial | P43 |
| 2556 | 32272_at | K-ALPHA-1 | K00558 | tubby like protein 3 | |
| 2557 | 39332_at | TUBB | AF035316 | tubulin, alpha, ubiquitous | tubulin, alpha, ubiquitous |
| 2558 | 39331_at | TUBB | X79535 | tubulin, beta polypeptide | |
| 2559 | 33346_r_at | TUBG1 | M61764 | tubulin, beta polypeptide | beta tubulin |
| 2560 | 36176_at | TBCC | U61234 | tubulin, gamma 1 | gamma-tubulin |
| 2561 | 35159_at | TBCE | U61232 | tubulin-specific chaperone c | cofactor C |
| 2562 | 37007_at | TDE1 | U49188 | tubulin-specific chaperone e | cofactor E |
| 2563 | 34892_at | TNFRSF10B | AF016266 | tumor differentially expressed 1 | tumor differentially expressed 1 |
| | | | | tumor necrosis factor receptor | |
| | | | | superfamily, member 10b | TRAIL receptor 2 |
| 2564 | 41190_at | TNFRSF12 | U83598 | tumor necrosis factor receptor | |
| | | | | superfamily, member 12 (translocating | |
| | | | | chain-association membrane protein) | death domain receptor 3 soluble form |
| 2565 | 1563_s_at | TNFRSF1A | M58286 | tumor necrosis factor receptor | |
| | | | | superfamily, member 1A | tumor necrosis factor receptor |
| 2566 | 35150_at | TNFRSF5 | X60592 | tumor necrosis factor receptor | |
| | | | | superfamily, member 5 | CDw40 |
| 2567 | 37643_at | TNFRSF6 | X63717 | tumor necrosis factor receptor | |
| | | | | superfamily, member 6 | APO-1 cell surface antigen precursor |
| 2568 | 36988_at | TNFAIP1 | M80783 | tumor necrosis factor, alpha-induced | |
| | | | | protein 1 (endothelial) | B12 protein |
| 2569 | 38631_at | TNFAIP2 | M92357 | tumor necrosis factor, alpha-induced | |
| | | | | protein 2 | B94 protein |
| 2570 | 595_at | TNFAIP3 | M59465 | tumor necrosis factor, alpha-induced | |
| | | | | protein 3 | A20 |
| 2571 | 40076_at | TPD52L2 | AF004430 | tumor necrosis factor, alpha-induced | |
| | | | | tumor protein D52-like 2 | hD54+ins2 isoform |
| 2572 | 1711_at | TP53BP1 | U09477 | tumor protein p53 binding protein, 1 | p53-binding protein |
| 2573 | 34822_at | TP53BP2 | U58334 | tumor protein p53 binding protein, 2 | Bbp/53BP2 |
| 2574 | 38568_at | TP53BPL | U82939 | tumor protein p53-binding protein | p53 binding protein |

Fig. 21

| A | B | C | D | E |
|-----------------|--------|----------|---|--|
| 2575 31584_at | TPT1 | X16064 | tumor protein, translationally-controlled 1 | tumor protein, translationally-controlled 1 |
| 2576 31888_s_at | TSSC3 | AF001294 | tumor suppressing subtransferable candidate 3 | IPL |
| 2577 147_at | TSG101 | U82130 | tumor susceptibility gene 101 | tumor susceptibility protein |
| 2578 40328_at | TWIST | X99268 | twist homolog (acrocephalosyndactyly 3; Saethre-Chotzen syndrome) (Drosophila) | B-HLH DNA binding protein |
| 2579 2086_s_at | TYRO3 | D17517 | TYRO3 protein tyrosine kinase | Sky |
| 2580 35246_at | TYRO3 | U18934 | TYRO3 protein tyrosine kinase | receptor tyrosine kinase |
| 2581 32324_at | YWHAH | X57346 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide |
| 2582 409_at | YWHAQ | X56468 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide | 14.3.3 protein |
| 2583 32530_at | YWHAQ | X56468 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide | 14.3.3 protein |
| 2584 1235_at | YWHAZ | M86400 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide | phospholipase A2 |
| 2585 32718_at | TPST1 | AF038009 | tyrosylprotein sulfotransferase 1 | tyrosylprotein sulfotransferase-1 |
| 2586 35172_at | TPST2 | AF049891 | tyrosylprotein sulfotransferase 2 | tyrosylprotein sulfotransferase-2 |
| 2587 38977_at | YARS | U89436 | tyrosyl-tRNA synthetase | tyrosyl-tRNA synthetase |
| 2588 36517_at | U2AF1 | M96982 | U2(RNU2) small nuclear RNA auxiliary factor 1 | U2 snRNP auxiliary factor small subunit |
| 2589 32858_at | UBN1 | A1341565 | ubiquitin 1 | ubiquitin 2 |
| 2590 34824_at | UBQLN2 | AB015344 | ubiquitin 2 | ubiquitin 2 |
| 2591 38451_at | UQCR | T58471 | ubiquinol-cytochrome c reductase (6.4kD) subunit | |
| 2592 39427_at | UQCRB | T79616 | ubiquinol-cytochrome c reductase binding protein | |
| 2593 40854_at | UQCRC2 | J04973 | ubiquinol-cytochrome c reductase core protein II | ubiquinol-cytochrome c reductase core protein II |

Fig-21

| A | B | C | D | E |
|----------------|--------|----------|---|---|
| 2594 36104_at | UQCRH | AA526497 | ubiquinol-cytochrome c reductase hinge protein | |
| 2595 1366_i_at | UBC | M26880 | ubiquitin C | ubiquitin C |
| 2596 1367_f_at | UBC | M26880 | ubiquitin C | ubiquitin C |
| 2597 36990_at | UCHL1 | X04741 | ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase) | ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase) |
| 2598 811_at | UFD1L | U64444 | ubiquitin fusion degradation 1-like | ubiquitin fusion-degradation 1 like protein |
| 2599 40623_at | UBE3B | A1749193 | ubiquitin protein ligase | |
| 2600 41205_at | UBE3A | U84404 | ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) | E6-associated protein E6-AP/ubiquitin-protein ligase |
| 2601 34383_at | USP1 | AB014458 | ubiquitin specific protease 1 | ubiquitin specific protease |
| 2602 37683_at | USP10 | D80012 | ubiquitin specific protease 10 | |
| 2603 162_at | USP11 | U44839 | ubiquitin specific protease 11 | UHX1 protein |
| 2604 36982_at | USP14 | U30888 | ubiquitin specific protease 14 (tRNA-guanine transglycosylase) | tRNA-Guanine Transglycosylase |
| 2605 39866_at | USP22 | AB028986 | ubiquitin specific protease 22 | KIAA1063 protein |
| 2606 35847_at | USP24 | AB028980 | ubiquitin specific protease 24 | KIAA1057 protein |
| 2607 1357_at | USP4 | U20657 | ubiquitin specific protease 4 (proto-oncogene) | ubiquitin protease |
| 2608 34405_at | USP5 | U47927 | ubiquitin specific protease 5 (isopeptidase T) | isopeptidase T |
| 2609 37672_at | USP7 | Z72499 | ubiquitin specific protease 7 (herpes virus-associated) | herpesvirus associated ubiquitin-specific protease (HAUSP) |
| 2610 39794_at | USP8 | D29956 | ubiquitin specific protease 8 | ubiquitin specific protease 8 |
| 2611 32572_at | USP9X | X98296 | ubiquitin specific protease 9, X chromosome (fat facets-like Drosophila) | ubiquitin hydrolase |
| 2612 40066_at | UBE1C | AF046024 | ubiquitin-activating enzyme E1C (UBA3 homolog, yeast) | UBA3 |
| 2613 36579_at | UBE4A | D50916 | ubiquitination factor E4A (UFD2 homolog, yeast) | ubiquitination factor E4A (UFD2 homolog, yeast) |
| 2614 41339_at | UBE4B | AF043117 | ubiquitination factor E4B (UFD2 homolog, yeast) | ubiquitin-fusion degradation protein 2 |
| 2615 36959_at | UBE2V1 | U49278 | ubiquitin-conjugating enzyme E2 variant 1 | UEV-1 |

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| A | B | C | D | E |
|-----------------|---------|----------|--|---|
| 2616 890_at | UBE2A | M74524 | ubiquitin-conjugating enzyme E2A (RAD6 homolog) | ubiquitin-conjugating enzyme E2A (RAD6 homolog) |
| 2617 37826_at | UBE2D1 | AF020761 | ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast) | |
| 2618 38705_at | UBE2D2 | A1310002 | ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast) | |
| 2619 832_at | UBE2D2 | U39317 | ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast) | UbcH5B |
| 2620 39083_at | UBE2D3 | U39318 | ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast) | UbcH5C |
| 2621 504_at | UBE2D3 | U39318 | ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast) | UbcH5C |
| 2622 34850_at | UBE2E3 | AB017644 | ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) | ubiquitin-conjugating enzyme E2 |
| 2623 32236_at | UBE2G2 | AF032456 | ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast) | ubiquitin conjugating enzyme G2 |
| 2624 38480_s_at | UBE2I | U66867 | ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast) | ubiquitin conjugating enzyme 9 |
| 2625 838_s_at | UBE2I | U45328 | ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast) | ubiquitin-conjugating enzyme |
| 2626 223_at | UBE2L3 | S81003 | ubiquitin-conjugating enzyme E2L 3 | L-UBC |
| 2627 40505_at | UBE2L6 | AA883502 | ubiquitin-conjugating enzyme E2L 6 | |
| 2628 36604_at | UBE2N | D83004 | ubiquitin-conjugating enzyme E2N | ubiquitin-conjugating enzyme E2 UbcH-ben |
| 2629 457_s_at | UBL1 | U67122 | (UBC13 homolog, yeast) | SUMO-1 |
| 2630 155_s_at | UBL1 | U61397 | ubiquitin-like 1 (sentrin) | ubiquitin-homology domain protein PIC1 |
| 2631 40839_at | UBL3 | AL080177 | ubiquitin-like 3 | hypothetical protein |
| 2632 37336_at | UBXD2 | D87684 | UBX domain-containing 2 | KIAA0242 protein |
| 2633 40960_at | B4GALT1 | D29805 | UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1 | beta-1,4-galactosyltransferase |
| 2634 34177_at | B4GALT2 | AF038660 | UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 2 | beta-1,4-galactosyltransferase |
| 2635 39445_at | B4GALT3 | AF038661 | UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3 | beta-1,4-galactosyltransferase |
| 2636 40215_at | UGCG | D50840 | UDP-glucose ceramide glucosyltransferase | ceramide glucosyltransferase |

fig. 21

| A | B | C | D | E |
|-----------------|------------|----------|--|--|
| 2637 35214_at | UGDH | AF061016 | UDP-glucose dehydrogenase | UDP-glucose dehydrogenase |
| 2638 37373_at | UGP2 | U27460 | UDP-glucose pyrophosphorylase 2 | uridine diphosphoglucose pyrophosphorylase |
| 2639 38041_at | GALNT1 | U41514 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 1 (GalNAc-T1) | UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase |
| 2640 36515_at | GNE | AJ238764 | UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase | UDP-N-acetylglucosamine-2-epimerase / N-acetylmannosamine kinase |
| 2641 41242_at | UAP1 | AB011004 | UDP-N-acetylglucosamine pyrophosphorylase 1 | UDP-N-acetylglucosamine pyrophosphorylase |
| 2642 34827_at | ULK1 | AF045458 | unc-51-like kinase 1 (C. elegans) | serine/threonine kinase ULK1 |
| 2643 37315_f_at | BM036 | AI057607 | uncharacterized bone marrow protein BM036 | |
| 2644 35750_at | HT010 | ALO49948 | uncharacterized hypothalamus protein HT010 | |
| 2645 41058_g_at | HT012 | AI760162 | uncharacterized hypothalamus protein HT012 | |
| 2646 41057_at | HT012 | AI760162 | uncharacterized hypothalamus protein HT012 | |
| 2647 38610_s_at | KRT10; KPP | X14487 | unnamed protein product; Human gene for acidic (type I) cytokeratin 10. | keratin 10 |
| 2648 34402_at | UNRIP | AB024327 | unr-interacting protein | WD-40 repeat protein |
| 2649 34372_at | UREB1 | AB002310 | upstream regulatory element binding protein 1 | upstream regulatory element binding protein 1 |
| 2650 37686_s_at | UNG | Y09008 | uracil-DNA glycosylase | uracil-DNA glycosylase |
| 2651 33815_at | UMPS | J03626 | uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) | uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) |
| 2652 41859_at | UST | AB020316 | uronyl-2-sulfotransferase | dermatan/chondroitin sulfate 2-sulfotransferase |
| 2653 39429_at | UVRAG | X99050 | UV Radiation Resistance Associated Gene; H.sapiens mRNA; UV Radiation Resistance Associated Gene. | p63 (processed form) |

Fig-21

| | A | B | C | D | E |
|-----------------|----------------|---|----------|---|--|
| | | | | v-abl Abelson murine leukemia viral oncogene homolog 1 | v-abl Abelson murine leukemia viral oncogene homolog 1 isoform a; v-abl |
| 2654 39730_at | ABL1 | | X16416 | oncogene homolog 1 | Abelson murine leukemia viral oncogene homolog 1 isoform b |
| 2655 35779_at | VPS45A | | AJ133421 | vacuolar protein sorting 45A (yeast) | vacuolar protein sorting |
| 2656 38801_at | VAPA | | AI742846 | VAMP (vesicle-associated membrane protein)-associated protein A (33kD) | |
| | | | | | vascular cell adhesion molecule 1, isoform a precursor; vascular cell adhesion molecule 1, isoform b precursor |
| 2657 583_s_at | VCAM1 | | M30257 | vascular cell adhesion molecule 1 | |
| 2658 1953_at | VEGF | | AF024710 | vascular endothelial growth factor | vascular endothelial growth factor |
| 2659 36100_at | VEGF | | AF022375 | vascular endothelial growth factor | vascular endothelial growth factor |
| 2660 37268_at | VEGFB | | U43368 | vascular endothelial growth factor B | VEGF related factor isoform VRF186 precursor |
| 2661 159_at | VEGFC | | U43142 | vascular endothelial growth factor C | vascular endothelial growth factor related protein |
| | | | | VDAC protein; similar to mouse VDAC 3; Homo sapiens voltage dependent anion channel protein mRNA, complete cds. | voltage dependent anion channel protein |
| 2662 36102_at | VDAC3; HD-VDAC | | AF038962 | | vesicle amine transport protein 1 |
| 2663 40147_at | VAT1 | | U18009 | vesicle amine transport protein 1 | KIAA0917 protein |
| 2664 33930_at | RA410 | | AB020724 | vesicle transport-related protein | |
| 2665 32254_at | VAMP2 | | AL050223 | vesicle-associated membrane protein 2 (synaptobrevin 2) | |
| 2666 35783_at | VAMP3 | | H93123 | vesicle-associated membrane protein 3 (cellubrevin) | |
| 2667 40103_at | VIL2 | | X51521 | villin 2 (ezrin) | villin 2 |
| 2668 34091_s_at | VIM | | Z19554 | vimentin | vimentin |
| 2669 36601_at | VCL | | M33308 | vinculin | vinculin isoform VCL; VCL isoform meta-VCL |
| 2670 39091_at | JWA | | AF070523 | vitamin A responsive; cytoskeleton related | JWA protein |
| 2671 1388_g_at | VDR | | J03258 | vitamin D (1,25-dihydroxyvitamin D3) receptor | vitamin D (1,25-dihydroxyvitamin D3) receptor |
| 2672 1940_at | KRAS2 | | M54968 | v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog | K-ras oncogene protein |

fig-21

| A | B | C | D | E |
|-----------------|--------|----------|---|--|
| 2673 41504_s_at | MAF | AF055376 | v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) | short form transcription factor C-MAF |
| 2674 32835_at | MAFF | AA725102 | v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian) | |
| 2675 40198_at | VDAC1 | L06132 | voltage-dependent anion channel 1 | voltage-dependent anion channel |
| 2676 37696_at | VDAC2 | L06328 | voltage-dependent anion channel 2 | voltage-dependent anion channel |
| 2677 171_at | VBP1 | U56833 | von Hippel-Lindau binding protein 1 | VHL binding protein-1 |
| 2678 38743_f_at | RAF1 | X06409 | v-raf-1 murine leukemia viral oncogene homolog 1 | |
| 2679 32776_at | RALB | M35416 | v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein) | v-ral simian leukemia viral oncogene homolog B |
| 2680 36645_at | RELA | L19067 | v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian) | NF-kappa-B transcription factor subunit |
| 2681 1295_at | RELA | L19067 | v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian) | |
| 2682 1674_at | YES1 | M15990 | v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 | NF-kappa-B transcription factor subunit |
| 2683 1402_at | LYN | M16038 | v-yes-1 Yamaguchi sarcoma viral related oncogene homolog | homolog 1 |
| 2684 1058_at | WASF3 | S69790 | WAS protein family, member 3 | v-yes-1 Yamaguchi sarcoma viral related oncogene homolog |
| 2685 38736_at | WDR1 | AL050108 | WD repeat domain 1 | hypothetical protein |
| 2686 41430_at | WDR7 | AB011113 | WD repeat domain 7 | KIAA0541 protein |
| 2687 36009_at | CL683 | AF091092 | weakly similar to glutathione peroxidase 2 | weakly similar to glutathione peroxidase 2 |
| 2688 36909_at | WEE1 | X62048 | WEE1 + homolog (S. pombe) | wee1 tyrosine kinase |
| 2689 41212_r_at | WBCSR1 | D26068 | Williams-Beuren syndrome chromosome region 1 | eukaryotic translation initiation factor 4H, isoform 1; eukaryotic translation initiation factor 4H, isoform 2 |
| 2690 41635_at | WTAP | D14661 | Wilms' tumour 1-associating protein | Wilms' tumour 1-associating protein |
| 2691 31862_at | WNT5A | L20861 | wingless-type MMTV integration site family, member 5A | wingless-type MMTV integration site family, member 5A precursor |

fig-21

| A | B | C | D | E |
|-----------------|----------|----------|--|---|
| 2692 34225_at | WHSC2 | AF101434 | Wolff-Hirschhorn syndrome candidate 2 | Wolff-Hirschhorn syndrome candidate 2 protein |
| 2693 33438_at | WBP2 | AL049981 | WW domain binding protein 2 | |
| 2694 35213_at | WBP4 | AF071185 | WW domain binding protein 4 (formin binding protein 21) | formin binding protein 21 |
| 2695 39995_s_at | WBOX | U13395 | WW domain containing oxidoreductase | oxidoreductase |
| 2696 36822_at | WAC | U51334 | WW domain-containing adapter with a coiled-coil region | putative RNA binding protein RBP56 |
| 2697 1307_at | XPA | D14533 | xeroderma pigmentosum, complementation group A | XPAC protein |
| 2698 1873_at | XPC | D21089 | xeroderma pigmentosum, complementation group C | XP-C repair complementing protein (p125) |
| 2699 41756_at | NTPBP | AJ010842 | XPA binding protein 1; putative ATP(GTP)-binding protein | ATP(GTP)-binding protein |
| 2700 38733_at | XRCC5 | M30938 | X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen; 80kD) | ATP-dependant DNA helicase II |
| 2701 585_at | XRCC5 | M30938 | X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen; 80kD) | ATP-dependant DNA helicase II |
| 2702 2093_s_at | XRCC5 | J04977 | X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen; 80kD) | ATP-dependant DNA helicase II |
| 2703 35827_at | KIAA0905 | AB020712 | yeast Sec31p homolog | KIAA0905 protein |
| 2704 40988_at | YME1L1 | AJ132637 | YME1-like 1 (S. cerevisiae) | ATP-dependent metalloprotease YME1L |
| 2705 891_at | YY1 | M77698 | YY1 transcription factor | GLI-Krupple related protein |
| 2706 34887_at | | N92548 | zb29g04.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305046 3', mRNA sequence. | |
| 2707 36308_at | ZIC1 | D76435 | Zic family member 1 (odd-paired homolog, Drosophila) | Zic protein |
| 2708 35681_r_at | ZFX1B | AB011141 | zinc finger homeobox 1b | KIAA0569 protein |

fig. 21

| | A | B | C | D | E |
|------|------------|------------|---------------|---|---|
| 2709 | 34786_at | TSGA | AB018285 | zinc finger protein | KIAA0742 protein |
| 2710 | 39977_at | ZNF-U69274 | U69274 | zinc finger protein | zinc finger protein |
| 2711 | 40140_at | ZFP103 | D76444 | zinc finger protein 103 homolog (mouse) | zinc finger protein 103 homolog |
| 2712 | 36295_at | ZNF134 | U09412 | zinc finger protein 134 (clone pHZ-15) | zinc finger protein ZNF134 |
| 2713 | 32192_g_at | ZNF144 | D13969 | zinc finger protein 144 (Mel-18) | Mel-18 protein |
| 2714 | 36928_at | ZNF146 | X70394 | zinc finger protein 146 | zinc finger protein |
| 2715 | 41532_at | ZNF151 | Y09723 | zinc finger protein 151 (pHZ-67) | Miz-1 protein |
| 2716 | 32628_at | ZNF161 | D28118 | zinc finger protein 161 | DB1 |
| 2717 | 41436_at | ZNF198 | AJ224901 | zinc finger protein 198 | ZNF198 protein |
| 2718 | 40724_at | ZNF200 | Y14443 | zinc finger protein 200 | zinc finger protein |
| 2719 | 35368_at | ZNF207 | AF046001 | zinc finger protein 207 | zinc finger protein 207 |
| 2720 | 41542_at | ZNF216 | AF062346 | zinc finger protein 216 | zinc finger protein 216 splice variant 1 |
| 2721 | 840_at | ZNF220 | U47742 | zinc finger protein 220 | monocytic leukaemia zinc finger protein |
| 2722 | 39762_at | ZNF262 | AB007885 | zinc finger protein 262 | zinc finger protein 262 |
| 2723 | 34299_at | ZNF278 | AL096880 | zinc finger protein 278 | hypothetical protein |
| 2724 | 39005_s_at | ZNF294 | AB018257 | zinc finger protein 294 | KIAA0714 protein |
| 2725 | 37860_at | ZNF337 | AL049942 | zinc finger protein 337 | hypothetical protein |
| 2726 | 40448_at | ZFP36 | M92843 | zinc finger protein 36, C3H type, homolog (mouse) | zinc finger transcriptional regulator |
| 2727 | 38740_at | ZFP36L1 | X79067 | zinc finger protein 36, C3H type-like 1 | butyrate response factor 1 |
| 2728 | 36046_at | ZNF363 | AL050144 | zinc finger protein 363 | hypothetical protein |
| 2729 | 32129_at | ZNF364 | AL079314 | zinc finger protein 364 | hypothetical protein, similar to (U06944) |
| 2730 | 41033_at | ZNF84 | M27878 | zinc finger protein 84 (HPF2) | PRAJA1 [Mus musculus] |
| 2731 | 40610_at | ZFR | AI743507 | zinc finger RNA binding protein | DNA binding protein |
| 2732 | 39751_at | ZDHHC3 | AF052182 | zinc finger, DHHC domain containing 3 | |
| 2733 | 33912_at | ZMPSTE24 | Y13834 | zinc metalloproteinase (STE24 homolog, yeast) | farnesylated-proteins converting enzyme 1 |
| 2734 | 36521_at | DZIP1 | AB023213 | zinc-finger protein DZIP1 | KIAA0996 protein |
| 2735 | 35995_at | ZWINT | AF067656 | ZW10 interactor | ZW10 interactor Zwint |
| 2736 | 706_at | | HG4582-HT4987 | | |
| 2737 | 960_g_at | | HG2463-HT2559 | | |
| 2738 | 956_at | | HG1980-HT2023 | | |
| 2739 | 955_at | | HG1862-HT1897 | | |
| 2740 | 324_f_at | | HG1515-HT1515 | | |

F5.21

| | A | B | C | D | E |
|------|------------|-----------|---------------|---|--|
| 2741 | 327_f_at | | HG1800-HT1823 | | |
| 2742 | 333_s_at | | HG2639-HT2735 | | |
| 2743 | 1840_g_at | | HG1112-HT1112 | | |
| 2744 | 1664_at | | HG3543-HT3739 | | |
| 2745 | 1624_at | | HG2036-HT2090 | | |
| 2746 | 1278_at | | HG162-HT3165 | | |
| 2747 | 1179_at | | HG2855-HT2995 | | |
| 2748 | 1180_g_at | | HG2855-HT2995 | | |
| 2749 | 32243_g_at | | AL038340 | | |
| 2750 | 311_s_at | | HG3044-HT3742 | | |
| 2751 | 297_g_at | | HG4322-HT4592 | | |
| 2752 | 296_at | | HG4322-HT4592 | | |
| 2753 | 1839_at | | HG1112-HT1112 | | |
| 2754 | 723_s_at | | HG1322-HT5143 | | |
| 2755 | 33300_at | dJ283E3.1 | AL031282 | | guanine nucleotide binding protein (G protein), beta polypeptide 1 |
| 2756 | 41249_at | dJ283E3.1 | AL031282 | | guanine nucleotide binding protein (G protein), beta polypeptide 1 |

Fig. 21